



## SEQUENCE LISTING

<110> Pompejus, Markus  
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Haberhauer, Gregor

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
INVOLVED IN CARBON METABOLISM AND ENERGY  
PRODUCTION

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<140> US 09/602,740

<141> 2000-06-23

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	Met Val Asp Val Val	
	1 5	
cgc gca cgc gat act gaa gat ttg gtt gca cag gct gcc tcc aaa ttc	163	
Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln Ala Ala Ser Lys Phe		
10 15 20		
att gag gtt gtt gaa gca gca act gcc aat aat ggc acc gca cag gta	211	
Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn Gly Thr Ala Gln Val		
25 30 35		
gtg ctc acc ggt ggt ggc gcc ggc atc aag ttg ctg gaa aag ctc agc	259	
Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu Leu Glu Lys Leu Ser		
40 45 50		
gtt gat gcg gct gac ctt gcc tgg gat cgc att cat gtg ttc ttc ggc	307	
Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile His Val Phe Phe Gly		
55 60 65		
gat gag cgc aat gtc cct gtc agt gat tct gag tcc aat gag ggc cag	355	
Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu Ser Asn Glu Gly Gln		
70 75 80 85		
gct cgt gag gca ctg ttg tcc aag gtt tct atc cct gaa gcc aac att	403	
Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile Pro Glu Ala Asn Ile		
90 95 100		
cac gga tat ggt ctc ggc gac gta gat ctt gca gag gca gcc cgc gct	451	
His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala		
105 110 115		
tac gaa gct gtg ttg gat gaa ttc gca cca aac ggc ttt gat ctt cac	499	
Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His		
120 125 130		
ctg ctc ggc atg ggt ggc gaa ggc cat atc aac tcc ctg ttc cct cac	547	
Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn Ser Leu Phe Pro His		
135 140 145		
acc gat gca gtc aag gaa tcc tcc gca aag gtc atc gcg gtg ttt gat	595	
Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val Ile Ala Val Phe Asp		
150 155 160 165		
tcc cct aag cct cct tca gag cgt gca act cta acc ctt cct gcg gtt	643	
Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu Thr Leu Pro Ala Val		
170 175 180		
cac tcc gca aag cgc gtg tgg ttg ctg gtt tct ggt gcg gag aag gct	691	
His Ser Ala Lys Arg Val Trp Leu Leu Val Ser Gly Ala Glu Lys Ala		
185 190 195		
gag gca gct gcg gcg atc gtc aac ggt gag cct gct gtt gag tgg cct	739	
Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro Ala Val Glu Trp Pro		
200 205 210		
gct gct gga gct acc gga tct gag gaa acg gta ttg ttc ttg gct gat	787	
Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val Leu Phe Leu Ala Asp		
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35 40 45

Leu Glu Lys Leu Ser Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile  
50 55 60

His Val Phe Phe Gly Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu  
65 70 75 80

Ser Asn Glu Gly Gln Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile  
85 90 95

Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala  
100 105 110

Glu Ala Ala Arg Ala Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn  
115 120 125

Gly Phe Asp Leu His Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn  
130 135 140

Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val  
145 150 155 160

Ile Ala Val Phe Asp Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu  
165 170 175

Thr Leu Pro Ala Val His Ser Ala Lys Arg Val Trp Leu Leu Val Ser  
180 185 190

Gly Ala Glu Lys Ala Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro  
195 200 205

Ala Val Glu Trp Pro Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val  
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Leu Phe Leu Ala Asp Asp Ala Ala Gly Asn Leu  
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&lt;223&gt; RXA01626

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 Met Ser Lys Thr Ile  
 1 5

atc gtg cgc acc gaa att gaa atc cct gga cac cca acc gcc atc cat 163  
 Ile Val Arg Thr Glu Ile Glu Ile Pro Gly His Pro Thr Ala Ile His  
 10 15 20

atc gca gag atg cag gag ctt ccc cca tct gag gct caa ggc ggc gtg 211  
 Ile Ala Glu Met Gln Glu Leu Pro Pro Ser Glu Ala Gln Gly Gly Val  
 25 30 35

cag atg tgc aaa atg cag cgc att att gaa cta gca gga act gcc gaa 259  
 Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu Ala Gly Thr Ala Glu  
 40 45 50

ggg gat gtc gtt act ggt gca ggt gtt att ggc gga tct aat ttc cag 307  
 Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly Gly Ser Asn Phe Gln  
 55 60 65

ctg aat aac gag cca aat gaa gtg gtt ccc cat cca gat acc tat gcg 355  
 Leu Asn Asn Glu Pro Asn Glu Val Val Pro His Pro Asp Thr Tyr Ala  
 70 75 80 85

gat ttc ccc gat atc aag gcg gtt gtt atc tcc gcg gag act ttt gaa 403  
 Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser Ala Glu Thr Phe Glu  
 90 95 100

ggc ctg tgg ctg gaa gcg gga gcg aag ttc cct ggc tta aat 445  
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Pro Thr Ala Ile His Ile Ala Glu Met Gln Glu Leu Pro Pro Ser Glu  
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Ala Gln Gly Gly Val Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu  
 35 40 45

Ala Gly Thr Ala Glu Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly  
 50 55 60

Gly Ser Asn Phe Gln Leu Asn Asn Glu Pro Asn Glu Val Val Pro His  
 65 70 75 80

Pro Asp Thr Tyr Ala Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser  
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Ala Glu Thr Phe Glu Gly Leu Trp Leu Glu Ala Gly Ala Lys Phe Pro  
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 Met Ala Gln Arg Thr  
 1 5

cca cta atc gcc cca tcc att ctt gct gct gat ttc tcc cgc tta ggg 163  
 Pro Leu Ile Ala Pro Ser Ile Leu Ala Ala Asp Phe Ser Arg Leu Gly  
 10 15 20

gag cag gtg ttg gct gtt cct gat gct gac tgg att cac gtc gac atc 211  
 Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp Ile His Val Asp Ile  
 25 30 35

atg gac gga cac ttc gtt cca aac ttg agc ttt ggc gcg gat atc aca 259  
 Met Asp Gly His Phe Val Pro Asn Leu Ser Phe Gly Ala Asp Ile Thr  
 40 45 50

gct gcg gtc aac cgc gtt acg gac aaa gaa cta gac gtc cac ctg atg 307  
 Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu Asp Val His Leu Met  
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atc gaa aac cca gag aag tgg gtg gac aac tac atc gac gct ggc gcg 355  
 Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr Ile Asp Ala Gly Ala  
 70 75 80 85

gac tgc att gtt ttc cac gtt gaa gcc acc gaa ggt cac gtt gag ttg 403  
 Asp Cys Ile Val Phe His Val Glu Ala Thr Glu Gly His Val Glu Leu  
 90 95 100

gct aag tac atc cgt tcc aag ggt gtg cgt gca ggt ttc tcc ctg cgc 451  
 Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala Gly Phe Ser Leu Arg  
 105 110 115

cct gga act ccc atc gag gat tac ttg gat gac ctc gag cac ttc gat 499  
 Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp Leu Glu His Phe Asp  
 120 125 130

gaa gtc atc gtc atg agc gtc gag cct gga ttc ggt ggc caa agc ttc 547  
 Glu Val Ile Val Met Ser Val Glu Pro Gly Phe Gly Gly Gln Ser Phe  
 135 140 145

atg cct gaa caa ctg gaa aag gtt cgt acc ctg cgc aag gtc atc gat 595  
 Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu Arg Lys Val Ile Asp  
 150 155 160 165

gag cgc ggt ctg aac acc gtc atc gag atc gac ggc ggc att agc gcc 643  
 Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp Gly Gly Ile Ser Ala  
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aag acc atc aag cag gct gcc gac gct ggc gtg gat gcc ttc gtt gca 691  
 Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val Asp Ala Phe Val Ala  
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ggt tcc gct gtg tac ggc gct gag gat ccc aac aag gcg atc cag gag 739  
 Gly Ser Ala Val Tyr Gly Ala Glu Asp Pro Asn Lys Ala Ile Gln Glu  
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Ile His Val Asp Ile Met Asp Gly His Phe Val Pro Asn Leu Ser Phe  
 35 40 45

Gly Ala Asp Ile Thr Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu  
 50 55 60

Asp Val His Leu Met Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr  
 65 70 75 80

Ile Asp Ala Gly Ala Asp Cys Ile Val Phe His Val Glu Ala Thr Glu  
 85 90 95

Gly His Val Glu Leu Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala  
 100 105 110

Gly Phe Ser Leu Arg Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp  
 115 120 125

Leu Glu His Phe Asp Glu Val Ile Val Met Ser Val Glu Pro Gly Phe  
 130 135 140

Gly Gly Gln Ser Phe Met Pro Glu Gln Leu Glu Lys Val Arg Thr Leu  
 145 150 155 160

Arg Lys Val Ile Asp Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp  
 165 170 175

Gly Gly Ile Ser Ala Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val  
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 Met Arg Val Tyr Leu  
 1 5

gga gca gac cac gct ggt ttc gaa act aaa aat gca atc gca gaa cac 163  
 Gly Ala Asp His Ala Gly Phe Glu Thr Lys Asn Ala Ile Ala Glu His  
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 Leu Lys Ala His Gly His Glu Val Ile Asp Cys Gly Ala His Thr Tyr  
 25 30 35

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 Asp Ala Glu Asp Asp Tyr Pro Ala Phe Cys Ile Glu Ala Ala Ser Arg  
 40 45 50

aca gta aac gac cca ggc tca ctc ggc atc gtc ctg ggt gga tcc gga 307  
 Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val Leu Gly Gly Ser Gly  
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 Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys Gly Ala Arg Cys Ala  
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 Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala Arg Glu His Asn Asn  
 90 95 100

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 35 40 45  
 Glu Ala Ala Ser Arg Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val  
 50 55 60  
 Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys  
 65 70 75 80  
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 Met Ser Thr His Ser  
 1 5  
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 Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val Ser Val Leu Pro Glu  
 10 15 20  
 gtc tca gct ggt acg gtc ctt gac gct gca gag cca gca ggc gtt ccc 211  
 Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu Pro Ala Gly Val Pro  
 25 30 35  
 acc aaa gat atg tgg gaa tac caa aaa gac cac atg aac ctg gtc tcc 259  
 Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His Met Asn Leu Val Ser  
 40 45 50  
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 Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val Val Gly Thr Gly Leu

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aag gcg ttc acc tac cac gac gca cct cgc cgt gcg cac tcc att gct Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg Ala His Ser Ile Ala 90 95 100			403
gca cag ggt ggc gtt aac tcc gcc cgc ggc aag aag gta gac aac gac Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys Lys Val Asp Asn Asp 105 110 115			451
ggc gca tac cgc cac gtc aag gac acc gtc aag ggc ggc gac tac cgt Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys Gly Gly Asp Tyr Arg 120 125 130			499
ggt cgc gag tcc gac tgc tgg cgt ctc gcc gtc gag tcc gtc cgc gtc Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val Glu Ser Val Arg Val 135 140 145			547
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ggc gcc ttg gca acc cgt tcc ttc ggt ggt gtg cag gtc tcc cgt acc Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val Gln Val Ser Arg Thr 170 175 180			643
tac tac acc cgt gga caa acc gga cag cag ctg cag ttc tcc acc gca Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu Gln Phe Ser Thr Ala 185 190 195			691
tcc gca cta cag cgc cag atc cac ctc ggc tcc gta gaa atc ttc acc Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser Val Glu Ile Phe Thr 200 205 210			739
cat aac gaa atg gtt gac gtc att gtc acc gaa cgt aac ggt gaa aag His Asn Glu Met Val Asp Val Ile Val Thr Glu Arg Asn Gly Glu Lys 215 220 225			787
cgc tgc gaa ggc ctg atc atg cgc aac ctg atc acc ggc gag ctc acc Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile Thr Gly Glu Leu Thr 230 235 240 245			835
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cct aag gaa ccg aac gat aac cgc gat cca aac acc atc cct gag gat Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp 330 335 340	1123
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agc cca atg cgt att gca ccg acc tgc cac ttc acc atg ggt ggc ctc Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu 425 430 435	1411
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gat gca cca gaa gca cag gca gcg att gcg cgt gca cag gct cgc att Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile 505 510 515	1651
gac cgc ctc atg ggc aac cgc cca gag tgg gtc ggt gac aac gtt cac Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val Gly Asp Asn Val His 520 525 530	1699
gga cct gag tac tac cac cgc cag ctt ggc gat atc ctg tac ttc tcc Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser 535 540 545	1747

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 Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys  
 550 555 560 565

atc cgt gcc ctc cgc gat gac ttc tgg aag aac atg cgc atc acc ggc 1843  
 Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly  
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agc acc gat gag atg aac cag gtt ctc gaa tac gca gca cgc gta gcc 1891  
 Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala  
 585 590 595

gac tac atc gac ctc ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc 1939  
 Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg  
 600 605 610

gac gag tcc tgt ggc gct cac ttc cgc gac gac cac ctc tcc gaa gat 1987  
 Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp His Leu Ser Glu Asp  
 615 620 625

ggc gaa gca caa cgt gac gac caa aac tgg tgc ttc gtc tcc gca tgg 2035  
 Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp  
 630 635 640 645

gaa cca ggc gag aat gga acc ttc gtc tgc cac gca gaa cca ctg ttc 2083  
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 650 655 660

ttc gaa tct gtc cca ctg cag aca agg aac tac aag taatgaaact 2129  
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<213> Corynebacterium glutamicum

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Pro Ala Gly Val Pro Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His  
 35 40 45

Met Asn Leu Val Ser Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val  
 50 55 60

Val Gly Thr Gly Leu Ser Gly Gly Ala Ala Ala Ala Ala Leu Gly Glu  
 65 70 75 80

Leu Gly Tyr Asp Val Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg  
 85 90 95

Ala His Ser Ile Ala Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys  
 100 105 110

Lys Val Asp Asn Asp Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys  
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 Gly Gly Asp Tyr Arg Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val  
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 Glu Ser Val Arg Val Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe  
 145 150 155 160  
 Ala Arg Glu Tyr Gly Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val  
 165 170 175  
 Gln Val Ser Arg Thr Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu  
 180 185 190  
 Gln Phe Ser Thr Ala Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser  
 195 200 205  
 Val Glu Ile Phe Thr His Asn Glu Met Val Asp Val Ile Val Thr Glu  
 210 215 220  
 Arg Asn Gly Glu Lys Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile  
 225 230 235 240  
 Thr Gly Glu Leu Thr Ala His Thr Gly His Ala Val Ile Leu Ala Thr  
 245 250 255  
 Gly Gly Tyr Gly Asn Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser  
 260 265 270  
 Asn Ala Ser Ala Ile Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala  
 275 280 285  
 Ser Pro Ser Phe Ile Gln Phe His Pro Thr Gly Leu Pro Val Asn Ser  
 290 295 300  
 Thr Trp Gln Ser Lys Thr Ile Leu Met Ser Glu Ser Leu Arg Asn Asp  
 305 310 315 320  
 Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn Asp Asn Arg Asp Pro Asn  
 325 330 335  
 Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe Leu Glu Arg Arg Tyr Pro  
 340 345 350  
 Ala Phe Gly Asn Leu Val Pro Arg Asp Val Ala Ser Arg Ala Ile Ser  
 355 360 365  
 Gln Gln Ile Asn Ala Gly Leu Gly Val Gly Pro Leu Asn Asn Ala Ala  
 370 375 380  
 Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg Leu Gly Gln Asp Thr Ile  
 385 390 395 400  
 Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met Tyr Glu Glu Ala Ile Gly  
 405 410 415  
 Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile Ala Pro Thr Cys His Phe  
 420 425 430

Thr Met Gly Gly Leu Trp Thr Asp Phe Asn Glu Met Thr Ser Leu Pro  
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 Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp Thr Tyr His Gly Ala Asn  
           450                                  455                                  460  
 Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala Ser Val Asp Gly Trp Phe  
 465                                  470                                  475                                  480  
 Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser  
                                   485                                  490                                  495  
 Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala Gln Ala Ala Ile Ala Arg  
                                   500                                  505                                  510  
 Ala Gln Ala Arg Ile Asp Arg Leu Met Gly Asn Arg Pro Glu Trp Val  
                                   515                                  520                                  525  
 Gly Asp Asn Val His Gly Pro Glu Tyr Tyr His Arg Gln Leu Gly Asp  
           530                                  535                                  540  
 Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg Asn Val Glu Asp Leu Gln  
 545                                  550                                  555                                  560  
 Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg Asp Asp Phe Trp Lys Asn  
                                   565                                  570                                  575  
 Met Arg Ile Thr Gly Ser Thr Asp Glu Met Asn Gln Val Leu Glu Tyr  
                                   580                                  585                                  590  
 Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu Gly Glu Leu Met Cys Val  
                                   595                                  600                                  605  
 Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp  
           610                                  615                                  620  
 His Leu Ser Glu Asp Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys  
 625                                  630                                  635                                  640  
 Phe Val Ser Ala Trp Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His  
                                   645                                  650                                  655  
 Ala Glu Pro Leu Phe Phe Glu Ser Val Pro Leu Gln Thr Arg Asn Tyr  
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Lys

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 <213> Corynebacterium glutamicum

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gat	aac	cgc	gat	cca	aac	acc	atc	cct	gag	gat	gag	cgc	gac	tac	ttc		96
Asp	Asn	Arg	Asp	Pro	Asn	Thr	Ile	Pro	Glu	Asp	Glu	Arg	Asp	Tyr	Phe		
			20					25					30				
ctg	gag	cgc	cgc	tac	cca	gca	ttc	ggc	aac	ctc	gtc	cca	cgt	gac	gtt		144
Leu	Glu	Arg	Arg	Tyr	Pro	Ala	Phe	Gly	Asn	Leu	Val	Pro	Arg	Asp	Val		
		35					40					45					
gct	tcc	cgt	gcg	atc	tcc	cag	cag	atc	aat	gct	ggc	ctc	ggc	gtt	gga		192
Ala	Ser	Arg	Ala	Ile	Ser	Gln	Gln	Ile	Asn	Ala	Gly	Leu	Gly	Val	Gly		
	50					55					60						
cct	ctg	aac	aac	gct	gca	tac	ctg	gac	ttc	cgc	gac	gcc	acc	gag	cgc		240
Pro	Leu	Asn	Asn	Ala	Ala	Tyr	Leu	Asp	Phe	Arg	Asp	Ala	Thr	Glu	Arg		
	65				70					75					80		
ctc	gga	cag	gac	acc	atc	cgc	gag	cgt	tac	tcc	aac	ctc	ttc	acc	atg		288
Leu	Gly	Gln	Asp	Thr	Ile	Arg	Glu	Arg	Tyr	Ser	Asn	Leu	Phe	Thr	Met		
				85					90					95			
tac	gaa	gag	gca	att	ggc	gag	gac	cca	tac	tcc	agc	cca	atg	cgt	att		336
Tyr	Glu	Glu	Ala	Ile	Gly	Glu	Asp	Pro	Tyr	Ser	Ser	Pro	Met	Arg	Ile		
			100					105					110				
gca	ccg	acc	tgc	cac	ttc	acc	atg	ggc	ggc	ctc	tgg	act	gac	ttc	aac		384
Ala	Pro	Thr	Cys	His	Phe	Thr	Met	Gly	Gly	Leu	Trp	Thr	Asp	Phe	Asn		
		115					120					125					
gaa	atg	acg	tca	ctc	cca	ggc	ctg	ttc	tgc	gca	ggc	gaa	gca	tcc	tgg		432
Glu	Met	Thr	Ser	Leu	Pro	Gly	Leu	Phe	Cys	Ala	Gly	Glu	Ala	Ser	Trp		
	130					135					140						
acc	tac	cac	ggc	gca	aac	cgt	ctg	ggc	gca	aac	tcc	ctg	ctc	tcc	gct		480
Thr	Tyr	His	Gly	Ala	Asn	Arg	Leu	Gly	Ala	Asn	Ser	Leu	Leu	Ser	Ala		
	145				150					155					160		
tcc	gtc	gat	ggc	tgg	ttc	acc	ctg	cca	ttc	acc	atc	cct	aac	tac	ctc		528
Ser	Val	Asp	Gly	Trp	Phe	Thr	Leu	Pro	Phe	Thr	Ile	Pro	Asn	Tyr	Leu		
				165					170					175			
ggc	cca	ttg	ctt	ggc	tcc	gag	cgt	ctg	tca	gag	gat	gca	cca	gaa	gca		576
Gly	Pro	Leu	Leu	Gly	Ser	Glu	Arg	Leu	Ser	Glu	Asp	Ala	Pro	Glu	Ala		
			180					185					190				
cag	gca	gcg	att	gcg	cgt	gca	cag	gct	cgc	att	gac	cgc	ctc	atg	ggc		624
Gln	Ala	Ala	Ile	Ala	Arg	Ala	Gln	Ala	Arg	Ile	Asp	Arg	Leu	Met	Gly		
		195					200					205					
aac	cgc	cca	gag	tgg	gtc	ggc	gac	aac	gtt	cac	gga	cct	gag	tac	tac		672
Asn	Arg	Pro	Glu	Trp	Val	Gly	Asp	Asn	Val	His	Gly	Pro	Glu	Tyr	Tyr		
	210					215					220						
cac	cgc	cag	ctt	ggc	gat	atc	ctg	tac	ttc	tcc	tgt	ggc	gtt	tcc	cga		720
His	Arg	Gln	Leu	Gly	Asp	Ile	Leu	Tyr	Phe	Ser	Cys	Gly	Val	Ser	Arg		
	225				230					235					240		
aac	gta	gaa	gac	ctc	cag	gat	ggc	atc	aac	aag	atc	cgt	gcc	ctc	cgc		768
Asn	Val	Glu	Asp	Leu	Gln	Asp	Gly	Ile	Asn	Lys	Ile	Arg	Ala	Leu	Arg		

	245	250	255	
gat gac ttc tgg aag aac atg cgc atc acc ggc agc acc gat gag atg				816
Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met				
	260	265	270	
aac cag gtt ctc gaa tac gca gca cgc gta gcc gac tac atc gac ctc				864
Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu				
	275	280	285	
ggc gaa ctc atg tgt gtc gac gcc ctc gac cgc gac gag tcc tgt ggc				912
Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly				
	290	295	300	
gct cac ttc cgc gac gac cac ctc tcc gaa gat ggc gaa gca caa cgt				960
Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg				
	305	310	315	320
gac gac caa aac tgg tgc ttc gtc tcc gca tgg gaa cca ggc gag aat				1008
Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn				
	325	330	335	
gga acc ttc gtc tgc cac gca gaa cca ctg ttc ttc gaa tct gtc cca				1056
Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro				
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ctg cag aca agg aac tac aag taatgaaact tacacttgag atc				1100
Leu Gln Thr Arg Asn Tyr Lys				
	355			

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&lt;211&gt; 359

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 12

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Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe				
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Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val				
35	40	45		
Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly				
50	55	60		
Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg				
65	70	75	80	
Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met				
85	90	95		
Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile				
100	105	110		
Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn				
115	120	125		

Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp  
 130 135 140  
 Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala  
 145 150 155 160  
 Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu  
 165 170 175  
 Gly Pro Leu Leu Gly Ser Glu Arg Leu Ser Glu Asp Ala Pro Glu Ala  
 180 185 190  
 Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly  
 195 200 205  
 Asn Arg Pro Glu Trp Val Gly Asp Asn Val His Gly Pro Glu Tyr Tyr  
 210 215 220  
 His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg  
 225 230 235 240  
 Asn Val Glu Asp Leu Gln Asp Gly Ile Asn Lys Ile Arg Ala Leu Arg  
 245 250 255  
 Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met  
 260 265 270  
 Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu  
 275 280 285  
 Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly  
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 Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg  
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 Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn  
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 Leu Gln Thr Arg Asn Tyr Lys  
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 Met Thr Ile Asn Val

																1	5
ttc	gaa	cta	ctt	gtc	aaa	agt	ccc	acg	ggt	cta	ctg	att	ggt	gat	tcc	163	
Phe	Glu	Leu	Leu	Val	Lys	Ser	Pro	Thr	Gly	Leu	Leu	Ile	Gly	Asp	Ser		
10				15				20									
tgg	gtg	gaa	gca	tcc	gac	ggc	ggt	act	ttc	gat	gtg	gaa	aac	cca	gcg	211	
Trp	Val	Glu	Ala	Ser	Asp	Gly	Gly	Thr	Phe	Asp	Val	Glu	Asn	Pro	Ala		
25				30				35									
acg	ggt	gaa	aca	atc	gca	acg	ctc	gcg	tct	gct	act	tcc	gag	gat	gca	259	
Thr	Gly	Glu	Thr	Ile	Ala	Thr	Leu	Ala	Ser	Ala	Thr	Ser	Glu	Asp	Ala		
40				45				50									
ctg	gct	gct	ctt	gat	gct	gca	tgc	gct	gtt	cag	gcc	gag	tgg	gct	agg	307	
Leu	Ala	Ala	Leu	Asp	Ala	Ala	Cys	Ala	Val	Gln	Ala	Glu	Trp	Ala	Arg		
55				60				65									
atg	cca	gcg	cgc	gag	cgt	tct	aat	att	tta	cgc	cgc	ggt	ttt	gag	ctc	355	
Met	Pro	Ala	Arg	Glu	Arg	Ser	Asn	Ile	Leu	Arg	Arg	Gly	Phe	Glu	Leu		
70				75				80				85					
gta	gca	gaa	cgt	gca	gaa	gag	ttc	gcc	acc	ctc	atg	acc	ttg	gaa	atg	403	
Val	Ala	Glu	Arg	Ala	Glu	Glu	Phe	Ala	Thr	Leu	Met	Thr	Leu	Glu	Met		
90				95				100									
ggc	aag	cct	ttg	gct	gaa	gct	cgc	ggc	gaa	gtc	acc	tac	ggc	aac	gaa	451	
Gly	Lys	Pro	Leu	Ala	Glu	Ala	Arg	Gly	Glu	Val	Thr	Tyr	Gly	Asn	Glu		
105				110				115									
ttc	ctg	cgc	tgg	ttc	tct	gag	gaa	gca	gtt	cgt	ctg	tat	ggc	cgt	tac	499	
Phe	Leu	Arg	Trp	Phe	Ser	Glu	Glu	Ala	Val	Arg	Leu	Tyr	Gly	Arg	Tyr		
120				125				130									
gga	acc	aca	cca	gaa	ggc	aac	ttg	cgg	atg	ctg	acc	gcc	ctc	aag	cca	547	
Gly	Thr	Thr	Pro	Glu	Gly	Asn	Leu	Arg	Met	Leu	Thr	Ala	Leu	Lys	Pro		
135				140				145									
gtt	ggc	ccg	tgc	ctc	ctg	atc	acc	cca	tgg	aac	ttc	cca	cta	gca	atg	595	
Val	Gly	Pro	Cys	Leu	Leu	Ile	Thr	Pro	Trp	Asn	Phe	Pro	Leu	Ala	Met		
150				155				160				165					
gct	acc	cgc	aag	gtc	gca	cct	gcg	atc	gct	gca	ggt	tgt	gtc	atg	gtg	643	
Ala	Thr	Arg	Lys	Val	Ala	Pro	Ala	Ile	Ala	Ala	Gly	Cys	Val	Met	Val		
170				175				180									
ctc	aag	cca	gct	cga	ctt	acc	ccg	ctg	acc	tcc	cag	tat	ttt	gct	cag	691	
Leu	Lys	Pro	Ala	Arg	Leu	Thr	Pro	Leu	Thr	Ser	Gln	Tyr	Phe	Ala	Gln		
185				190				195									
acc	atg	ctt	gat	gcc	ggt	ctt	cca	gca	ggt	gtc	ctc	aat	gtg	gtc	tcc	739	
Thr	Met	Leu	Asp	Ala	Gly	Leu	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	Ser		
200				205				210									
ggt	gct	tcc	gcc	tct	gcg	att	tcc	aac	ccg	att	atg	gaa	gac	gat	cgc	787	
Gly	Ala	Ser	Ala	Ser	Ala	Ile	Ser	Asn	Pro	Ile	Met	Glu	Asp	Asp	Arg		
215				220				225									
ctt	cgt	aaa	gtc	tcc	ttc	acc	ggc	tcc	acc	cca	gtt	ggc	cag	cag	ctg	835	
Leu	Arg	Lys	Val	Ser	Phe	Thr	Gly	Ser	Thr	Pro	Val	Gly	Gln	Gln	Leu		
230				235				240				245					



ctc	aaa	aag	gct	gcc	gat	aaa	gtt	ctg	cgc	acc	tcc	atg	gaa	ctt	ggt	883
Leu	Lys	Lys	Ala	Ala	Asp	Lys	Val	Leu	Arg	Thr	Ser	Met	Glu	Leu	Gly	
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ggc	aac	gca	cct	ttc	att	gtc	ttc	gag	gac	gcc	gac	cta	gat	ctc	gcg	931
Gly	Asn	Ala	Pro	Phe	Ile	Val	Phe	Glu	Asp	Ala	Asp	Leu	Asp	Leu	Ala	
			265					270					275			
atc	gaa	ggt	gcc	atg	ggt	gcc	aaa	atg	cgc	aac	atc	ggc	gaa	gct	tgc	979
Ile	Glu	Gly	Ala	Met	Gly	Ala	Lys	Met	Arg	Asn	Ile	Gly	Glu	Ala	Cys	
		280					285					290				
acc	gca	gcc	aac	cgt	ttc	tta	gtc	cac	gaa	tcc	gtc	gcc	gat	gaa	ttc	1027
Thr	Ala	Ala	Asn	Arg	Phe	Leu	Val	His	Glu	Ser	Val	Ala	Asp	Glu	Phe	
	295					300					305					
ggc	cgt	cgc	ttc	gct	gcc	cgc	ctt	gaa	gag	caa	gtc	cta	ggc	aac	ggc	1075
Gly	Arg	Arg	Phe	Ala	Ala	Arg	Leu	Glu	Glu	Gln	Val	Leu	Gly	Asn	Gly	
310					315					320					325	
ctc	gac	gaa	ggc	gtc	acc	gtg	ggc	ccc	ctg	gtt	gag	gaa	aaa	gca	cga	1123
Leu	Asp	Glu	Gly	Val	Thr	Val	Gly	Pro	Leu	Val	Glu	Glu	Lys	Ala	Arg	
			330					335						340		
gac	agc	gtt	gca	tcg	ctt	gtc	gac	gcc	gcc	gtc	gcc	gaa	ggt	gcc	acc	1171
Asp	Ser	Val	Ala	Ser	Leu	Val	Asp	Ala	Ala	Val	Ala	Glu	Gly	Ala	Thr	
			345					350					355			
gtc	ctc	acc	ggc	ggc	aag	gcc	ggc	aca	ggt	gca	ggc	tac	ttc	tac	gaa	1219
Val	Leu	Thr	Gly	Gly	Lys	Ala	Gly	Thr	Gly	Ala	Gly	Tyr	Phe	Tyr	Glu	
		360					365					370				
cca	acg	gtg	ctc	acg	gga	gtt	tca	aca	gat	gcg	gct	atc	ctg	aac	gaa	1267
Pro	Thr	Val	Leu	Thr	Gly	Val	Ser	Thr	Asp	Ala	Ala	Ile	Leu	Asn	Glu	
	375					380					385					
gag	atc	ttc	ggt	ccc	gtc	gca	ccg	atc	gtc	acc	ttc	caa	acc	gag	gaa	1315
Glu	Ile	Phe	Gly	Pro	Val	Ala	Pro	Ile	Val	Thr	Phe	Gln	Thr	Glu	Glu	
390					395				400					405		
gaa	gcc	ctg	cgt	cta	gcc	aac	tcc	acc	gaa	tac	gga	ctg	gcc	tcc	tat	1363
Glu	Ala	Leu	Arg	Leu	Ala	Asn	Ser	Thr	Glu	Tyr	Gly	Leu	Ala	Ser	Tyr	
			410					415					420			
gtg	ttc	acc	cag	gac	acc	tca	cgt	att	ttc	cgc	gtc	tcc	gat	ggt	ctc	1411
Val	Phe	Thr	Gln	Asp	Thr	Ser	Arg	Ile	Phe	Arg	Val	Ser	Asp	Gly	Leu	
			425				430						435			
gag	ttc	ggc	cta	gtg	ggc	gtc	aat	tcc	ggt	gtc	atc	tct	aac	gct	gct	1459
Glu	Phe	Gly	Leu	Val	Gly	Val	Asn	Ser	Gly	Val	Ile	Ser	Asn	Ala	Ala	
		440					445					450				
gca	cct	ttt	ggt	ggc	gta	aaa	caa	tcc	gga	atg	ggc	cgc	gaa	ggt	ggt	1507
Ala	Pro	Phe	Gly	Gly	Val	Lys	Gln	Ser	Gly	Met	Gly	Arg	Glu	Gly	Gly	
	455					460					465					
ctc	gaa	gga	atc	gag	gag	tac	acc	tcc	gtg	cag	tac	atc	ggt	atc	cgg	1555
Leu	Glu	Gly	Ile	Glu	Glu	Tyr	Thr	Ser	Val	Gln	Tyr	Ile	Gly	Ile	Arg	
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 Asp Pro Tyr Ala Gly  
 490

1593

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 <213> Corynebacterium glutamicum

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 Val Glu Asn Pro Ala Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala  
 35 40 45  
 Thr Ser Glu Asp Ala Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln  
 50 55 60  
 Ala Glu Trp Ala Arg Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg  
 65 70 75 80  
 Arg Gly Phe Glu Leu Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu  
 85 90 95  
 Met Thr Leu Glu Met Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val  
 100 105 110  
 Thr Tyr Gly Asn Glu Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg  
 115 120 125  
 Leu Tyr Gly Arg Tyr Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu  
 130 135 140  
 Thr Ala Leu Lys Pro Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn  
 145 150 155 160  
 Phe Pro Leu Ala Met Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala  
 165 170 175  
 Gly Cys Val Met Val Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser  
 180 185 190  
 Gln Tyr Phe Ala Gln Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val  
 195 200 205  
 Leu Asn Val Val Ser Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile  
 210 215 220  
 Met Glu Asp Asp Arg Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro  
 225 230 235 240  
 Val Gly Gln Gln Leu Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr  
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 Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala  
 260 265 270

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tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt 115  
Met Lys Leu Thr Leu  
1 5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc	163
Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr	
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Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu	
25 30 35	
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Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala	
40 45 50	
ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc	307
Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu	
55 60 65	
gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg	355
Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala	
70 75 80 85	
cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca	403
Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro	
90 95 100	
ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc	451
Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg	
105 110 115	
tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac	499
Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn	
120 125 130	
gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc	547
Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr	
135 140 145	
gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt	595
Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys	
150 155 160 165	
gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag	643
Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys	
170 175 180	
ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg	691
Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu	
185 190 195	
cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc	739
Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys	
200 205 210	
tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg	787
Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu	
215 220 225	
acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga	835
Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg	
230 235 240 245	
ggc aaa gac gac tagtctttaa tccaagtaag tac	870

Gly Lys Asp Asp

<210> 16

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

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Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser  
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Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly  
35 40 45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly  
50 55 60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn  
65 70 75 80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr  
85 90 95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp  
100 105 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly  
115 120 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His  
130 135 140

Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile  
145 150 155 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu  
165 170 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys  
180 185 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr  
195 200 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro  
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Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala  
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Arg Ala Ala Phe Arg Gly Lys Asp Asp  
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<210> 17

<211> 1530

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1507)

&lt;223&gt; RXA01535

&lt;400&gt; 17

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                               1 5
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Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys
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Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile
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Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu
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Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala
                               55 60 65
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Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys Glu Ile Ala Ser Gly
70 75 80 85
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Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe Gln Thr Gly Ser Gly
90 95 100
act tcc tcc aac atg aac acc aat gag gtt atc gct tcc atc gcg aag 451
Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile Ala Ser Ile Ala Lys
105 110 115
gct aac ggc gtt gag gtt cac cca aat gac cac gtc aac atg ggt cag 499
Ala Asn Gly Val Glu Val His Pro Asn Asp His Val Asn Met Gly Gln
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tcc tcc aat gac acc ttc cct act gca act cac gtt gct gca acc gaa 547
Ser Ser Asn Asp Thr Phe Pro Thr Ala Thr His Val Ala Ala Thr Glu
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Ala Ala Val Asn Asp Leu Ile Pro Gly Leu Lys Val Leu His Glu Ser
150 155 160 165
ttg gcg aag aag gct aac gag tgg tct gag gtt gtt aag tcc ggc cgc 643
Leu Ala Lys Lys Ala Asn Glu Trp Ser Glu Val Val Lys Ser Gly Arg
170 175 180
acc cac ctg atg gac gct gtt cca gta acc ctg ggc cag gag ttc ggt 691
Thr His Leu Met Asp Ala Val Pro Val Thr Leu Gly Gln Glu Phe Gly

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185								190				195				
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ctt	cct	cgc	ctt	ggt	gag	ctg	gct	att	ggt	ggc	acc	gct	gct	ggt	acc	787
Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly	Thr	Ala	Ala	Gly	Thr	
215				220				225								
ggt	atc	aac	acc	tcc	gct	gat	ttc	ggc	ggc	aag	gtt	gtt	gct	gaa	ctg	835
Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys	Val	Val	Ala	Glu	Leu	
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Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu	Ala	Glu	Asn	His	Phe	
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Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu	Phe	Ser	Gly	Ala	Met	
265								270				275				
cgc	gtt	atc	gct	gtc	tcc	ttg	tac	aag	atc	gct	aac	gat	atc	cgc	ctc	979
Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	
280								285				290				
atg	ggc	tcc	ggc	cca	ctg	acc	ggt	ctt	ggc	gag	atc	cgt	ctc	cca	gac	1027
Met	Gly	Ser	Gly	Pro	Leu	Thr	Gly	Leu	Gly	Glu	Ile	Arg	Leu	Pro	Asp	
295				300				305								
ctg	cag	cca	ggt	tcc	tcc	atc	atg	cca	ggc	aag	gtc	aac	cca	gtt	ctc	1075
Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Leu	
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Cys	Glu	Thr	Ala	Thr	Gln	Val	Ser	Ala	Gln	Val	Ile	Gly	Asn	Asp	Ala	
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gct	gtt	gcg	ttc	tcc	ggc	acc	cag	ggc	cag	ttc	gag	ctc	aac	gtg	ttc	1171
Ala	Val	Ala	Phe	Ser	Gly	Thr	Gln	Gly	Gln	Phe	Glu	Leu	Asn	Val	Phe	
345								350				355				
atc	cca	gtg	atg	gct	cgc	aac	gtg	ctt	gag	tcc	gct	cgc	ctg	ctg	gct	1219
Ile	Pro	Val	Met	Ala	Arg	Asn	Val	Leu	Glu	Ser	Ala	Arg	Leu	Leu	Ala	
360				365				370								
aac	act	tcc	cgc	gtg	ttc	gca	acc	cgt	ctc	gtt	gat	ggc	att	gag	cca	1267
Asn	Thr	Ser	Arg	Val	Phe	Ala	Thr	Arg	Leu	Val	Asp	Gly	Ile	Glu	Pro	
375				380				385								
aac	gag	gca	cac	atg	aag	gag	ctc	gct	gag	tct	tca	cct	tcc	atc	gtt	1315
Asn	Glu	Ala	His	Met	Lys	Glu	Leu	Ala	Glu	Ser	Ser	Pro	Ser	Ile	Val	
390				395				400				405				
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Thr	Pro	Leu	Asn	Ser	Ala	Ile	Gly	Tyr	Glu							

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 Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu Glu Glu Leu Asp Lys  
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cgc ctc gac gtt ctt gct atg gct cac acc gag cgc gag aac aag ttc 1507  
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<210> 18

<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 18

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                           20                          25                          30

Glu Asn Phe Pro Ile Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg  
                           35                          40                          45

Ala Met Gly Leu Leu Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser  
       50                          55                          60

Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys  
       65                          70                          75                          80

Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe  
                           85                          90                          95

Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile  
                           100                          105                          110

Ala Ser Ile Ala Lys Ala Asn Gly Val Glu Val His Pro Asn Asp His  
                           115                          120                          125

Val Asn Met Gly Gln Ser Ser Asn Asp Thr Phe Pro Thr Ala Thr His  
       130                          135                          140

Val Ala Ala Thr Glu Ala Ala Val Asn Asp Leu Ile Pro Gly Leu Lys  
       145                          150                          155                          160

Val Leu His Glu Ser Leu Ala Lys Lys Ala Asn Glu Trp Ser Glu Val  
                           165                          170                          175

Val Lys Ser Gly Arg Thr His Leu Met Asp Ala Val Pro Val Thr Leu  
                           180                          185                          190

Gly Gln Glu Phe Gly Gly Tyr Ala Arg Gln Ile Gln Leu Gly Ile Glu  
                           195                          200                          205

Arg Val Glu Ala Thr Leu Pro Arg Leu Gly Glu Leu Ala Ile Gly Gly  
       210                          215                          220

Thr Ala Ala Gly Thr Gly Ile Asn Thr Ser Ala Asp Phe Gly Gly Lys



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225                230                235                240
Val Val Ala Glu Leu Ile Asn Leu Thr Asp Val Lys Glu Leu Lys Glu
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Ala Glu Asn His Phe Glu Ala Gln Ala Ala Arg Asp Ala Leu Val Glu
                260                265                270
Phe Ser Gly Ala Met Arg Val Ile Ala Val Ser Leu Tyr Lys Ile Ala
                275                280                285
Asn Asp Ile Arg Leu Met Gly Ser Gly Pro Leu Thr Gly Leu Gly Glu
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Ile Arg Leu Pro Asp Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys
305                310                315                320
Val Asn Pro Val Leu Cys Glu Thr Ala Thr Gln Val Ser Ala Gln Val
                325                330                335
Ile Gly Asn Asp Ala Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe
                340                345                350
Glu Leu Asn Val Phe Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser
                355                360                365
Ala Arg Leu Leu Ala Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val
                370                375                380
Asp Gly Ile Glu Pro Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser
385                390                395                400
Ser Pro Ser Ile Val Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala
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Ala Ala Lys Val Ala Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg
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Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu
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Glu Glu Leu Asp Lys Arg Leu Asp Val Leu Ala Met Ala His Thr Glu
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Arg Glu Asn Lys Phe
465

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&lt;210&gt; 19

&lt;211&gt; 1164

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1141)

&lt;223&gt; RXA00517

&lt;400&gt; 19

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gtc aac gcc caa caa ctc act gtt ctc tgc aca gac atc ctc acc aaa	163								
Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr Asp Ile Leu Thr Lys									
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act gga gta cct gca gca gac gcc cat ctt gtc ggt gat agt ttg gtg	211								
Thr Gly Val Pro Ala Ala Asp Ala His Leu Val Gly Asp Ser Leu Val									
	25	30	35						
cag gct gat ctt tgg ggt cac ccc tcc cac ggt gtg ctt cga ctg cct	259								
Gln Ala Asp Leu Trp Gly His Pro Ser His Gly Val Leu Arg Leu Pro									
	40	45	50						
tgg tat gtg cgc aga ctc cac agt ggc gcg atg act aca cat gca cac	307								
Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met Thr Thr His Ala His									
	55	60	65						
gtg gag gtt ctc aat gat ttg ggt gcc gtg ttg gcg ttg gat gga cac	355								
Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu Ala Leu Asp Gly His									
	70	75	80	85					
aat gga atc ggc caa gtt tta gct gat cat gct cgt aaa gaa gca gtg	403								
Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala Arg Lys Glu Ala Val									
	90	95	100						
act agg gca atg atg ttc ggc atc ggt gcg gtg tcg gtg cgc aac tcc	451								
Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val Ser Val Arg Asn Ser									
	105	110	115						
aat cat ttt gga act gcc atg tac tac acc cgg aaa gcg gca gcg caa	499								
Asn His Phe Gly Thr Ala Met Tyr Thr Arg Lys Ala Ala Ala Gln									
	120	125	130						
gga tgt gtt tcc att ctc acc acc aat gca tct ccg gcg atg gcg ccc	547								
Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser Pro Ala Met Ala Pro									
	135	140	145						
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Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn Pro Trp Ser Ile Ala									
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gca cct ttt gga gaa acg gct acg gta gtc gat ata gcc aat act gcg	643								
Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp Ile Ala Asn Thr Ala									
	170	175	180						
gtt gcg cgc gga aag atc tac cac gca cga cag aca aac atg ccc att	691								
Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln Thr Asn Met Pro Ile									
	185	190	195						
cct gag act tgg gcg atc acg agt gag ggc gca ccc acc acg gat cct	739								
Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala Pro Thr Thr Asp Pro									
	200	205	210						
gct gag gca atc aac ggt gtc gtc ctt ccc atg gct ggt cac aaa ggt	787								
Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met Ala Gly His Lys Gly									
	215	220	225						
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Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser Gly Val Leu Thr Gly  
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 Ser Gln His Ser Thr Lys Val His Gly Pro Tyr Asp Pro Thr Pro Pro  
 250 255 260  
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 Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp Val Ala Ala Phe Arg  
 265 270 275  
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 Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp Leu Val Gly Glu Val  
 280 285 290  
 aaa tcc act ccg aaa gca caa aac acc gag gag att ttc tac ccc ggt 1027  
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 295 300 305  
 gaa tcg gaa gac cgt gcg cat cgg aaa aac tct gcg cac ggt att tca 1075  
 Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser Ala His Gly Ile Ser  
 310 315 320 325  
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 His Val Val Thr His Arg  
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&lt;210&gt; 20

&lt;211&gt; 347

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 20

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 Gly Asp Ser Leu Val Gln Ala Asp Leu Trp Gly His Pro Ser His Gly  
 35 40 45  
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 Thr Thr His Ala His Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu  
 65 70 75 80  
 Ala Leu Asp Gly His Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala  
 85 90 95  
 Arg Lys Glu Ala Val Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val  
 100 105 110  
 Ser Val Arg Asn Ser Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg  
 115 120 125

Lys Ala Ala Ala Gln Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser  
 130 135 140  
 Pro Ala Met Ala Pro Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn  
 145 150 155 160  
 Pro Trp Ser Ile Ala Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp  
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 Ile Ala Asn Thr Ala Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln  
 180 185 190  
 Thr Asn Met Pro Ile Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala  
 195 200 205  
 Pro Thr Thr Asp Pro Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met  
 210 215 220  
 Ala Gly His Lys Gly Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser  
 225 230 235 240  
 Gly Val Leu Thr Gly Ser Gln His Ser Thr Lys Val His Gly Pro Tyr  
 245 250 255  
 Asp Pro Thr Pro Pro Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp  
 260 265 270  
 Val Ala Ala Phe Arg Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp  
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 Ile Phe Tyr Pro Gly Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser  
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 <223> RXA01350

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 Met Asn Ser Pro Gln  
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Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr	
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gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc	259
Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro Gln Ala Leu Gly	
40 45 50	
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Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu	
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ctg cga aac atc acc atc acc gcg gat gcc aat gag gca ttc gac ggc	355
Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu Ala Phe Asp Gly	
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gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc gga aaa ggc gaa	403
Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Lys Gly Glu	
90 95 100	
gag cgc gca gat ttg ctg gct aac aac ggc aag att ttc gga cct caa	451
Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile Phe Gly Pro Gln	
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ggt aaa gct atc aat gac aac gcc gca gat gac att cgt gtc cta gtt	499
Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val	
120 125 130	
gtt gga aac cca gcg aac acc aac gcg ttg att gct tca gct gcg gcc	547
Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Ser Ala Ala Ala	
135 140 145	
cca gat gtt cca gca tcc cgc ttc aac gca atg atg cgc ctt gat cac	595
Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met Met Arg Leu Asp His	
150 155 160 165	
aac cgt gcg atc tcc cag ctg gcc acc aag ctt ggc cgt gga tct gcg	643
Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu Gly Arg Gly Ser Ala	
170 175 180	
gaa ttt aac aac att gtg gtc tgg gga aat cac tcc gca acc cag ttc	691
Glu Phe Asn Asn Ile Val Val Trp Gly Asn His Ser Ala Thr Gln Phe	
185 190 195	
cca gac atc acc tac gca acc gtt ggt gga gaa aag gtc act gac ctg	739
Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu Lys Val Thr Asp Leu	
200 205 210	
gtt gat cac gat tgg tat gtg gag gag ttc att cct cgc gtg gct aac	787
Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile Pro Arg Val Ala Asn	
215 220 225	
cgt ggc gct gaa atc att gag gtc cgt gga aag tct tct gca gct tct	835
Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala Ser	
230 235 240 245	
gca gca tcc tct gcg att gat cac atg cgc gat tgg gta cag ggc acc	883

Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp Trp Val Gln Gly Thr  
 250 255 260

gag gcg tgg tcc tct gcg gca att cct tcc acc ggt gca tac ggc att 931  
 Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr Gly Ala Tyr Gly Ile  
 265 270 275

cct gag ggc att ttt gtc ggt ctg cca acc gta tcc cgc aac ggt gag 979  
 Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val Ser Arg Asn Gly Glu  
 280 285 290

tgg gaa atc gtt gaa ggc ctg gag att tcc gat ttc cag cgc gcc cgc 1027  
 Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp Phe Gln Arg Ala Arg  
 295 300 305

atc gac gcg aat gct cag gaa ttg cag gcc gag cgc gag gca gtg cgc 1075  
 Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu Arg Glu Ala Val Arg  
 310 315 320 325

gac ttg ctc taatctttaa cgcattgactt cgc 1107  
 Asp Leu Leu

<210> 22  
 <211> 328  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 22  
 Met Asn Ser Pro Gln Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly  
 1 5 10 15

Ala Ala Gly Gln Ile Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly  
 20 25 30

Glu Val Phe Gly Thr Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile  
 35 40 45

Pro Gln Ala Leu Gly Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp  
 50 55 60

Ser Ala Phe Pro Leu Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn  
 65 70 75 80

Glu Ala Phe Asp Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro  
 85 90 95

Arg Gly Lys Gly Glu Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys  
 100 105 110

Ile Phe Gly Pro Gln Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp  
 115 120 125

Ile Arg Val Leu Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile  
 130 135 140

Ala Ser Ala Ala Ala Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met  
 145 150 155 160

Met Arg Leu Asp His Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu

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<210> 23
<211> 1092
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1069)
<223> RXA02149
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<400> 23																
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aattcaccta	aatcctgtgt	agaacgcgag	gggcactctt	atg	cca	caa	aaa	ccg								115
				Met	Pro	Gln	Lys	Pro								
				1				5								
gcc	agt	ttc	gcg	gtg	ggc	ttt	gac	atc	ggc	ggc	acc	aac	atg	cga	gcc	163
Ala	Ser	Phe	Ala	Val	Gly	Phe	Asp	Ile	Gly	Gly	Thr	Asn	Met	Arg	Ala	
				10					15					20		
ggg	ctt	gtc	gac	gaa	tcc	ggg	cgc	atc	gtg	acc	agt	ttg	tcg	gcg	ccg	211
Gly	Leu	Val	Asp	Glu	Ser	Gly	Arg	Ile	Val	Thr	Ser	Leu	Ser	Ala	Pro	
			25					30					35			
tcg	ccg	cgc	acg	acg	cag	gca	atg	gaa	cag	ggg	att	ttt	gat	cta	gtc	259
Ser	Pro	Arg	Thr	Thr	Gln	Ala	Met	Glu	Gln	Gly	Ile	Phe	Asp	Leu	Val	
		40					45					50				

gaa cag ctc aag gcc gaa tac ccg gtt ggt gct gtg gga ctt gcc gtc Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala Val Gly Leu Ala Val 55 60 65	307
gcg gga ttt ttg gat cct gag tgc gag gtt gtt cga ttt gcc ccg cac Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val Arg Phe Ala Pro His 70 75 80 85	355
ctt cct tgg cgc gat gag cca gtg cgt gaa aag ttg gaa aac ctt ttg Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys Leu Glu Asn Leu Leu 90 95 100	403
ggc ctg cct gtt cgt ttg gaa cat gat gcc aac tca gca gcg tgg ggt Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn Ser Ala Ala Trp Gly 105 110 115	451
gag cat cgt ttt ggt gca gct caa ggc gct gac aac tgg gtt ttg ttg Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp Asn Trp Val Leu Leu 120 125 130	499
gca ctc ggc act gga att ggt gca gcg ctg att gaa aaa ggc gaa att Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile Glu Lys Gly Glu Ile 135 140 145	547
tac cgt ggt gca tat ggc acg gca cca gaa ttt ggt cat ttg cgt gtt Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe Gly His Leu Arg Val 150 155 160 165	595
gtt cgt ggc gga cgc gca tgt gcg tgt ggc aaa gaa ggc tgc ctg gag Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys Glu Gly Cys Leu Glu 170 175 180	643
cgt tac tgt tcc ggt act gcc ttg gtt tac act gcg cgt gaa ttg gct Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr Ala Arg Glu Leu Ala 185 190 195	691
tcg cat ggc tca ttc cgc aac agc ggg ctg ttt gac aag atc aaa gcc Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe Asp Lys Ile Lys Ala 200 205 210	739
gat ccg aat tcc atc aat gga aaa acg atc act gcg gca gcg cgc caa Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr Ala Ala Ala Arg Gln 215 220 225	787
gaa gac cca ctt gct ctc gcc gtt ctg gaa gat ttc agc gag tgg ctg Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp Phe Ser Glu Trp Leu 230 235 240 245	835
ggc gaa act ttg gcg atc att gct gat gtc ctt gac cca ggc atg atc Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile 250 255 260	883
atc att ggt ggc gga ctg tcc aat gct gcc gac ctt tat ttg gat cgc Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp Leu Tyr Leu Asp Arg 265 270 275	931
tcg gtc aac cac tat tcc acc cgc atc gtc ggc gca gga tat cgc cct Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly Ala Gly Tyr Arg Pro 280 285 290	979



taggtgtttt tcggtgggct gcg 1092

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<210> 24
<211> 323
<212> PRT
<213> Corynebacterium glutamicum
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<400> 24																
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Thr	Asn	Met	Arg	Ala	Gly	Leu	Val	Asp	Glu	Ser	Gly	Arg	Ile	Val	Thr	
			20					25					30			
Ser	Leu	Ser	Ala	Pro	Ser	Pro	Arg	Thr	Thr	Gln	Ala	Met	Glu	Gln	Gly	
		35					40					45				
Ile	Phe	Asp	Leu	Val	Glu	Gln	Leu	Lys	Ala	Glu	Tyr	Pro	Val	Gly	Ala	
	50					55					60					
Val	Gly	Leu	Ala	Val	Ala	Gly	Phe	Leu	Asp	Pro	Glu	Cys	Glu	Val	Val	
65					70					75					80	
Arg	Phe	Ala	Pro	His	Leu	Pro	Trp	Arg	Asp	Glu	Pro	Val	Arg	Glu	Lys	
				85					90					95		
Leu	Glu	Asn	Leu	Leu	Gly	Leu	Pro	Val	Arg	Leu	Glu	His	Asp	Ala	Asn	
			100					105					110			
Ser	Ala	Ala	Trp	Gly	Glu	His	Arg	Phe	Gly	Ala	Ala	Gln	Gly	Ala	Asp	
		115					120					125				
Asn	Trp	Val	Leu	Leu	Ala	Leu	Gly	Thr	Gly	Ile	Gly	Ala	Ala	Leu	Ile	
		130				135					140					
Glu	Lys	Gly	Glu	Ile	Tyr	Arg	Gly	Ala	Tyr	Gly	Thr	Ala	Pro	Glu	Phe	
145					150					155					160	
Gly	His	Leu	Arg	Val	Val	Arg	Gly	Gly	Arg	Ala	Cys	Ala	Cys	Gly	Lys	
				165					170					175		
Glu	Gly	Cys	Leu	Glu	Arg	Tyr	Cys	Ser	Gly	Thr	Ala	Leu	Val	Tyr	Thr	
			180					185					190			
Ala	Arg	Glu	Leu	Ala	Ser	His	Gly	Ser	Phe	Arg	Asn	Ser	Gly	Leu	Phe	
		195					200					205				
Asp	Lys	Ile	Lys	Ala	Asp	Pro	Asn	Ser	Ile	Asn	Gly	Lys	Thr	Ile	Thr	
	210					215					220					
Ala	Ala	Ala	Arg	Gln	Glu	Asp	Pro	Leu	Ala	Leu	Ala	Val	Leu	Glu	Asp	
225					230					235					240	

[illegible]

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<210> 25
<211> 1785
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1762)
<223> RXA01814
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<400> 25																	
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ggaagatgaa gagaaagtat tggtgtttta aggagcaaac																115	
Met Ala His Glu Arg																	
1 5																	
gcc	ggg	caa	ctc	gcc	caa	cca	gaa	gat	ctc	atc	gat	gtt	gcg	gaa	ctg		163
Ala	Gly	Gln	Leu	Ala	Gln	Pro	Glu	Asp	Leu	Ile	Asp	Val	Ala	Glu	Leu		
10 15 20																	
gtc	acc	gca	tat	ttc	acc	cg	aag	ccg	gac	gtg	aac	aac	cct	gat	cag		211
Val	Thr	Ala	Tyr	Phe	Thr	Arg	Lys	Pro	Asp	Val	Asn	Asn	Pro	Asp	Gln		
25 30 35																	
cag	gtc	gct	ttc	ggc	acc	tcc	gga	cac	cg	ggc	ttc	gcg	ctg	gac	agc		259
Gln	Val	Ala	Phe	Gly	Thr	Ser	Gly	His	Arg	Gly	Phe	Ala	Leu	Asp	Ser		
40 45 50																	
gct	ttc	aac	gag	gac	cac	atc	ctg	gca	acc	acc	cag	gcg	atc	gtc	gac		307
Ala	Phe	Asn	Glu	Asp	His	Ile	Leu	Ala	Thr	Thr	Gln	Ala	Ile	Val	Asp		
55 60 65																	
tac	cg	aac	cag	cag	cca	aaa	aac	tgg	gtc	ggc	ccg	ctg	ttt	atc	ggc		355
Tyr	Arg	Asn	Gln	Gln	Pro	Lys	Asn	Trp	Val	Gly	Pro	Leu	Phe	Ile	Gly		
70 75 80 85																	
cg	gat	acg	cac	gcg	ctg	tcc	gaa	cca	gcg	atg	atc	agc	gcg	ctt	gag		403
Arg	Asp	Thr	His	Ala	Leu	Ser	Glu	Pro	Ala	Met	Ile	Ser	Ala	Leu	Glu		
90 95 100																	

gtc ctc att gcc aac gac gtc gaa gtg ctt gtc gac gcc gac ggc cgc	451
Val Leu Ile Ala Asn Asp Val Glu Val Leu Val Asp Ala Asp Gly Arg	
105 110 115	
tac acc ccg acg ccc gca gtg tcc cac gcg atc cta cga cac aac gat	499
Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile Leu Arg His Asn Asp	
120 125 130	
ggc atc atc ctt ggc acc gca gga ccc tcc cgc ccc tac gcc gac ggc	547
Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg Pro Tyr Ala Asp Gly	
135 140 145	
atc gtg atc acc cca tcc cac aac cct cct cgt gat ggc gga ttc aaa	595
Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg Asp Gly Gly Phe Lys	
150 155 160 165	
tac aac cca gcc aac ggt ggc cct gca gat acc gac gcc acc gac tgg	643
Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr Asp Ala Thr Asp Trp	
170 175 180	
atc gcc aac cgc gcc aac gat att ctg cgc ggc gac ctt gca gac gtg	691
Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly Asp Leu Ala Asp Val	
185 190 195	
aag cga gtt cca gtt tcc ggt gtc ctc gac gag cgc acc act gcc tac	739
Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu Arg Thr Thr Ala Tyr	
200 205 210	
gac ttc aag ggc att tac atc gct gac ctg cca aac gtg gtc aac atc	787
Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro Asn Val Val Asn Ile	
215 220 225	
gat gcc atc cgc gaa gct ggt gtt cga atc ggc gca gac cca atg ggt	835
Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly Ala Asp Pro Met Gly	
230 235 240 245	
ggc gca tcc gtg gat tac tgg ggt gcc atc gca gaa acc cat ggc ctc	883
Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala Glu Thr His Gly Leu	
250 255 260	
aac ctc acc gtg gtc aac cca cac gtt gat tcc acc ttc cgc ttc atg	931
Asn Leu Thr Val Val Asn Pro His Val Asp Ser Thr Phe Arg Phe Met	
265 270 275	
aca ttg gac acc gac ggc aag atc cgc atg gac tgc tcc agc cca cac	979
Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp Cys Ser Ser Pro His	
280 285 290	
gca atg gca tcg ctg att gac aac cga gac aag ttc gat gtg gca acc	1027
Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys Phe Asp Val Ala Thr	
295 300 305	
ggc aac gac gcc gac gcc gac cgc cac ggc atc gtc acc cca gac gct	1075
Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile Val Thr Pro Asp Ala	
310 315 320 325	
ggc ttg atg aac ccc aac cac tac ctc gca gta gca att gag tac ctc	1123
Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val Ala Ile Glu Tyr Leu	
330 335 340	
ttt gct cac cgc cca ggt tgg tcc gca gat acc gca gtg ggc aaa acc	1171

Phe	Ala	His	Arg	Pro	Gly	Trp	Ser	Ala	Asp	Thr	Ala	Val	Gly	Lys	Thr		
			345					350					355				
ctg	gtc	agc	tcc	tcc	atg	atc	gac	cgc	gtt	gtg	gcg	cag	ctt	ggc	cgc	1219	
Leu	Val	Ser	Ser	Ser	Met	Ile	Asp	Arg	Val	Val	Ala	Gln	Leu	Gly	Arg		
		360					365					370					
acc	ctc	gtt	gag	gtt	cca	gtc	gga	ttc	aag	tgg	ttt	gtc	cca	ggg	ttg	1267	
Thr	Leu	Val	Glu	Val	Pro	Val	Gly	Phe	Lys	Trp	Phe	Val	Pro	Gly	Leu		
		375				380					385						
atc	tcc	ggc	gaa	atc	gga	ttc	ggg	ggg	gaa	gaa	tcc	gca	ggg	gca	tcc	1315	
Ile	Ser	Gly	Glu	Ile	Gly	Phe	Gly	Gly	Glu	Glu	Ser	Ala	Gly	Ala	Ser		
390					395				400						405		
ttc	ctc	cgc	atg	gac	ggc	acc	acc	tgg	tcc	acc	gac	aag	gac	ggc	ctc	1363	
Phe	Leu	Arg	Met	Asp	Gly	Thr	Thr	Trp	Ser	Thr	Asp	Lys	Asp	Gly	Leu		
			410					415						420			
atc	ctt	gac	ctc	ctg	gca	gct	gag	atc	att	gca	gta	acc	ggc	aag	acc	1411	
Ile	Leu	Asp	Leu	Leu	Ala	Ala	Glu	Ile	Ile	Ala	Val	Thr	Gly	Lys	Thr		
			425				430						435				
cca	tca	cag	cgc	tac	gca	gaa	ctc	gcc	gaa	gaa	ttc	ggg	gca	cct	gcc	1459	
Pro	Ser	Gln	Arg	Tyr	Ala	Glu	Leu	Ala	Glu	Glu	Phe	Gly	Ala	Pro	Ala		
		440					445					450					
tac	gcc	cgc	acc	gat	gca	gaa	gcc	aac	cga	gaa	caa	aag	gcc	atc	ctg	1507	
Tyr	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Asn	Arg	Glu	Gln	Lys	Ala	Ile	Leu		
		455				460					465						
aag	gca	ctg	tcc	cca	gaa	cag	gtc	acc	gcc	acc	gaa	cta	gcc	ggc	gaa	1555	
Lys	Ala	Leu	Ser	Pro	Glu	Gln	Val	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Glu		
470					475				480					485			
gca	atc	acc	gct	aag	ctc	acc	gaa	gct	ccc	ggc	aat	ggc	gca	gcc	atc	1603	
Ala	Ile	Thr	Ala	Lys	Leu	Thr	Glu	Ala	Pro	Gly	Asn	Gly	Ala	Ala	Ile		
			490					495					500				
gga	gga	cta	aaa	gtg	acc	acc	gaa	aac	gcc	tgg	ttc	gca	gca	cgc	cca	1651	
Gly	Gly	Leu	Lys	Val	Thr	Thr	Glu	Asn	Ala	Trp	Phe	Ala	Ala	Arg	Pro		
		505						510				515					
tcc	ggc	acc	gaa	gac	aag	tac	aag	atc	tac	gca	gaa	tcc	ttc	aag	ggc	1699	
Ser	Gly	Thr	Glu	Asp	Lys	Tyr	Lys	Ile	Tyr	Ala	Glu	Ser	Phe	Lys	Gly		
		520					525					530					
gaa	gag	cac	ctc	gcc	cag	gtt	cag	aag	gaa	gcc	caa	gcg	ttg	gtc	agc	1747	
Glu	Glu	His	Leu	Ala	Gln	Val	Gln	Lys	Glu	Ala	Gln	Ala	Leu	Val	Ser		
		535				540					545						
gaa	gta	ctc	gga	cag	taaaactgcg	gacttgctga	caa									1785	
Glu	Val	Leu	Gly	Gln													
550																	

&lt;210&gt; 26

&lt;211&gt; 554

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 26

Met	Ala	His	Glu	Arg	Ala	Gly	Gln	Leu	Ala	Gln	Pro	Glu	Asp	Leu	Ile	1	5	10	15
Asp	Val	Ala	Glu	Leu	Val	Thr	Ala	Tyr	Phe	Thr	Arg	Lys	Pro	Asp	Val	20	25	30	
Asn	Asn	Pro	Asp	Gln	Gln	Val	Ala	Phe	Gly	Thr	Ser	Gly	His	Arg	Gly	35	40	45	
Phe	Ala	Leu	Asp	Ser	Ala	Phe	Asn	Glu	Asp	His	Ile	Leu	Ala	Thr	Thr	50	55	60	
Gln	Ala	Ile	Val	Asp	Tyr	Arg	Asn	Gln	Gln	Pro	Lys	Asn	Trp	Val	Gly	65	70	75	80
Pro	Leu	Phe	Ile	Gly	Arg	Asp	Thr	His	Ala	Leu	Ser	Glu	Pro	Ala	Met	85	90	95	
Ile	Ser	Ala	Leu	Glu	Val	Leu	Ile	Ala	Asn	Asp	Val	Glu	Val	Leu	Val	100	105	110	
Asp	Ala	Asp	Gly	Arg	Tyr	Thr	Pro	Thr	Pro	Ala	Val	Ser	His	Ala	Ile	115	120	125	
Leu	Arg	His	Asn	Asp	Gly	Ile	Ile	Leu	Gly	Thr	Ala	Gly	Pro	Ser	Arg	130	135	140	
Pro	Tyr	Ala	Asp	Gly	Ile	Val	Ile	Thr	Pro	Ser	His	Asn	Pro	Pro	Arg	145	150	155	160
Asp	Gly	Gly	Phe	Lys	Tyr	Asn	Pro	Ala	Asn	Gly	Gly	Pro	Ala	Asp	Thr	165	170	175	
Asp	Ala	Thr	Asp	Trp	Ile	Ala	Asn	Arg	Ala	Asn	Asp	Ile	Leu	Arg	Gly	180	185	190	
Asp	Leu	Ala	Asp	Val	Lys	Arg	Val	Pro	Val	Ser	Gly	Val	Leu	Asp	Glu	195	200	205	
Arg	Thr	Thr	Ala	Tyr	Asp	Phe	Lys	Gly	Ile	Tyr	Ile	Ala	Asp	Leu	Pro	210	215	220	
Asn	Val	Val	Asn	Ile	Asp	Ala	Ile	Arg	Glu	Ala	Gly	Val	Arg	Ile	Gly	225	230	235	240
Ala	Asp	Pro	Met	Gly	Gly	Ala	Ser	Val	Asp	Tyr	Trp	Gly	Ala	Ile	Ala	245	250	255	
Glu	Thr	His	Gly	Leu	Asn	Leu	Thr	Val	Val	Asn	Pro	His	Val	Asp	Ser	260	265	270	
Thr	Phe	Arg	Phe	Met	Thr	Leu	Asp	Thr	Asp	Gly	Lys	Ile	Arg	Met	Asp	275	280	285	
Cys	Ser	Ser	Pro	His	Ala	Met	Ala	Ser	Leu	Ile	Asp	Asn	Arg	Asp	Lys	290	295	300	
Phe	Asp	Val	Ala	Thr	Gly	Asn	Asp	Ala	Asp	Ala	Asp	Arg	His	Gly	Ile	305	310	315	320

Val Thr Pro Asp Ala Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val  
 325 330 335  
 Ala Ile Glu Tyr Leu Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr  
 340 345 350  
 Ala Val Gly Lys Thr Leu Val Ser Ser Ser Met Ile Asp Arg Val Val  
 355 360 365  
 Ala Gln Leu Gly Arg Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp  
 370 375 380  
 Phe Val Pro Gly Leu Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu  
 385 390 395 400  
 Ser Ala Gly Ala Ser Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr  
 405 410 415  
 Asp Lys Asp Gly Leu Ile Leu Asp Leu Leu Ala Ala Glu Ile Ile Ala  
 420 425 430  
 Val Thr Gly Lys Thr Pro Ser Gln Arg Tyr Ala Glu Leu Ala Glu Glu  
 435 440 445  
 Phe Gly Ala Pro Ala Tyr Ala Arg Thr Asp Ala Glu Ala Asn Arg Glu  
 450 455 460  
 Gln Lys Ala Ile Leu Lys Ala Leu Ser Pro Glu Gln Val Thr Ala Thr  
 465 470 475 480  
 Glu Leu Ala Gly Glu Ala Ile Thr Ala Lys Leu Thr Glu Ala Pro Gly  
 485 490 495  
 Asn Gly Ala Ala Ile Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp  
 500 505 510  
 Phe Ala Ala Arg Pro Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala  
 515 520 525  
 Glu Ser Phe Lys Gly Glu Glu His Leu Ala Gln Val Gln Lys Glu Ala  
 530 535 540  
 Gln Ala Leu Val Ser Glu Val Leu Gly Gln  
 545 550

&lt;210&gt; 27

&lt;211&gt; 680

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(657)

&lt;223&gt; RXN02803

&lt;400&gt; 27

gtc tct gga gag atg ctc gcg gca gca ctt tca gca ggc atg gcc agc  
 Val Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser  
 1 5 10 15

48

cag ggt gtt gat gtc att cgt gtt ggt gtc atc cca acc cca gct gtt	96
Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val	
20 25 30	
gca ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct	144
Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser	
35 40 45	
gca tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca	192
Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala	
50 55 60	
ggt gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt	240
Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val	
65 70 75 80	
atg gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt	288
Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg	
85 90 95	
gtc atc gaa gaa gca acc gat gca cag gac cgt tac cta gag cac ctg	336
Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu	
100 105 110	
aag gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat	384
Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp	
115 120 125	
gca gcc aat ggt gcg gca agt gtt gta gct cca acg gct tat gag gct	432
Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala	
130 135 140	
gcg ggt gca act gta att gct att cat aac aag cca gac tca tac aac	480
Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn	
145 150 155 160	
atc aac atg gac tgc ggt tcc acc cac att gat cag gcg cag ccg cca	528
Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro	
165 170 175	
gtc ttg aag cac ggt gct gac ctt gga ctc gcg cat gac ggt gat gct	576
Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala	
180 185 190	
gac cgt tgt ttg gct gtg aac aag gat gcc aac ctt gtt gat ggt gac	624
Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp	
195 200 205	
caa atc atg gcg ctg tta gcc att gcg atg aaa taaaacggcg agctgcgcaa	677
Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys	
210 215	
gaa	680

&lt;210&gt; 28

&lt;211&gt; 219

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 28

Val Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser  
 1 5 10 15  
 Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val  
 20 25 30  
 Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser  
 35 40 45  
 Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala  
 50 55 60  
 Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val  
 65 70 75 80  
 Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg  
 85 90 95  
 Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu  
 100 105 110  
 Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp  
 115 120 125  
 Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala  
 130 135 140  
 Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn  
 145 150 155 160  
 Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro  
 165 170 175  
 Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala  
 180 185 190  
 Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp  
 195 200 205  
 Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys  
 210 215

<210> 29  
 <211> 399  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(399)  
 <223> FRXA02803

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 Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln  
 1 5 10 15  
 ggt gtt gat gtc att cgt gtt ggt gtc atc cca acc cca gct gtt gca 96  
 Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala  
 20 25 30



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ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct gca 144
Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala
      35              40              45

tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca ggt 192
Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly
      50              55              60

gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt atg 240
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met
      65              70              75              80

gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt gtc 288
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val
              85              90              95

atc gaa gaa gca acc gat gca cag gac cgc tac cta gag cac ctg aag 336
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys
              100              105              110

gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat gca 384
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala
              115              120              125

gcc aat ggt gcg gca 399
Ala Asn Gly Ala Ala
      130

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&lt;210&gt; 30

&lt;211&gt; 133

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 30

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Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln
  1              5              10              15

Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala
      20              25              30

Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala
      35              40              45

Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly
      50              55              60

Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met
      65              70              75              80

Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val
              85              90              95

Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys
      100              105              110

Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala
      115              120              125

Ala Asn Gly Ala Ala

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<210> 31
<211> 1713
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101) .. (1690)
<223> RXN03076
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tctaatagtg atcccacgaa aacaaaggat cggggtgttc atg gac gag tct cgt 115															
Met Asp Glu Ser Arg 5															
1															
cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg 163															
Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala 20															
10															
15															
cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt 211															
Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val 35															
25															
30															
35															
gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg 259															
Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu 50															
40															
45															
50															
gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat 307															
Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp 65															
55															
60															
65															
ggc ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tgc cat 355															
Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His 85															
70															
75															
80															
act ttt gct gca acc act gcg gag gtg ttc gcg ggt gct ggt ttt gag 403															
Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu 100															
90															
95															
100															
gtg acg ttg ctc ccc acg cct agc cct acg ccg ttg att ccg tgg ttg 451															
Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu 115															
105															
110															
115															
gtg aac aag cat ggg ttg gat gcg ggc gtt cag atc acg gct tgc cat 499															
Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His 130															
120															
125															
130															
aat ggt gcg gcg gac aat ggc tac aag gtg ttt ttg tct aat ggt cgc 547															
Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe Leu Ser Asn Gly Arg 145															
135															
140															
145															
cag ctt tat tct gaa ctg gag cct gag ctt gag gcg cat atc aat gct 595															
Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala 165															
150															
155															
160															
165															
gtg gaa gat ccg att ccg gtt cct ccg gtg acg gtg cgc ccc act gct 643															

Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr	Val	Arg	Pro	Thr	Ala		
				170					175					180			
gat	cag	ctg	cgt	cga	tat	gtt	gat	gag	atg	gtg	tcg	ttg	gtg	act	cct	691	
Asp	Gln	Leu	Arg	Arg	Tyr	Val	Asp	Glu	Met	Val	Ser	Leu	Val	Thr	Pro		
			185					190					195				
gat	cag	gct	gat	ttg	ttg	cgg	gtg	aat	tct	gag	cgg	ggc	aat	ctt	cgc	739	
Asp	Gln	Ala	Asp	Leu	Leu	Arg	Val	Asn	Ser	Glu	Arg	Gly	Asn	Leu	Arg		
		200					205					210					
gtg	gtg	tat	acc	gct	ctg	cat	ggc	gtg	ggc	ggc	cgc	gcg	atg	gcc	aat	787	
Val	Val	Tyr	Thr	Ala	Leu	His	Gly	Val	Gly	Gly	Arg	Ala	Met	Ala	Asn		
	215					220					225						
gct	ttc	caa	ttt	gct	ggc	ttt	ccc	cat	act	cat	ggc	gtg	aag	gct	cag	835	
Ala	Phe	Gln	Phe	Ala	Gly	Phe	Pro	His	Thr	His	Gly	Val	Lys	Ala	Gln		
230				235						240					245		
cag	tat	cct	gat	ccc	acc	ttc	ccc	act	gtg	gcg	ttc	ccc	aat	ccg	gaa	883	
Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	Phe	Pro	Asn	Pro	Glu		
				250					255					260			
gag	cct	tct	gcg	att	gag	ttg	ttg	ttg	gaa	cgc	gca	aag	gaa	aag	aac	931	
Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	Ala	Lys	Glu	Lys	Asn		
			265					270					275				
gct	gac	att	ttg	ttt	gcg	ctt	gat	cct	gat	gcc	gat	cgt	tgt	gct	gtg	979	
Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	Asp	Arg	Cys	Ala	Val		
		280					285					290					
ggt	att	cgt	acc	gct	gat	ggc	ggc	cac	cga	atg	ctc	tct	ggc	gat	gag	1027	
Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met	Leu	Ser	Gly	Asp	Glu		
	295					300					305						
gtg	ggc	aca	ctt	ttg	gct	act	cgt	ttg	gtt	ccg	gag	tat	tcc	ggc	gaa	1075	
Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	Glu	Tyr	Ser	Gly	Glu		
310				315						320					325		
ggc	cca	cgt	ccc	gtg	gtt	gcc	acc	acg	gtg	gtg	tct	tcg	cag	ctt	ctg	1123	
Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val	Ser	Ser	Gln	Leu	Leu		
				330					335					340			
ggt	atc	atc	gcc	gag	gat	aaa	ggg	tgg	gat	tat	tcc	gag	aca	ctg	acg	1171	
Gly	Ile	Ile	Ala	Glu	Asp	Lys	Gly	Trp	Asp	Tyr	Ser	Glu	Thr	Leu	Thr		
			345					350					355				
gga	ttc	aaa	aat	ctg	tcg	agg	gct	gcc	gat	ggc	ctc	gac	gga	ccg	ctt	1219	
Gly	Phe	Lys	Asn	Leu	Ser	Arg	Ala	Ala	Asp	Gly	Leu	Asp	Gly	Pro	Leu		
		360					365					370					
gct	ttc	gct	tat	gag	gaa	gct	gtg	ggc	acc	tgc	ccg	gtt	cca	gat	gtc	1267	
Ala	Phe	Ala	Tyr	Glu	Glu	Ala	Val	Gly	Thr	Cys	Pro	Val	Pro	Asp	Val		
	375					380					385						
gtg	ccg	gat	aag	gac	ggc	atc	tct	aca	gcg	ttg	ttc	atg	gcg	tcg	tgg	1315	
Val	Pro	Asp	Lys	Asp	Gly	Ile	Ser	Thr	Ala	Leu	Phe	Met	Ala	Ser	Trp		
390					395				400						405		
gct	gcc	gaa	ctg	aag	gct	cag	ggc	gca	agc	ctg	cag	caa	aaa	ctc	aat	1363	
Ala	Ala	Glu	Leu	Lys	Ala	Gln	Gly	Ala	Ser	Leu	Gln	Gln	Lys	Leu	Asn		

	410	415	420	
gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg				1411
Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val				
	425	430	435	
cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct				1459
Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro				
	440	445	450	
cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa				1507
Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu				
	455	460	465	
aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt				1555
Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg				
	470	475	480	485
gct att ggt cga gtc tct gga act gag gcg aaa gcc aag ctc tat ttg				1603
Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu				
	490	495	500	
gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat				1651
Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His				
	505	510	515	
cag ctg gag gat gaa gtc caa agc tgg ttg agc aag ctt tagtttcctg				1700
Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser Lys Leu				
	520	525	530	
gctgctcccg gtt				1713

&lt;210&gt; 32

&lt;211&gt; 530

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 32

Met Asp Glu Ser Arg Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala
1 5 10 15

Pro Val Gly Pro Ala Arg His Gln Met Asn Val Leu Gln Val Thr Arg
20 25 30

Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn
35 40 45

Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala
50 55 60

Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala
65 70 75 80

Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala
85 90 95

Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro
100 105 110

Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
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115					120					125					
Ile	Thr	Ala	Ser	His	Asn	Gly	Ala	Ala	Asp	Asn	Gly	Tyr	Lys	Val	Phe
130						135					140				
Leu	Ser	Asn	Gly	Arg	Gln	Leu	Tyr	Ser	Glu	Leu	Glu	Pro	Glu	Leu	Glu
145					150					155					160
Ala	His	Ile	Asn	Ala	Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr
				165					170					175	
Val	Arg	Pro	Thr	Ala	Asp	Gln	Leu	Arg	Arg	Tyr	Val	Asp	Glu	Met	Val
			180					185					190		
Ser	Leu	Val	Thr	Pro	Asp	Gln	Ala	Asp	Leu	Leu	Arg	Val	Asn	Ser	Glu
		195					200					205			
Arg	Gly	Asn	Leu	Arg	Val	Val	Tyr	Thr	Ala	Leu	His	Gly	Val	Gly	Gly
	210					215					220				
Arg	Ala	Met	Ala	Asn	Ala	Phe	Gln	Phe	Ala	Gly	Phe	Pro	His	Thr	His
225					230					235					240
Gly	Val	Lys	Ala	Gln	Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala
				245					250					255	
Phe	Pro	Asn	Pro	Glu	Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg
			260					265						270	
Ala	Lys	Glu	Lys	Asn	Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala
		275					280					285			
Asp	Arg	Cys	Ala	Val	Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met
	290					295					300				
Leu	Ser	Gly	Asp	Glu	Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro
305					310					315					320
Glu	Tyr	Ser	Gly	Glu	Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val
			325						330					335	
Ser	Ser	Gln	Leu	Leu	Gly	Ile	Ile	Ala	Glu	Asp	Lys	Gly	Trp	Asp	Tyr
			340					345					350		
Ser	Glu	Thr	Leu	Thr	Gly	Phe	Lys	Asn	Leu	Ser	Arg	Ala	Ala	Asp	Gly
		355					360					365			
Leu	Asp	Gly	Pro	Leu	Ala	Phe	Ala	Tyr	Glu	Glu	Ala	Val	Gly	Thr	Cys
	370					375					380				
Pro	Val	Pro	Asp	Val	Val	Pro	Asp	Lys	Asp	Gly	Ile	Ser	Thr	Ala	Leu
385					390					395					400
Phe	Met	Ala	Ser	Trp	Ala	Ala	Glu	Leu	Lys	Ala	Gln	Gly	Ala	Ser	Leu
				405					410					415	
Gln	Gln	Lys	Leu	Asn	Glu	Leu	Tyr	Arg	Arg	Tyr	Gly	Tyr	Phe	Ala	Ser
			420					425					430		
Ser	Gln	Ile	Ala	Val	Arg	Thr	Ser	Ser	Pro	Arg	Glu	Leu	Val	Asp	His
		435					440					445			

Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro  
 450 455 460

His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly  
 465 470 475 480

His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys  
 485 490 495

Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala  
 500 505 510

Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser  
 515 520 525

Lys Leu  
 530

<210> 33  
 <211> 1684  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1684)  
 <223> FRXA02854

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tctaatagtg atcccacgaa aacaaaggat cggggtgttc atg gac gag tct cgt 115  
 Met Asp Glu Ser Arg  
 1 5

cag ctt agt ttc ggc aca gca ggg ttg cgt gca cca gtt ggc ccg gcg 163  
 Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala  
 10 15 20

cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt 211  
 Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val  
 25 30 35

gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg 259  
 Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu  
 40 45 50

gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat 307  
 Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp  
 55 60 65

ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat 355  
 Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His  
 70 75 80 85

act ttt gct gca acc act gcg gag gtg ttc gcg ggt gct ggt ttt gag 403  
 Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu  
 90 95 100

gtg	acg	ttg	ctc	ccc	acg	cct	agc	cct	acg	ccg	ttg	att	ccg	tgg	ttg	451
Val	Thr	Leu	Leu	Pro	Thr	Pro	Ser	Pro	Thr	Pro	Leu	Ile	Pro	Trp	Leu	
			105						110					115		
gtg	aac	aag	cat	ggg	ttg	gat	gcg	ggc	gtt	cag	atc	acg	gct	tcg	cat	499
Val	Asn	Lys	His	Gly	Leu	Asp	Ala	Gly	Val	Gln	Ile	Thr	Ala	Ser	His	
		120					125					130				
aat	ggt	gcg	gcg	gac	aat	ggc	tac	aag	gtg	ttt	ttg	tct	aat	ggt	cg	547
Asn	Gly	Ala	Ala	Asp	Asn	Gly	Tyr	Lys	Val	Phe	Leu	Ser	Asn	Gly	Arg	
	135					140					145					
cag	ctt	tat	tct	gaa	ctg	gag	cct	gag	ctt	gag	gcg	cat	atc	aat	gct	595
Gln	Leu	Tyr	Ser	Glu	Leu	Glu	Pro	Glu	Leu	Glu	Ala	His	Ile	Asn	Ala	
150					155					160					165	
gtg	gaa	gat	ccg	att	cg	gtt	cct	cg	gtg	acg	gtg	cg	ccc	act	gct	643
Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr	Val	Arg	Pro	Thr	Ala	
				170					175					180		
gat	cag	ctg	cgt	cga	tat	gtt	gat	gag	atg	gtg	tcg	ttg	gtg	act	cct	691
Asp	Gln	Leu	Arg	Arg	Tyr	Val	Asp	Glu	Met	Val	Ser	Leu	Val	Thr	Pro	
			185					190					195			
gat	cag	gct	gat	ttg	ttg	cg	gtg	aat	tct	gag	cg	ggc	aat	ctt	cg	739
Asp	Gln	Ala	Asp	Leu	Leu	Arg	Val	Asn	Ser	Glu	Arg	Gly	Asn	Leu	Arg	
		200					205					210				
gtg	gtg	tat	acc	gct	ctg	cat	ggt	gtg	ggt	ggc	cg	gcg	atg	gcc	aat	787
Val	Val	Tyr	Thr	Ala	Leu	His	Gly	Val	Gly	Gly	Arg	Ala	Met	Ala	Asn	
	215					220				225						
gct	ttc	caa	ttt	gct	ggt	ttt	ccc	cat	act	cat	ggc	gtg	aag	gct	cag	835
Ala	Phe	Gln	Phe	Ala	Gly	Phe	Pro	His	Thr	His	Gly	Val	Lys	Ala	Gln	
230					235					240					245	
cag	tat	cct	gat	ccc	acc	ttc	ccc	act	gtg	gcg	ttc	ccc	aat	ccg	gaa	883
Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	Phe	Pro	Asn	Pro	Glu	
				250					255					260		
gag	cct	tct	gcg	att	gag	ttg	ttg	ttg	gaa	cg	gca	aag	gaa	aag	aac	931
Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	Ala	Lys	Glu	Lys	Asn	
			265				270						275			
gct	gac	att	ttg	ttt	gcg	ctt	gat	cct	gat	gcc	gat	cgt	tgt	gct	gtg	979
Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	Asp	Arg	Cys	Ala	Val	
		280					285					290				
ggt	att	cgt	acc	gct	gat	ggc	ggc	cac	cga	atg	ctc	tct	ggc	gat	gag	1027
Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met	Leu	Ser	Gly	Asp	Glu	
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gtg	ggc	aca	ctt	ttg	gct	act	cgt	ttg	gtt	ccg	gag	tat	tcc	ggt	gaa	1075
Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	Glu	Tyr	Ser	Gly	Glu	
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ggc	cca	cgt	ccc	gtg	gtt	gcc	acc	acg	gtg	gtg	tct	tcg	cag	ctt	ctg	1123
Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val	Ser	Ser	Gln	Leu	Leu	
				330					335					340		
ggt	atc	atc	gcc	gag	gat	aaa	ggg	tgg	gat	tat	tcc	gag	aca	ctg	acg	1171

Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr  
 345 350 355  
 gga ttc aaa aat ctg tcg agg gct gcc gat ggt ctc gac gga ccg ctt 1219  
 Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu  
 360 365 370  
 gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc 1267  
 Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val  
 375 380 385  
 gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg 1315  
 Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp  
 390 395 400 405  
 gct gcc gaa ctg aag gct cag ggc gca agc ctg cag caa aaa ctc aat 1363  
 Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn  
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 gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg 1411  
 Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val  
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 Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro  
 440 445 450  
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 Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu  
 455 460 465  
 aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt 1555  
 Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg  
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 Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys Ala Lys Leu Tyr Leu  
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 gaa gtt ggt cag gcc agc tcc cat gat gaa gca gct cag ttg ttg cat 1651  
 Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala Ala Gln Leu Leu His  
 505 510 515  
 cag ctg gag gat gaa gtc caa agc tgg ttg agc 1684  
 Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser  
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&lt;210&gt; 34

&lt;211&gt; 528

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 34

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 Pro Val Gly Pro Ala Arg His Gln Met Asn Val Leu Gln Val Thr Arg  
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 Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn



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Arg	Tyr	Gly	Ser	His	Thr	Phe	Ala	Ala	Thr	Thr	Ala	Glu	Val	Phe	Ala	
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Gly	Ala	Gly	Phe	Glu	Val	Thr	Leu	Leu	Pro	Thr	Pro	Ser	Pro	Thr	Pro	
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Leu	Ile	Pro	Trp	Leu	Val	Asn	Lys	His	Gly	Leu	Asp	Ala	Gly	Val	Gln	
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Ile	Thr	Ala	Ser	His	Asn	Gly	Ala	Ala	Asp	Asn	Gly	Tyr	Lys	Val	Phe	
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Leu	Ser	Asn	Gly	Arg	Gln	Leu	Tyr	Ser	Glu	Leu	Glu	Pro	Glu	Leu	Glu	
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Ala	His	Ile	Asn	Ala	Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr	
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Val	Arg	Pro	Thr	Ala	Asp	Gln	Leu	Arg	Arg	Tyr	Val	Asp	Glu	Met	Val	
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Ser	Leu	Val	Thr	Pro	Asp	Gln	Ala	Asp	Leu	Leu	Arg	Val	Asn	Ser	Glu	
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Gly	Val	Lys	Ala	Gln	Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	
245					250					255						
Phe	Pro	Asn	Pro	Glu	Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	
260					265					270						
Ala	Lys	Glu	Lys	Asn	Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	
275					280					285						
Asp	Arg	Cys	Ala	Val	Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met	
290					295					300						
Leu	Ser	Gly	Asp	Glu	Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	
305					310					315					320	
Glu	Tyr	Ser	Gly	Glu	Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val	
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Ser	Ser	Gln	Leu	Leu	Gly	Ile	Ile	Ala	Glu	Asp	Lys	Gly	Trp	Asp	Tyr	
340					345					350						
Ser	Glu	Thr	Leu	Thr	Gly	Phe	Lys	Asn	Leu	Ser	Arg	Ala	Ala	Asp	Gly	
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Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys  
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 Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu  
 385 390 395 400  
 Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu  
 405 410 415  
 Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser  
 420 425 430  
 Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His  
 435 440 445  
 Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro  
 450 455 460  
 His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly  
 465 470 475 480  
 His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys  
 485 490 495  
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 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA00511

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 Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys  
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 gta gga gac cgc tac gtg ctg gaa gac ctc aat gca ggt gga ttc agc 144  
 Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser  
 35 40 45  
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 Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr  
 50 55 60

act ggc gat gga act ttg act ggt ctt tcc atc atg gcg cgc atg gct 240  
 Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala  
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 Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu  
 85 90 95

cca cag gtt ctg atc aat gtg cca gtt tcc gat aag tcc acc atc gtg 336  
 Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val  
 100 105 110

agc cac cca agc gtt gtg gct gcg atc gcg gaa gca gaa gct gag ttg 384  
 Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu  
 115 120 125

ggc gcc acc ggt cgc gtt ctt ctt cgt gct tct ggc acc gaa gag ctt 432  
 Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu  
 130 135 140

ttc cgc gtg atg gtt gag gct gga gac aag gaa caa gct cgt cgt atc 480  
 Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile  
 145 150 155 160

gcg gga cgt ctt gct gca gtg gtt gca gaa gtc taattcactt cagtcacagc 533  
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gca 536

<210> 36

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

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Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys  
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Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser  
 35 40 45

Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr  
 50 55 60

Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala  
 65 70 75 80

Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu  
 85 90 95

Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val  
 100 105 110

Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu  
 115 120 125

Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu  
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145 150 155 160

Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val  
165 170

<210> 37

<211> 1497

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1474)

<223> RXN01365

<400> 37

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Met Arg Thr Arg Glu  
1 5

tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163  
Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly  
10 15 20

gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211  
Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly  
25 30 35

cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259  
Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp  
40 45 50

atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg 307  
Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val  
55 60 65

act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat 355  
Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp  
70 75 80 85

gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt 403  
Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe  
90 95 100

act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt 451  
Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly Ile Lys Leu Cys Arg  
105 110 115

gcg ggt gct cgt ccg gtc ggt cag gat tct ggt ttg gcc aac atc att 499  
Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly Leu Ala Asn Ile Ile  
120 125 130

gat gat ctg gtt gag ggt gtt cca gcg ttt gat ggt gag tca ggt tcg 547

Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser	
135						140					145					
ggt	tct	gag	cag	gat	ttg	ctg	agc	gca	tat	gcc	gag	tac	ctc	aat	gag	595
Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu	
150					155					160					165	
ctt	ggt	gat	ctg	aag	aac	atc	cgc	ccg	atg	aag	ggt	gct	gtg	gat	gcg	643
Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala	
				170					175					180		
gca	aac	ggc	atg	ggt	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggt	ctg	691
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu	
			185					190					195			
cca	ctt	gat	ggt	gcg	cca	ctg	tat	ttt	gag	ctt	gac	ggc	aat	ttc	ccc	739
Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro	
		200				205						210				
aac	cat	gag	gcc	aat	cct	ctg	gag	cct	gcc	aac	ctg	ggt	gat	ttg	cag	787
Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln	
	215					220					225					
aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggt	ttg	gcg	ttc	gac	ggc	835
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly	
230					235					240					245	
gat	gcg	gat	cgt	tgc	ttc	gtg	gtc	gat	gag	aag	ggc	cag	cca	gtc	agc	883
Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser	
				250					255					260		
cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu	
			265					270					275			
ccg	ggt	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro	
		280					285					290				
gag	gtg	att	gct	gaa	aac	ggt	ggc	act	gcg	gtg	cgt	act	cgc	gtg	ggt	1027
Glu	Val	Ile	Ala	Glu	Asn	Gly	Gly	Thr	Ala	Val	Arg	Thr	Arg	Val	Gly	
	295					300					305					
cac	tcc	ttc	atc	aag	gcg	aag	atg	gca	gag	acc	ggt	gcg	gcc	ttt	ggt	1075
His	Ser	Phe	Ile	Lys	Ala	Lys	Met	Ala	Glu	Thr	Gly	Ala	Ala	Phe	Gly	
310					315					320					325	
ggc	gag	cac	tct	gcg	cac	tac	tac	ttc	act	gag	ttc	ttc	aat	gcg	gac	1123
Gly	Glu	His	Ser	Ala	His	Tyr	Tyr	Phe	Thr	Glu	Phe	Phe	Asn	Ala	Asp	
				330					335					340		
tcc	ggc	att	ttg	gct	gcg	atg	cac	gtg	ctg	gct	gcg	ctg	gga	agc	cag	1171
Ser	Gly	Ile	Leu	Ala	Ala	Met	His	Val	Leu	Ala	Ala	Leu	Gly	Ser	Gln	
			345					350					355			
gac	cag	cca	ctc	agt	gag	atg	atg	gct	agg	tat	aac	cgg	tac	ggt	gct	1219
Asp	Gln	Pro	Leu	Ser	Glu	Met	Met	Ala	Arg	Tyr	Asn	Arg	Tyr	Val	Ala	
		360					365					370				
tca	ggc	gag	ttg	aac	tcc	cgt	ttg	gct	aat	gca	gag	gcg	cag	caa	gag	1267
Ser	Gly	Glu	Leu	Asn	Ser	Arg	Leu	Ala	Asn	Ala	Glu	Ala	Gln	Gln	Glu	

375	380	385	
cgc acc cag gct gtg ctc gat gcg ttc gct gat cgc acc gag tcc gtg			1315
Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp Arg Thr Glu Ser Val			
390	395	400	405
gac acc ctt gac ggc gtg act gtg gaa ctc aag gac acc tcc gcg tgg			1363
Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys Asp Thr Ser Ala Trp			
	410	415	420
ttc aac gtg cgt gcg tcc aac acc gag ccg ctg ctt cgc ctc aat gtt			1411
Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu Leu Arg Leu Asn Val			
	425	430	435
gaa gct gca tcg aag gaa gaa gtc gat gcg ttg gta gcg gag att cta			1459
Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu Val Ala Glu Ile Leu			
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ggg att atc cgc gca taatccatt ttccggcgagg cat			1497
Gly Ile Ile Arg Ala			
455			

&lt;210&gt; 38

&lt;211&gt; 458

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 38

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Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr
20 25 30

Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
35 40 45

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
50 55 60

Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
65 70 75 80

Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
85 90 95

Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
100 105 110

Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
115 120 125

Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
130 135 140

Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
145 150 155 160

Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
165 170 175

Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu  
 180 185 190  
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu  
 195 200 205  
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn  
 210 215 220  
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly  
 225 230 235 240  
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys  
 245 250 255  
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg  
 260 265 270  
 Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr  
 275 280 285  
 Ser Lys Ala Val Pro Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val  
 290 295 300  
 Arg Thr Arg Val Gly His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr  
 305 310 315 320  
 Gly Ala Ala Phe Gly Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu  
 325 330 335  
 Phe Phe Asn Ala Asp Ser Gly Ile Leu Ala Ala Met His Val Leu Ala  
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 Ala Leu Gly Ser Gln Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr  
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 Asn Arg Tyr Val Ala Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala  
 370 375 380  
 Glu Ala Gln Gln Glu Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp  
 385 390 395 400  
 Arg Thr Glu Ser Val Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys  
 405 410 415  
 Asp Thr Ser Ala Trp Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu  
 420 425 430  
 Leu Arg Leu Asn Val Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu  
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 Val Ala Glu Ile Leu Gly Ile Ile Arg Ala  
 450 455

&lt;210&gt; 39

&lt;211&gt; 994

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(994)

&lt;223&gt; FRXA01365

&lt;400&gt; 39

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Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
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Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
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Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
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Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
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Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
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Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
                        90 95 100

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Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly Ile Lys Leu Cys Arg
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gcg ggt gct cgt ccg gtc ggt cag gat tct ggt ttg gcc aac atc att 499
Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly Leu Ala Asn Ile Ile
                        120 125 130

gat gat ctg gtt gag ggt gtt cca gcg ttt gat ggt gag tca ggt tcg 547
Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp Gly Glu Ser Gly Ser
                        135 140 145

gtt tct gag cag gat ttg ctg agc gca tat gcc gag tac ctc aat gag 595
Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala Glu Tyr Leu Asn Glu
                        150 155 160 165

ctt gtt gat ctg aag aac atc cgc ccg atg aag gtt gct gtg gat gcg 643
Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys Val Ala Val Asp Ala
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gca aac ggc atg ggt ggg ttc act gtc cct gag gta ttc aag ggt ctg 691
Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu Val Phe Lys Gly Leu
                        185 190 195

cca ctt gat gtt gcg cca ctg tat ttt gag ctt gac ggc aat ttc ccc 739

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Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu Asp Gly Asn Phe Pro  
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 Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn Leu Val Asp Leu Gln  
 215 220 225

aag ttt acc gta gag acc gga tct gat atc ggt ttg gcg ttc gac ggc 835  
 Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly Leu Ala Phe Asp Gly  
 230 235 240 245

gat gcg gat cgt tgc ttc gtg gtc gat gag aag ggc cag cca gtc agc 883  
 Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys Gly Gln Pro Val Ser  
 250 255 260

cct tcg gcg atc tgt gcg atc gta gcg gag cgt tac ttg gag aag ctt 931  
 Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg Tyr Leu Glu Lys Leu  
 265 270 275

ccg ggt tcc acc atc atc cac aac ctg att acc tct aag gct gtg cct 979  
 Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr Ser Lys Ala Val Pro  
 280 285 290

gag gtg att gct gaa 994  
 Glu Val Ile Ala Glu  
 295

&lt;210&gt; 40

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 40

Met Arg Thr Arg Glu Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val  
 1 5 10 15

Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr  
 20 25 30

Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val  
 35 40 45

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala  
 50 55 60

Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly  
 65 70 75 80

Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys  
 85 90 95

Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly  
 100 105 110

Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly  
 115 120 125

Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp  
 130 135 140

Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala  
 145 150 155 160  
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys  
 165 170 175  
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu  
 180 185 190  
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu  
 195 200 205  
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn  
 210 215 220  
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly  
 225 230 235 240  
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys  
 245 250 255  
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg  
 260 265 270  
 Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr  
 275 280 285  
 Ser Lys Ala Val Pro Glu Val Ile Ala Glu  
 290 295

<210> 41  
 <211> 1743  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1720)  
 <223> RXA00098

<400> 41  
 taaatttgtc gtgtttccca ctttgaacac tcttcgatgc gcttggccac aaaagcaagc 60  
 taacctgaag atgttattta acgacaataa aggagttttc atg gcg gac att tcg 115  
 Met Ala Asp Ile Ser  
 1 5  
 acc acc cag gtt tgg caa gac ctg acc gat cat tac tca aac ttc cag 163  
 Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His Tyr Ser Asn Phe Gln  
 10 15 20  
 gca acc act ctg cgt gaa ctt ttc aag gaa gaa aac cgc gcc gag aag 211  
 Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu Asn Arg Ala Glu Lys  
 25 30 35  
 tac acc ttc tcc gcg gct ggc ctc cac gtc gac ctg tcg aag aat ctg 259  
 Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp Leu Ser Lys Asn Leu  
 40 45 50  
 ctt gac gac gcc acc ctc acc aag ctc ctt gca ctg acc gaa gaa tct 307

Leu	Asp	Asp	Ala	Thr	Leu	Thr	Lys	Leu	Leu	Ala	Leu	Thr	Glu	Glu	Ser	
55						60					65					
ggc	ctt	cgc	gaa	cgc	att	gac	gcg	atg	ttt	gcc	ggc	gaa	cac	ctc	aac	355
Gly	Leu	Arg	Glu	Arg	Ile	Asp	Ala	Met	Phe	Ala	Gly	Glu	His	Leu	Asn	
70					75					80					85	
aac	acc	gaa	gac	cgc	gct	gtc	ctc	cac	acc	gcg	ctg	cgc	ctt	cct	gcc	403
Asn	Thr	Glu	Asp	Arg	Ala	Val	Leu	His	Thr	Ala	Leu	Arg	Leu	Pro	Ala	
				90					95					100		
gaa	gct	gat	ctg	tca	gta	gat	ggc	caa	gat	gtt	gct	gct	gat	gtc	cac	451
Glu	Ala	Asp	Leu	Ser	Val	Asp	Gly	Gln	Asp	Val	Ala	Ala	Asp	Val	His	
			105					110					115			
gaa	gtt	ttg	gga	cgc	atg	cgt	gac	ttc	gct	act	gcg	ctg	cgc	tca	ggc	499
Glu	Val	Leu	Gly	Arg	Met	Arg	Asp	Phe	Ala	Thr	Ala	Leu	Arg	Ser	Gly	
	120						125				130					
aac	tgg	ttg	gga	cac	acc	ggc	cac	acg	atc	aag	aag	atc	gtc	aac	att	547
Asn	Trp	Leu	Gly	His	Thr	Gly	His	Thr	Ile	Lys	Lys	Ile	Val	Asn	Ile	
	135					140					145					
ggt	atc	ggt	ggc	tct	gac	ctc	gga	cca	gcc	atg	gct	acg	aag	gct	ctg	595
Gly	Ile	Gly	Gly	Ser	Asp	Leu	Gly	Pro	Ala	Met	Ala	Thr	Lys	Ala	Leu	
150					155				160						165	
cgt	gca	tac	gcg	acc	gct	ggc	atc	tca	gca	gaa	ttc	gtc	tcc	aac	gtc	643
Arg	Ala	Tyr	Ala	Thr	Ala	Gly	Ile	Ser	Ala	Glu	Phe	Val	Ser	Asn	Val	
				170					175					180		
gac	cca	gca	gac	ctc	gtt	tct	gtg	ttg	gaa	gac	ctc	gat	gca	gaa	tcc	691
Asp	Pro	Ala	Asp	Leu	Val	Ser	Val	Leu	Glu	Asp	Leu	Asp	Ala	Glu	Ser	
			185					190					195			
aca	ttg	ttc	gtg	atc	gct	tcg	aaa	act	ttc	acc	acc	cag	gag	acg	ctg	739
Thr	Leu	Phe	Val	Ile	Ala	Ser	Lys	Thr	Phe	Thr	Thr	Gln	Glu	Thr	Leu	
	200						205					210				
tcc	aac	gct	cgt	gca	gct	cgt	gct	tgg	ctg	gta	gag	aag	ctc	ggc	gaa	787
Ser	Asn	Ala	Arg	Ala	Ala	Arg	Ala	Trp	Leu	Val	Glu	Lys	Leu	Gly	Glu	
	215					220				225						
gag	gct	gtc	gcg	aag	cac	ttc	gtc	gca	gtg	tcc	acc	aat	gct	gaa	aag	835
Glu	Ala	Val	Ala	Lys	His	Phe	Val	Ala	Val	Ser	Thr	Asn	Ala	Glu	Lys	
230					235					240					245	
gtc	gca	gag	ttc	ggc	atc	gac	acg	gac	aac	atg	ttc	ggc	ttc	tgg	gac	883
Val	Ala	Glu	Phe	Gly	Ile	Asp	Thr	Asp	Asn	Met	Phe	Gly	Phe	Trp	Asp	
				250					255					260		
tgg	gtc	gga	ggc	cgt	tac	tcc	gtg	gac	tcc	gca	gtt	ggc	ctt	tcc	ctc	931
Trp	Val	Gly	Gly	Arg	Tyr	Ser	Val	Asp	Ser	Ala	Val	Gly	Leu	Ser	Leu	
			265					270					275			
atg	gca	gtg	atc	ggc	cct	cgc	gac	ttc	atg	cgt	ttc	ctc	ggc	gga	ttc	979
Met	Ala	Val	Ile	Gly	Pro	Arg	Asp	Phe	Met	Arg	Phe	Leu	Gly	Gly	Phe	
		280					285					290				
cac	gcg	atg	gat	gaa	cac	ttc	cgc	acc	acc	aag	ttc	gaa	gag	aac	gtt	1027
His	Ala	Met	Asp	Glu	His	Phe	Arg	Thr	Thr	Lys	Phe	Glu	Glu	Asn	Val	

295	300	305	
cca atc ttg atg gct ctg ctc ggt gtc tgg tac tcc gat ttc tat ggt Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr Ser Asp Phe Tyr Gly 310 315 320 325			1075
gca gaa acc cac gct gtc cta cct tat tcc gag gat ctc agc cgt ttt Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu Asp Leu Ser Arg Phe 330 335 340			1123
gct gct tac ctc cag cag ctg acc atg gaa tca aat ggc aag tca gtc Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser Asn Gly Lys Ser Val 345 350 355			1171
cac cgc gac ggc tcc cct gtt tcc act ggc act ggc gaa att tac tgg His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr Gly Glu Ile Tyr Trp 360 365 370			1219
ggt gag cct ggc aca aat ggc cag cac gct ttc ttc cag ctg atc cac Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe Phe Gln Leu Ile His 375 380 385			1267
cag ggc act cgc ctt gtt cca gct gat ttc att ggt ttc gct cgt cca Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile Gly Phe Ala Arg Pro 390 395 400 405			1315
aag cag gat ctt cct gcc ggt gag cgc acc atg cat gac ctt ttg atg Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met His Asp Leu Leu Met 410 415 420			1363
agc aac ttc ttc gca cag acc aag gtt ttg gct ttc ggt aag aac gct Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala Phe Gly Lys Asn Ala 425 430 435			1411
gaa gag atc gct gcg gaa ggt gtc gca cct gag ctg gtc aac cac aag Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu Leu Val Asn His Lys 440 445 450			1459
gtc atg cca ggt aat cgc cca acc acc acc att ttg gcg gag gaa ctt Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu 455 460 465			1507
acc cct tct att ctc ggt gcg ttg atc gct ttg tac gaa cac atc gtg Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Ile Val 470 475 480 485			1555
atg gtt cag ggc gtg att tgg gac atc aac tcc ttc gac caa tgg ggt Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly 490 495 500			1603
gtt gaa ctg ggc aaa cag cag gca aat gac ctc gct ccg gct gtc tct Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser 505 510 515			1651
ggt gaa gag gat gtt gac tcg gga gat tct tcc act gat tca ctg att Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile 520 525 530			1699
aag tgg tac cgc gca aat agg tagtcgcttg cttatagggt cag Lys Trp Tyr Arg Ala Asn Arg 535 540			1743

<210> 42  
 <211> 540  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 42

Met Ala Asp Ile Ser Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His  
 1 5 10 15

Tyr Ser Asn Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu  
 20 25 30

Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp  
 35 40 45

Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala  
 50 55 60

Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala  
 65 70 75 80

Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala  
 85 90 95

Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val  
 100 105 110

Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr  
 115 120 125

Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys  
 130 135 140

Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met  
 145 150 155 160

Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu  
 165 170 175

Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp  
 180 185 190

Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr  
 195 200 205

Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val  
 210 215 220

Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser  
 225 230 235 240

Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met  
 245 250 255

Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala  
 260 265 270

Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg  
 275 280 285

Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys  
 290 295 300  
 Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr  
 305 310 315 320  
 Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu  
 325 330 335  
 Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser  
 340 345 350  
 Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr  
 355 360 365  
 Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe  
 370 375 380  
 Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile  
 385 390 395 400  
 Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met  
 405 410 415  
 His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala  
 420 425 430  
 Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu  
 435 440 445  
 Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile  
 450 455 460  
 Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu  
 465 470 475 480  
 Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser  
 485 490 495  
 Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu  
 500 505 510  
 Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser  
 515 520 525  
 Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg  
 530 535 540

&lt;210&gt; 43

&lt;211&gt; 630

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(630)

&lt;223&gt; RXA01989

&lt;400&gt; 43

gtt aaa tca att cac aaa aca att cat gaa ggt act ggt gca ggt agt	48
Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser	
1 5 10 15	
gac ttc tta ggc tgg gtt gat tta cca gtt gat tac gac aaa gaa gaa	96
Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu	
20 25 30	
ttt tca aga att gtt gaa gca tca aaa cgc att aaa gaa aat tct gat	144
Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp	
35 40 45	
gtt tta gta gtc atc ggt att ggt ggt tct tac tta ggt gca cgt gca	192
Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala	
50 55 60	
gca atc gaa atg tta acg tca tca ttt aga aac agc aat gaa tac cct	240
Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro	
65 70 75 80	
gaa att gta ttt gtt ggt aat cac tta tca tca aca tat acg aaa gag	288
Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu	
85 90 95	
tta gtt gat tat tta gca gac aaa gat ttc tct gta aac gtt att tct	336
Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser	
100 105 110	
aaa tct ggt aca act aca gaa cca gca gtt gca ttt aga ttg ttc aaa	384
Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys	
115 120 125	
caa tta gtt gaa gaa aga tac ggt aaa gaa gaa gca caa aaa cgt ata	432
Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile	
130 135 140	
ttt gca aca acg gat aaa gaa aaa ggt gct tta aaa cag ttg gct aca	480
Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr	
145 150 155 160	
aac gaa ggt tat gaa acg ttt atc gta cct gat gat gta ggt gga aga	528
Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg	
165 170 175	
tat tct gtt tta aca gca gta gga tta tta cca att gca aca gct gga	576
Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly	
180 185 190	
att aac atc gaa gct atg atg att ggt gct gca aaa gca cgt gaa gaa	624
Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu	
195 200 205	
tta tct	630
Leu Ser	
210	

&lt;210&gt; 44

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 44

Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser  
 1 5 10 15

Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu  
 20 25 30

Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp  
 35 40 45

Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala  
 50 55 60

Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro  
 65 70 75 80

Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu  
 85 90 95

Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser  
 100 105 110

Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys  
 115 120 125

Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile  
 130 135 140

Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr  
 145 150 155 160

Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg  
 165 170 175

Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly  
 180 185 190

Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu  
 195 200 205

Leu Ser  
 210

&lt;210&gt; 45

&lt;211&gt; 1269

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1246)

&lt;223&gt; RXA00340

&lt;400&gt; 45

cggtatctcc gacatccgca acacccccaa agatgaggtt ccacagtgcc cagaatgtgg 60

ctcttacctc atcactgaca tctcttagaa agaccacca gtg aaa tta gtc atc 115  
 Val Lys Leu Val Ile  
 1 5



gag gcc gac ggc ggc tcc cgc gga aac ccc ggc gtc gcc ggc tcc ggc Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly	163
10 15 20	
acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala	211
25 30 35	
tat gtt gtc gga aca aaa gcc acc aac aac gtc gcc gaa tac cgc gga Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly	259
40 45 50	
cta ctc gaa ggc ctc aaa gca gcc cgc gag ctc ggc gct acc tcc gtg Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val	307
55 60 65	
gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg	355
70 75 80 85	
tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys	403
90 95 100	
gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg	451
105 110 115	
gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala	499
120 125 130	
gca gcg gca ggt aag ccg gta ggt gtt gta ggg gat tct gct tct gta Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly Asp Ser Ala Ser Val	547
135 140 145	
tct tct gct tct tcg gtt gcg ggc tca gag aaa gaa gac ctc aac tgc Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys Glu Asp Leu Asn Cys	595
150 155 160 165	
acc gaa acc aaa ccc acc aac tgg aac ggc gca acc aca gat ccc act Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala Thr Thr Asp Pro Thr	643
170 175 180	
cgt ttc ttg ttg ctt cgc cac ggc caa act gct atg tca gtg gca cgc Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala Met Ser Val Ala Arg	691
185 190 195	
ctt tac tcc ggt agg tcc aac cca gag ctg tct gaa ctt ggt gaa aaa Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser Glu Leu Gly Glu Lys	739
200 205 210	
caa gca gca gcg gca gca cga cga ctc gct caa acc ggt ggc atc gac Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln Thr Gly Gly Ile Asp	787
215 220 225	
gct att gtg agt tct ccg ctc acc cgc acg atg caa acc gca gaa gca Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met Gln Thr Ala Glu Ala	835
230 235 240 245	

gca gcg gcc gca ctg gga atg aaa gta cgt gtt atc gat gat ctc atc 883  
 Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val Ile Asp Asp Leu Ile  
 250 255 260

gaa act gac ttt gga ctg tgg gat gga aaa tca ttt tca gaa gcc cac 931  
 Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser Phe Ser Glu Ala His  
 265 270 275

gaa caa gat cca gaa ctg cac acc aag tgg ctc act gac tca tct gta 979  
 Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val  
 280 285 290

gcc cca ccc ggt ggt gag tcc ctg cag acg gtt aat cga cgt gtg aaa 1027  
 Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val Asn Arg Arg Val Lys  
 295 300 305

aag gct cgt gaa agc ctc caa cgc gaa tac ggt gca gcg aat gtt ttg 1075  
 Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu  
 310 315 320 325

gtg gtc agc cac gtc acc cca atc aaa gcc atc atg agg caa gca ttg 1123  
 Val Val Ser His Val Thr Pro Ile Lys Ala Ile Met Arg Gln Ala Leu  
 330 335 340

gac gca ggc cca tcc ttc ttt cag aag gca cac ctt gac ttg gcg tcg 1171  
 Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser  
 345 350 355

ctg tcg atc gca gag ttt tac gaa gac ggc cca acc tgc gta aga ctg 1219  
 Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu  
 360 365 370

ttc aac gac acc tca cac ctg gaa gcg tgacgacagt ctgacggaag 1266  
 Phe Asn Asp Thr Ser His Leu Glu Ala  
 375 380

ctc 1269

&lt;210&gt; 46

&lt;211&gt; 382

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 46

Val Lys Leu Val Ile Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly  
 1 5 10 15

Val Ala Gly Ser Gly Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val  
 20 25 30

Leu Lys Glu Ile Ala Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val  
 35 40 45

Ala Glu Tyr Arg Gly Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu  
 50 55 60

Gly Ala Thr Ser Val Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu  
 65 70 75 80

Gln Met Ser Gly Arg Trp Lys Ile Lys His Pro Asp Met Lys Val Leu

85										90					95				
Ala	Ile	Glu	Ala	Lys	Glu	Ile	Ala	Ser	Glu	Ile	Gly	Ser	Val	Ser	Tyr				
			100					105					110						
Thr	Trp	Ile	Pro	Arg	Glu	Lys	Asn	Lys	Arg	Ala	Asp	Ala	Leu	Ser	Asn				
		115					120					125							
Val	Ala	Met	Asp	Ala	Ala	Ala	Ala	Gly	Lys	Pro	Val	Gly	Val	Val	Gly				
	130					135					140								
Asp	Ser	Ala	Ser	Val	Ser	Ser	Ala	Ser	Ser	Val	Ala	Gly	Ser	Glu	Lys				
145					150					155					160				
Glu	Asp	Leu	Asn	Cys	Thr	Glu	Thr	Lys	Pro	Thr	Asn	Trp	Asn	Gly	Ala				
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Thr	Thr	Asp	Pro	Thr	Arg	Phe	Leu	Leu	Leu	Arg	His	Gly	Gln	Thr	Ala				
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Met	Ser	Val	Ala	Arg	Leu	Tyr	Ser	Gly	Arg	Ser	Asn	Pro	Glu	Leu	Ser				
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Glu	Leu	Gly	Glu	Lys	Gln	Ala	Ala	Ala	Ala	Ala	Arg	Arg	Leu	Ala	Gln				
	210					215					220								
Thr	Gly	Gly	Ile	Asp	Ala	Ile	Val	Ser	Ser	Pro	Leu	Thr	Arg	Thr	Met				
225					230					235					240				
Gln	Thr	Ala	Glu	Ala	Ala	Ala	Ala	Ala	Leu	Gly	Met	Lys	Val	Arg	Val				
			245						250					255					
Ile	Asp	Asp	Leu	Ile	Glu	Thr	Asp	Phe	Gly	Leu	Trp	Asp	Gly	Lys	Ser				
			260					265					270						
Phe	Ser	Glu	Ala	His	Glu	Gln	Asp	Pro	Glu	Leu	His	Thr	Lys	Trp	Leu				
		275					280					285							
Thr	Asp	Ser	Ser	Val	Ala	Pro	Pro	Gly	Gly	Glu	Ser	Leu	Gln	Thr	Val				
	290					295					300								
Asn	Arg	Arg	Val	Lys	Lys	Ala	Arg	Glu	Ser	Leu	Gln	Arg	Glu	Tyr	Gly				
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Ala	Ala	Asn	Val	Leu	Val	Val	Ser	His	Val	Thr	Pro	Ile	Lys	Ala	Ile				
			325						330					335					
Met	Arg	Gln	Ala	Leu	Asp	Ala	Gly	Pro	Ser	Phe	Phe	Gln	Lys	Ala	His				
			340					345					350						
Leu	Asp	Leu	Ala	Ser	Leu	Ser	Ile	Ala	Glu	Phe	Tyr	Glu	Asp	Gly	Pro				
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Thr	Cys	Val	Arg	Leu	Phe	Asn	Asp	Thr	Ser	His	Leu	Glu	Ala						
	370					375					380								

&lt;210&gt; 47

&lt;211&gt; 840

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(817)

&lt;223&gt; RXA02492

&lt;400&gt; 47

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aaacgcgcgt cgtggaacat aaagtggcaa actagtagctt atg act aac gga aaa 115
                                         Met Thr Asn Gly Lys
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ttg att ctt ctt cgt cac ggt cag agc gaa tgg aac gca tcc aac cag 163
Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp Asn Ala Ser Asn Gln
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Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu Gln Gly Glu Ala Glu
                               25                               30                               35

gcc aaa ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgt cgc 259
Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg
                               40                               45                               50

gcg atc cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg 307
Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp
                               55                               60                               65

atc cca gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca 355
Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala
                               70                               75                               80                               85

ctg cag ggc ctt gac aag gct gca acc aag gaa aaa tac ggc gac gac 403
Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp
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cag ttc atg gaa tgg cgc cgc tcc tac gac acc cca cca cca gag ctc 451
Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu
                               105                               110                               115

gcg gat gac gca gag tac tcc cag gca aat gac cct cgt tac gcg gac 499
Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp
                               120                               125                               130

ctc gac gta gtt cca cgc acc gaa tgc ctc aag gac gtt gtg gtt cgt 547
Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg
                               135                               140                               145

ttt gtt cct tac ttc gag gaa gaa atc ctg cca cgc gca aag aag ggc 595
Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly
                               150                               155                               160                               165

gaa acc gtc ctc atc gca gca cac ggc aac tcc ctg cgt gcg ctg gtt 643
Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val
                               170                               175                               180

aag cac ctt gac ggc atc tcc gat gct gat atc gca gag ctc aac atc 691
Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile
                               185                               190                               195

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cca acc ggc atc cca ctg gtc tac gaa atc gcc gaa gac ggt tcc gta 739  
 Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala Glu Asp Gly Ser Val  
           200                                  205                                  210

gta aac cca ggc ggc acc tac ctc gat cct gag gca gca gca gcc ggc 787  
 Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly  
           215                                  220                                  225

gca gca gca gta gca aac cag ggt aat aag tagctatttg taggtgagca 837  
 Ala Ala Ala Val Ala Asn Gln Gly Asn Lys  
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ctc 840

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 <213> Corynebacterium glutamicum

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                                   20                                  25                                  30

Gln Gly Glu Ala Glu Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr  
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Ser Leu Leu Arg Arg Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala  
           50                                  55                                  60

Ala Asp Arg His Trp Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu  
           65                                  70                                  75                                  80

Arg His Tyr Gly Ala Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu  
                                   85                                  90                                  95

Lys Tyr Gly Asp Asp Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr  
                                   100                                  105                                  110

Pro Pro Pro Glu Leu Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp  
           115                                  120                                  125

Pro Arg Tyr Ala Asp Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys  
           130                                  135                                  140

Asp Val Val Val Arg Phe Val Pro Tyr Phe Glu Glu Ile Leu Pro  
           145                                  150                                  155                                  160

Arg Ala Lys Lys Gly Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser  
                                   165                                  170                                  175

Leu Arg Ala Leu Val Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile  
                                   180                                  185                                  190

Ala Glu Leu Asn Ile Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala  
           195                                  200                                  205

Glu Asp Gly Ser Val Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu

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 Met Thr Gln Thr Ile  
 1 5

gtc cat cta gtt cgc cac ggc gaa gtc cac aac cca gag aaa atc ctg 163  
 Val His Leu Val Arg His Gly Glu Val His Asn Pro Glu Lys Ile Leu  
 10 15 20

tac gga cgc atg ccc gga tac agg ttg tct tcc cgt gga cgc agc caa 211  
 Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser Arg Gly Arg Ser Gln  
 25 30 35

gcc gcc cgc act gca gct tct ttt gaa ggc cac gat gtc acc tac att 259  
 Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His Asp Val Thr Tyr Ile  
 40 45 50

gcg gcc tcc cca ttg cag cgt gtg cag gaa acc tcc gaa ccg ttc atc 307  
 Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr Ser Glu Pro Phe Ile  
 55 60 65

aag gtc aca ggc cta gaa ctg atc acc gac gag gat ctt ctg gaa gca 355  
 Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala  
 70 75 80 85

ggc aac cgt ttc gaa ggc ctg cgc acc aaa ggt tgg cgt tcc cag ttg 403  
 Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu  
 90 95 100

tgg aac ccc gtg cgt tgg cct ttg atg tac aac ccc acg ctt ccc agc 451  
 Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser  
 105 110 115

tgg ggc gaa cac tac acc gac att ttg gaa aga atg atg gcg gct gtg 499  
 Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg Met Met Ala Ala Val  
 120 125 130

gaa cga gct cgg gtg gca gcg gaa gga cac gaa gca atc ctg gtg acc 547  
 Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu Ala Ile Leu Val Thr  
 135 140 145

cac cag ttg ccg atc gtg tgc gtg caa cgc cac gcc cgc gga caa agc 595  
 His Gln Leu Pro Ile Val Cys Val Gln Arg His Ala Arg Gly Gln Ser

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<210> 50
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<212> PRT
<213> Corynebacterium glutamicum
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			20					25					30		
Arg	Gly	Arg	Ser	Gln	Ala	Ala	Arg	Thr	Ala	Ala	Ser	Phe	Glu	Gly	His
		35					40					45			
Asp	Val	Thr	Tyr	Ile	Ala	Ala	Ser	Pro	Leu	Gln	Arg	Val	Gln	Glu	Thr
	50					55					60				
Ser	Glu	Pro	Phe	Ile	Lys	Val	Thr	Gly	Leu	Glu	Leu	Ile	Thr	Asp	Glu
65					70					75					80
Asp	Leu	Leu	Glu	Ala	Gly	Asn	Arg	Phe	Glu	Gly	Leu	Arg	Thr	Lys	Gly
				85					90					95	
Trp	Arg	Ser	Gln	Leu	Trp	Asn	Pro	Val	Arg	Trp	Pro	Leu	Met	Tyr	Asn
			100					105					110		
Pro	Thr	Leu	Pro	Ser	Trp	Gly	Glu	His	Tyr	Thr	Asp	Ile	Leu	Glu	Arg
		115					120					125			
Met	Met	Ala	Ala	Val	Glu	Arg	Ala	Arg	Val	Ala	Ala	Glu	Gly	His	Glu
		130				135					140				
Ala	Ile	Leu	Val	Thr	His	Gln	Leu	Pro	Ile	Val	Cys	Val	Gln	Arg	His
145					150					155					160
Ala	Arg	Gly	Gln	Ser	Leu	Ser	His	Asn	Pro	Ala	Thr	Arg	Gln	Cys	Asp
				165					170					175	
Leu	Ala	Ser	Val	Thr	Ser	Leu	Val	Phe	Gln	Asp	Asp	Gln	Ile	Val	Gly
			180					185					190		
Val	His	Tyr	Asn	Glu	Pro	Ala	Gln	Glu	Ile						
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Met Leu His Val Met															5
1															
aag ccg ggt tca cac gca gct gcc gaa aag act caa tcc act gtg gtt	163														
Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr Gln Ser Thr Val Val	20														
10 15															
tta ctc att cgg cat ggg caa acc cca aca act ggt cag gtt ctg cct	211														
Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr Gly Gln Val Leu Pro	35														
25 30															
ggt cag acg ccg ggt tta cac ctg tct gat aag ggt gaa gag cag gcg	259														
Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys Gly Glu Glu Gln Ala	50														
40 45															
cgg gag gtg gca cag cgt ctg gcg gag gtg ccg att acc gct gtg tat	307														
Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro Ile Thr Ala Val Tyr	65														
55 60															
tca tcg ccg atg gag cgt gcg cag gaa aca gca gca ccg acg gtc agc	355														
Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala Ala Pro Thr Val Ser	85														
70 75 80															
gct cat ggc ctc gag ttg acg gtg gaa cct ggg ctt att gaa tgc gat	403														
Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly Leu Ile Glu Cys Asp	100														
90 95															
ttc ggc gag tgg acg ggc cgg aaa cta act gag ctc aat gcc cta gag	451														
Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu Leu Asn Ala Leu Glu	115														
105 110															
gag tgg aaa gcg gtg cag aag aca ccg tct acc ttc agg ttt cca ggt	499														
Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr Phe Arg Phe Pro Gly	130														
120 125															
ggt gag agt ttc gtg gaa atg cag gat cgg atg gtg gag gct atc ggc	547														
Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met Val Glu Ala Ile Gly	145														
135 140															
aac att gcg cag cag cat ccg gga gaa atc gtt gct gcg ttt agt cat	595														
Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val Ala Ala Phe Ser His	165														
150 155 160															
gcc gac acg atc aag gct gcg gtg gct cat ttt gta ggc act cca ctg	643														
Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe Val Gly Thr Pro Leu	180														
170 175															



gat tct ttt cag cgc att ttc atc gac acg gcg tca att tcc gca gtg 691  
 Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala Ser Ile Ser Ala Val  
                   185                                  190                                  195

gaa ttt acc ggg aaa tct tca ggc gtc tcc tcc cat atg ctg ctg aca 739  
 Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser His Met Leu Leu Thr  
                   200                                  205                                  210

aat tcc aga aca gga tcg ttg gga tac ctt cga gac aaa ctt ccg aaa 787  
 Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg Asp Lys Leu Pro Lys  
                   215                                  220                                  225

gct ccg caa cca tgatcacctc accatttgag cgc 822  
 Ala Pro Gln Pro  
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<210> 52

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

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Gln Ser Thr Val Val Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr  
                   20                                  25                                  30

Gly Gln Val Leu Pro Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys  
                   35                                  40                                  45

Gly Glu Glu Gln Ala Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro  
                   50                                  55                                  60

Ile Thr Ala Val Tyr Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala  
                   65                                  70                                  75                                  80

Ala Pro Thr Val Ser Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly  
                   85                                  90                                  95

Leu Ile Glu Cys Asp Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu  
                   100                                  105                                  110

Leu Asn Ala Leu Glu Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr  
                   115                                  120                                  125

Phe Arg Phe Pro Gly Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met  
                   130                                  135                                  140

Val Glu Ala Ile Gly Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val  
                   145                                  150                                  155                                  160

Ala Ala Phe Ser His Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe  
                   165                                  170                                  175

Val Gly Thr Pro Leu Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala  
                   180                                  185                                  190

Ser Ile Ser Ala Val Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser  
                   195                                  200                                  205

His Met Leu Leu Thr Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg  
 210 215 220

Asp Lys Leu Pro Lys Ala Pro Gln Pro  
 225 230

<210> 53

<211> 1161

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1138)

<223> RXA00206

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 Met Glu Asp Met Arg  
 1 5

att gct act ctc acg tca ggc ggc gac tgc ccc gga cta aac gcc gtc 163  
 Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val  
 10 15 20

atc cga gga atc gtc cgc aca gcc agc aat gaa ttt ggc tcc acc gtc 211  
 Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val  
 25 30 35

gtt ggt tat caa gac ggt tgg gaa gga ctg tta ggc gat cgt cgc gta 259  
 Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg Arg Val  
 40 45 50

cag ctg tat gac gat gaa gat att gac cga atc ctc ctt cga ggc ggc 307  
 Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly  
 55 60 65

acc att ttg ggc act ggt cgc ctc cat ccg gac aag ttt aag gcc gga 355  
 Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys Ala Gly  
 70 75 80 85

att gat cag att aag gcc aac tta gaa gac gcc ggc atc gat gcc ctt 403  
 Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp Ala Leu  
 90 95 100

atc cca atc ggt ggc gaa gga acc ctg aag ggt gcc aag tgg ctg tct 451  
 Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ser  
 105 110 115

gat aac ggt atc cct gtt gtc ggt gtc cca aag acc att gac aat gac 499  
 Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp  
 120 125 130

gtg aat ggc act gac ttc acc ttc ggt ttc gat act gct gtg gca gtg 547  
 Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val Ala Val  
 135 140 145

gct acc gac gct gtt gac cgc ctg cac acc acc gct gaa tct cac aac 595  
 Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser His Asn  
 150 155 160 165

cgt gtg atg atc gtg gag gtc atg ggc cgc cac gtg ggt tgg att gct 643  
 Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala  
 170 175 180

ctg cac gca ggt atg gcc ggc ggt gct cac tac acc gtt att cca gaa 691  
 Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu  
 185 190 195

gta cct ttc gat att gca gag atc tgc aag gcg atg gaa cgt cgc ttc 739  
 Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg Arg Phe  
 200 205 210

cag atg ggc gag aag tac ggc att atc gtc gtt gcg gaa ggt gcg ttg 787  
 Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu  
 215 220 225

cca cgc gaa ggc acc atg gag ctt cgt gaa ggc cac att gac cag ttc 835  
 Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe  
 230 235 240 245

ggt cac aag acc ttc acg gga att gga cag cag atc gct gat gag atc 883  
 Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Ile  
 250 255 260

cac gtg cgc ctc ggc cac gat gtt cgt acg acc gtt ctt ggc cac att 931  
 His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile  
 265 270 275

caa cgt ggt gga acc cca act gct ttc gac cgt gtt ctg gcc act cgt 979  
 Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg  
 280 285 290

tat ggt gtt cgt gca gct cgt gcg tgc cat gag gga agc ttt gac aag 1027  
 Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys  
 295 300 305

gtt gtt gct ttg aag ggt gag agc att gag atg atc acc ttt gaa gaa 1075  
 Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu  
 310 315 320 325

gca gtc gga acc ttg aag gaa gtt cca ttc gaa cgc tgg gtt act gcc 1123  
 Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val Thr Ala  
 330 335 340

cag gca atg ttt gga tagtttttcg ggctttttatc aac 1161  
 Gln Ala Met Phe Gly  
 345

&lt;210&gt; 54

&lt;211&gt; 346

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 54

Met Glu Asp Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro  
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Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu  
 20 25 30  
 Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu  
 35 40 45  
 Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile  
 50 55 60  
 Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp  
 65 70 75 80  
 Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala  
 85 90 95  
 Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly  
 100 105 110  
 Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys  
 115 120 125  
 Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp  
 130 135 140  
 Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr  
 145 150 155 160  
 Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His  
 165 170 175  
 Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr  
 180 185 190  
 Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala  
 195 200 205  
 Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val  
 210 215 220  
 Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly  
 225 230 235 240  
 His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln  
 245 250 255  
 Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr  
 260 265 270  
 Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg  
 275 280 285  
 Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu  
 290 295 300  
 Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met  
 305 310 315 320  
 Ile Thr Phe Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu  
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Arg Trp Val Thr Ala Gln Ala Met Phe Gly  
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 <211> 1083  
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 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1060)  
 <223> RXA01243

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 Met Ile Leu Thr Val  
 1 5  
 act gca agt ccg tat ctg ttg agc acc aat gag ctt gac ggc acc atc 163  
 Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu Leu Asp Gly Thr Ile  
 10 15 20  
 gaa att ggc gaa gca aac aaa atc cgg cag gtt tcc act gtt gcc ggt 211  
 Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val Ser Thr Val Ala Gly  
 25 30 35  
 ggt ttt ggc acc ggt gtg gct gcc acc ttg ttt tat ggc ggc aat gaa 259  
 Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe Tyr Gly Gly Asn Glu  
 40 45 50  
 act ttt gca gtt ttt ccc gct cca gaa atc tct cat tac atg cgc ctg 307  
 Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser His Tyr Met Arg Leu  
 55 60 65  
 gtg acg ttt gct ggg ttg cct cat gaa att att ccg gtg gca ggt ccc 355  
 Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile Pro Val Ala Gly Pro  
 70 75 80 85  
 atc ccc atg cat ttg acc atg cgt gat gca gag ggc aat gag act aag 403  
 Ile Pro Met His Leu Thr Met Arg Asp Ala Glu Gly Asn Glu Thr Lys  
 90 95 100  
 ttc aaa gac tcc ccc atg cct ttg gat gtg tcc cag ttg gca att ctt 451  
 Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser Gln Leu Ala Ile Leu  
 105 110 115  
 cgt gat cta gtg gtg cgt cga gcc gaa gat gcc gcg tgg gtg ttg ttg 499  
 Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala Ala Trp Val Leu Leu  
 120 125 130  
 ggt ggc aat ttg ccg tct atc gcg cct gct gcg tgg ttt gtg gat gtg 547  
 Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala Trp Phe Val Asp Val  
 135 140 145  
 gtg aga tca ctt cgc ttg tac cac cct cat gtg aag gta gct atc gca 595  
 Val Arg Ser Leu Arg Leu Tyr His Pro His Val Lys Val Ala Ile Ala  
 150 155 160 165

gca act ggt gct gcg ttg cgt gcg gtt att cga cag ctt gca gct acg 643  
 Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg Gln Leu Ala Ala Thr  
 170 175 180

tcc ccg gat gcg ctg att gtg gct gcg gaa gaa atc gaa att gcc act 691  
 Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu Ile Glu Ile Ala Thr  
 185 190 195

gga tta gaa ccc aaa acc ttg aga ggt cca tgg gta gag gga gat ctc 739  
 Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp Val Glu Gly Asp Leu  
 200 205 210

tcc ccg act gtg gcg gca gcg cgc gct tta att gat agc ggt gtc acc 787  
 Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile Asp Ser Gly Val Thr  
 215 220 225

gag gtg ttg gtt acc aac aag cgg acg gaa tct ttg tat gtt tcc gag 835  
 Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser Leu Tyr Val Ser Glu  
 230 235 240 245

tct gaa tca ctg tta gcc agc tac gac agc acc cct ggt aag cag ggc 883  
 Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr Pro Gly Lys Gln Gly  
 250 255 260

gtg aat tgg cgg gaa tct ttt act gca gga ttc ttg gca gca tcc aat 931  
 Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe Leu Ala Ala Ser Asn  
 265 270 275

gat gga aaa tcc act gag gac agc gtg atc aac gcg gtt gct tac gcc 979  
 Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn Ala Val Ala Tyr Ala  
 280 285 290

aac gct gaa ggc agt gag tgg gac aac tac att ccc aca ccc gat aag 1027  
 Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile Pro Thr Pro Asp Lys  
 295 300 305

ctt cgg gcg gag cac gtg gtc atc aaa tcg ctt tagaccacgc aaaaagcctc 1080  
 Leu Arg Ala Glu His Val Val Ile Lys Ser Leu  
 310 315 320

aaa 1083

&lt;210&gt; 56

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 56

Met Ile Leu Thr Val Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu  
 1 5 10 15

Leu Asp Gly Thr Ile Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val  
 20 25 30

Ser Thr Val Ala Gly Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe  
 35 40 45

Tyr Gly Gly Asn Glu Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser  
 50 55 60

His Tyr Met Arg Leu Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile  
 65 70 75 80  
 Pro Val Ala Gly Pro Ile Pro Met His Leu Thr Met Arg Asp Ala Glu  
 85 90 95  
 Gly Asn Glu Thr Lys Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser  
 100 105 110  
 Gln Leu Ala Ile Leu Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala  
 115 120 125  
 Ala Trp Val Leu Leu Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala  
 130 135 140  
 Trp Phe Val Asp Val Val Arg Ser Leu Arg Leu Tyr His Pro His Val  
 145 150 155 160  
 Lys Val Ala Ile Ala Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg  
 165 170 175  
 Gln Leu Ala Ala Thr Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu  
 180 185 190  
 Ile Glu Ile Ala Thr Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp  
 195 200 205  
 Val Glu Gly Asp Leu Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile  
 210 215 220  
 Asp Ser Gly Val Thr Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser  
 225 230 235 240  
 Leu Tyr Val Ser Glu Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr  
 245 250 255  
 Pro Gly Lys Gln Gly Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe  
 260 265 270  
 Leu Ala Ala Ser Asn Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn  
 275 280 285  
 Ala Val Ala Tyr Ala Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile  
 290 295 300  
 Pro Thr Pro Asp Lys Leu Arg Ala Glu His Val Val Ile Lys Ser Leu  
 305 310 315 320

<210> 57

<211> 1113

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1090)

<223> RXA01882

&lt;400&gt; 57

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ttccagtttt gcccgaccac aactttcagg tggtaacccc atg atc atc aca ttc 115
                                   Met Ile Ile Thr Phe
                                   1 5

acc cca aac ccg agt att gat tcc acg ctg tcg ctc ggc gaa gag ctc 163
Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu
                                   10 15 20

tcc cgt gga tcc gtc caa cga ctt gat tcc gtc acc gct gtc gca ggt 211
Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly
                                   25 30 35

ggt aaa ggc atc aat gtc gcc cac gct gtc ttg ctt gcg ggc ttt gaa 259
Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu
                                   40 45 50

acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg 307
Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu
                                   55 60 65

gtc cgc gac atc ggc ttg ccc gtg gaa act gtt gtg atc aac aag aac 355
Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn
                                   70 75 80 85

gtc cgc acc aac acc aca gtc acc gaa ccg gac ggc acc acc acc aag 403
Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys
                                   90 95 100

ctc aac ggc ccc ggc gcg ccg ctc agc gag cag aag ctc cgt agc ttg 451
Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln Lys Leu Arg Ser Leu
                                   105 110 115

gaa aag gtg ctt atc gac gcg ctc cgc ccc gaa gtc acc tgg gtt gtc 499
Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu Val Thr Trp Val Val
                                   120 125 130

ctg gcg ggc tcg ctg cca cca ggg gca cca gtt gac tgg tac gcg cgt 547
Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val Asp Trp Tyr Ala Arg
                                   135 140 145

ctc acc gcg ttg atc cat tca gca cgc cct gac gtt cgc gtg gct gtc 595
Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp Val Arg Val Ala Val
                                   150 155 160 165

gat acc tca gac aag cca ctg atg gcg ttg ggc gag agc ttg gat aca 643
Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly Glu Ser Leu Asp Thr
                                   170 175 180

cct ggc gct gct ccg aac ctg att aag cca aat ggt ctg gaa ctg ggc 691
Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn Gly Leu Glu Leu Gly
                                   185 190 195

cag ctg gct aac act gat ggt gaa gag ctg gag gcg cgt gct gcg caa 739
Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu Ala Arg Ala Ala Gln
                                   200 205 210

ggc gat tac gac gcc atc atc gca gct gcg gac gta ctg gtt aac cgt 787

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Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp Val Leu Val Asn Arg  
 215 220 225  
 ggc atc gaa cag gtg ctt gtc acc ttg ggt gcc gca gga gcg gtg ttg 835  
 Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala Ala Gly Ala Val Leu  
 230 235 240 245  
 gtc aac gca gaa ggt gcg tgg act gct act tct cca aag att gat gtt 883  
 Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser Pro Lys Ile Asp Val  
 250 255 260  
 gta tcc acc gtt gga gct gga gac tgt gct ctt gca ggt ttt gtt atg 931  
 Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu Ala Gly Phe Val Met  
 265 270 275  
 gca cgt tcc cag aag aaa aca ctg gag gaa tct ctg ctg aat gcc gtg 979  
 Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser Leu Leu Asn Ala Val  
 280 285 290  
 tct tac ggc tcg act gcg gcg tct ctt cct ggc act acc att cct cgt 1027  
 Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly Thr Thr Ile Pro Arg  
 295 300 305  
 cct gac caa ctc gcc aca gct ggt gca acg gtc acc caa gtc aaa gga 1075  
 Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val Thr Gln Val Lys Gly  
 310 315 320 325  
 ttg aaa gaa tca gca tgaatagcgt aaataattcc tcg 1113  
 Leu Lys Glu Ser Ala  
 330

&lt;210&gt; 58

&lt;211&gt; 330

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 58

Met Ile Ile Thr Phe Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser  
 1 5 10 15

Leu Gly Glu Glu Leu Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val  
 20 25 30

Thr Ala Val Ala Gly Gly Lys Gly Ile Asn Val Ala His Ala Val Leu  
 35 40 45

Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp  
 50 55 60

Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val  
 65 70 75 80

Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp  
 85 90 95

Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln  
 100 105 110

Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu  
 115 120 125

Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val  
 130 135 140  
 Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp  
 145 150 155 160  
 Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly  
 165 170 175  
 Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn  
 180 185 190  
 Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu  
 195 200 205  
 Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp  
 210 215 220  
 Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala  
 225 230 235 240  
 Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser  
 245 250 255  
 Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu  
 260 265 270  
 Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser  
 275 280 285  
 Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly  
 290 295 300  
 Thr Thr Ile Pro Arg Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val  
 305 310 315 320  
 Thr Gln Val Lys Gly Leu Lys Glu Ser Ala  
 325 330

<210> 59  
 <211> 1155  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1132)  
 <223> RXA01702

<400> 59  
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acatagttca gtgacagtca ccttttggag gagacacctt atg cct atc gca act 115  
 Met Pro Ile Ala Thr  
 1 5

ccc gag gtc tat aac gag atg ctc gat cgt gct aag gaa ggc gga ttc 163  
 Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala Lys Glu Gly Gly Phe  
 10 15 20

gcc ttc cca gcc atc aac tgc acc tcc tcg gaa acc atc aac gca gct	211
Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu Thr Ile Asn Ala Ala	
25 30 35	
ctc aag ggc ttc gca gag gct gaa tct gac gga atc atc cag ttc tcc	259
Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly Ile Ile Gln Phe Ser	
40 45 50	
acc ggt ggt gca gag ttc ggt tcc ggc ctg gca gta aag aac aag gtc	307
Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala Val Lys Asn Lys Val	
55 60 65	
aag ggc gca gtt gcg ctt gca gcc ttc gcc cac gag gca gca aag agc	355
Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His Glu Ala Ala Lys Ser	
70 75 80 85	
tac ggc atc aac gtt gct ctg cac act gac cac tgc cag aag gaa gtc	403
Tyr Gly Ile Asn Val Ala Leu His Thr Asp His Cys Gln Lys Glu Val	
90 95 100	
ctg gac gag tac gtc cgc cca ctg ctg gct atc tcc cag gag cgc gtc	451
Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile Ser Gln Glu Arg Val	
105 110 115	
gac cgc ggc gag ctt cca ctg ttc cag tcc cac atg tgg gat ggt tcc	499
Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His Met Trp Asp Gly Ser	
120 125 130	
gct gtc cca atc gac gag aac ctc gaa atc gca cag gag ctg ctg gct	547
Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala Gln Glu Leu Leu Ala	
135 140 145	
aag gcc aag gca gcg aac atc atc ttg gaa gtt gag atc ggt gtt gtc	595
Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val Glu Ile Gly Val Val	
150 155 160 165	
ggt ggc gaa gaa gac ggc gtt gag gct aag gct ggc gca aac ctc tac	643
Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala Gly Ala Asn Leu Tyr	
170 175 180	
acc tcc cca gaa gac ttt gag aag acc atc gat gca atc ggc acc ggt	691
Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp Ala Ile Gly Thr Gly	
185 190 195	
gag aag ggc cgc tac ctg cta gca gct acc ttc ggt aac gtc cac ggc	739
Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe Gly Asn Val His Gly	
200 205 210	
ggt tac aag cca ggc aac gtc aag ctg cgc cca gag gtc ctc ctt gag	787
Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro Glu Val Leu Leu Glu	
215 220 225	
ggc cag cag gtt gca cgc aag aag ctt gga ctt gca gac gac gca ctt	835
Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu Ala Asp Asp Ala Leu	
230 235 240 245	
cca ttc gac ttc gtc ttc cac ggt ggc tca ggc tcc gag aag gaa aag	883
Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly Ser Glu Lys Glu Lys	
250 255 260	

atc gaa gag gcg ctg acc tac ggc gtc atc aag atg aac gtt gat act 931  
 Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys Met Asn Val Asp Thr  
                   265                                  270                                  275

gac acc cag tac gca ttc acc cgc cca atc gtc tcc cac atg ttt gag 979  
 Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val Ser His Met Phe Glu  
                   280                                  285                                  290

aac tac aac ggc gtt ctc aag atc gac ggc gag gtc gga aac aag aag 1027  
 Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu Val Gly Asn Lys Lys  
                   295                                  300                                  305

gct tac gac cca cgc tct tac atg aag aag gct gag cag agc atg tct 1075  
 Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala Glu Gln Ser Met Ser  
 310                                  315                                  320                                  325

gag cgc att atc gag tct tgc cag gac ctc aag tct gtt gga aag acc 1123  
 Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys Ser Val Gly Lys Thr  
                   330                                  335                                  340

acc tct aag taatctcagc agttaaaaag ggc 1155  
 Thr Ser Lys

&lt;210&gt; 60

&lt;211&gt; 344

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 60

Met Pro Ile Ala Thr Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala  
   1                                  5                                  10                                  15

Lys Glu Gly Gly Phe Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu  
                   20                                  25                                  30

Thr Ile Asn Ala Ala Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly  
                   35                                  40                                  45

Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala  
                   50                                  55                                  60

Val Lys Asn Lys Val Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His  
   65                                  70                                  75                                  80

Glu Ala Ala Lys Ser Tyr Gly Ile Asn Val Ala Leu His Thr Asp His  
                   85                                  90                                  95

Cys Gln Lys Glu Val Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile  
                   100                                  105                                  110

Ser Gln Glu Arg Val Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His  
                   115                                  120                                  125

Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala  
   130                                  135                                  140

Gln Glu Leu Leu Ala Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val  
   145                                  150                                  155                                  160

Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala  
 165 170 175  
 Gly Ala Asn Leu Tyr Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp  
 180 185 190  
 Ala Ile Gly Thr Gly Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe  
 195 200 205  
 Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro  
 210 215 220  
 Glu Val Leu Leu Glu Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu  
 225 230 235 240  
 Ala Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly  
 245 250 255  
 Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys  
 260 265 270  
 Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val  
 275 280 285  
 Ser His Met Phe Glu Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu  
 290 295 300  
 Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala  
 305 310 315 320  
 Glu Gln Ser Met Ser Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys  
 325 330 335  
 Ser Val Gly Lys Thr Thr Ser Lys  
 340

<210> 61  
 <211> 900  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(877)  
 <223> RXA02258

<400> 61  
 cgttgcaatt ctcgctcagt aaatccgaca cggccctttg ttagaaaaca aaacataaag 60  
 ggccaccggg aaactttttt aagaaaggtg tgtttcacac atg gca cgt aag cca 115  
 Met Ala Arg Lys Pro  
 1 5  
 ctt atc gct ggt aac tgg aag atg aac ctg gat cac cag cag gca atc 163  
 Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp His Gln Gln Ala Ile  
 10 15 20  
 ggc act gtt cag aag ctt gca ttc gcc ctt cca aag gaa tac ttc gag 211  
 Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro Lys Glu Tyr Phe Glu  
 25 30 35

aag gtt gac gtt gca gtc acc gtt cct ttc act gac atc cgc tcc gtc	259
Lys Val Asp Val Ala Val Thr Val Pro Phe Thr Asp Ile Arg Ser Val	
40 45 50	
cag act ctc gtt gag ggc gac aag ctt gag gtc act ttc ggt gct cag	307
Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val Thr Phe Gly Ala Gln	
55 60 65	
gac gtc tcc cag cac gag tcc ggt gcg tac acc ggt gaa gtt tct gca	355
Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr Gly Glu Val Ser Ala	
70 75 80 85	
agc atg ctg gca aag ttg aac tgc tct tgg gtt gtc gtt gga cac tcc	403
Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val Val Val Gly His Ser	
90 95 100	
gag cgc cgc gag tac cac aac gag tct gat gag ttg gtt gct gcg aag	451
Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu Leu Val Ala Ala Lys	
105 110 115	
gca aag gca gct ctg tcc aac ggc atc agc ccg atc gtc tgc gtt ggt	499
Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro Ile Val Cys Val Gly	
120 125 130	
gag cca ctg gaa atc cgt gaa gct ggc acc cac gtt gag tac gtc gtc	547
Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His Val Glu Tyr Val Val	
135 140 145	
gag cag acc cgt aag tcc ctt gct ggc ctg gat gct gct gag ctg gcc	595
Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp Ala Ala Glu Leu Ala	
150 155 160 165	
aac acc gtt atc gcg tat gag cca gtg tgg gct atc ggc acc ggt aag	643
Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Lys	
170 175 180	
gtt gct tcc gca gct gac gct cag gaa gtg tgc aag gct atc cgc ggt	691
Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys Lys Ala Ile Arg Gly	
185 190 195	
ctg atc gtg gag ctt gca ggc gac gag gtc gct gag ggc ctg cgt att	739
Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile	
200 205 210	
ctt tac ggt ggt tct gtt aag gca gaa acc gtc gct gag atc gtc ggt	787
Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val Ala Glu Ile Val Gly	
215 220 225	
cag cct gac gtc gac ggc gga ctt gtc ggt ggc gct tcc ctc gac ggt	835
Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly	
230 235 240 245	
gaa gca ttc gcc aag ctg gct gcc aac gct gcg agc gtt gct	877
Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala Ser Val Ala	
250 255	
taaagtacag agctttaag cac	900

&lt;211&gt; 259

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 62

Met Ala Arg Lys Pro Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp  
 1 5 10 15

His Gln Gln Ala Ile Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro  
 20 25 30

Lys Glu Tyr Phe Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr  
 35 40 45

Asp Ile Arg Ser Val Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val  
 50 55 60

Thr Phe Gly Ala Gln Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr  
 65 70 75 80

Gly Glu Val Ser Ala Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val  
 85 90 95

Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu  
 100 105 110

Leu Val Ala Ala Lys Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro  
 115 120 125

Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His  
 130 135 140

Val Glu Tyr Val Val Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp  
 145 150 155 160

Ala Ala Glu Leu Ala Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala  
 165 170 175

Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys  
 180 185 190

Lys Ala Ile Arg Gly Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala  
 195 200 205

Glu Gly Leu Arg Ile Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val  
 210 215 220

Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly  
 225 230 235 240

Ala Ser Leu Asp Gly Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala  
 245 250 255

Ser Val Ala

&lt;210&gt; 63

&lt;211&gt; 1563

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1540)

&lt;223&gt; RXN01225

&lt;400&gt; 63

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tttgggctaa tgttggggggg agtgcttttca actatccacg agagctgccc agtgataaac 60

cccgggttaa cccacgcct aagtcagtga aggacttttt atg acg cac aac cac 115
                                         Met Thr His Asn His
                                         1                               5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
                                         10                               15                               20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
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cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
                                         40                               45                               50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
                                         55                               60                               65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tgc atc 355
Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
                                         70                               75                               80                               85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
                                         90                               95                               100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa 451
Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
                                         105                               110                               115

acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc 499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile
                                         120                               125                               130

ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac 547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp
                                         135                               140                               145

ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac 595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp
                                         150                               155                               160                               165

ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga 643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly
                                         170                               175                               180

ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc 691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala
                                         185                               190                               195

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gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr 215 220 225	787
ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys 230 235 240 245	835
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aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln 265 270 275	931
atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu 280 285 290	979
aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr 295 300 305	1027
gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys 310 315 320 325	1075
ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu 330 335 340	1123
acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly 345 350 355	1171
aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met 360 365 370	1219
gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val 375 380 385	1267
aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln 390 395 400 405	1315
atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly 410 415 420	1363
acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly 425 430 435	1411
cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc	1459

Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser  
 440 445 450

aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1507  
 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg  
 455 460 465

gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560  
 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu  
 470 475 480

cac 1563

<210> 64  
 <211> 480  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 64  
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Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val  
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Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile  
 35 40 45

Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro  
 50 55 60

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu  
 65 70 75 80

Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu  
 85 90 95

Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro  
 100 105 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr  
 115 120 125

Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg  
 130 135 140

Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys  
 145 150 155 160

Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp  
 165 170 175

Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn  
 180 185 190

Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn  
 195 200 205

Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val  
 210 215 220

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Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
225                230                235                240

His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
                245                250                255

Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
                260                265                270

Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
                275                280                285

Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
290                295                300

Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
305                310                315                320

Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
                325                330                335

Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
                340                345                350

Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
                355                360                365

Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
                370                375                380

Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
385                390                395                400

Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
                405                410                415

Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
                420                425                430

Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
                435                440                445

Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
450                455                460

Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
465                470                475                480

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&lt;210&gt; 65

&lt;211&gt; 1563

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1540)

&lt;223&gt; FRXA01225

&lt;400&gt; 65

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cccgggttaa ccccacgcct aagtcagtga aggacttttt atg acg cac aac cac 115
                                         Met Thr His Asn His
                                         1 5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
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atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
                        25 30 35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
                        40 45 50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
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gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tgc atc 355
Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
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gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
                        90 95 100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa 451
Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
                        105 110 115

acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc 499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile
                        120 125 130

ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac 547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp
                        135 140 145

ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac 595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp
                        150 155 160 165

ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga 643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly
                        170 175 180

ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc 691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala
                        185 190 195

aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att 739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile
                        200 205 210

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ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys 250 255 260	883
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gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val 375 380 385	1267
aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln 390 395 400 405	1315
atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly 410 415 420	1363
acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly 425 430 435	1411
cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser 440 445 450	1459
aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc	1507

Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg  
 455 460 465

gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560  
 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu  
 470 475 480

cac 1563

<210> 66

<211> 480

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

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Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile  
 35 40 45

Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro  
 50 55 60

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu  
 65 70 75 80

Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu  
 85 90 95

Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro  
 100 105 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr  
 115 120 125

Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg  
 130 135 140

Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys  
 145 150 155 160

Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp  
 165 170 175

Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn  
 180 185 190

Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn  
 195 200 205

Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val  
 210 215 220

Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln  
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<210> 67
<211> 1125
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1102)
<223> RXA02256
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ggt Gly	att Ile	aac Asn	gga Gly	ttt Phe	ggc Gly	cgt Arg	atc Ile	gga Gly	cgt Arg	aac Asn	ttc Phe	ttc Phe	cgc Arg	gca Ala	gtt Val	163		
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ctg Leu	gag Glu	cgc Arg	agc Ser	gac Asp	gat Asp	ctc Leu	gag Glu	gta Val	gtt Val	gca Ala	gtc Val	aac Asn	gac Asp	ctc Leu	acc Thr	211		
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ggc Gly	aag Lys	cgc Arg	atc Ile	gct Ala	gtt Val	tac Tyr	gca Ala	gag Glu	cgc Arg	gat Asp	cca Pro	aag Lys	aac Asn	ctg Leu	gac Asp	355		
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tgg Trp	gct Ala	gca Ala	cac His	aac Asn	gtt Val	gac Asp	atc Ile	gtg Val	atc Ile	gag Glu	tcc Ser	acc Thr	ggc Gly	ttc Phe	ttc Phe	403		
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acc Thr	gat Asp	gca Ala	aac Asn	gcg Ala	gct Ala	aag Lys	gct Ala	cac His	atc Ile	gaa Glu	gca Ala	ggt Gly	gcc Ala	aag Lys	aag Lys	451		
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gtc Val	atc Ile	atc Ile	tcc Ser	gca Ala	cca Pro	gca Ala	agc Ser	aac Asn	gaa Glu	gac Asp	gca Ala	acc Thr	ttc Phe	gtt Val	tac Tyr	499		
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ggt Gly	gtg Val	aac Asn	cac His	gag Glu	tcc Ser	tac Tyr	gat Asp	cct Pro	gag Glu	aac Asn	cac His	aac Asn	gtg Val	atc Ile	tcc Ser	547		
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ggc Gly	gca Ala	tct Ser	tgc Cys	acc Thr	acc Thr	aac Asn	tgc Cys	ctc Leu	gca Ala	cca Pro	atg Met	gca Ala	aag Lys	gtc Val	cta Leu	595		
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aac Asn	gac Asp	aag Lys	ttc Phe	ggc Gly	atc Ile	gag Glu	aac Asn	ggc Gly	ctc Leu	atg Met	acc Thr	acc Thr	gtt Val	cac His	gca Ala	643		
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tac Tyr	act Thr	ggc Gly	gac Asp	cag Gln	cgc Arg	ctg Leu	cac His	gat Asp	gca Ala	cct Pro	cac His	cgc Arg	gac Asp	ctg Leu	cgt Arg	691		
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cgt Arg	gca Ala	cgt Arg	gca Ala	gca Ala	gca Ala	gtc Val	aac Asn	atc Ile	gtt Val	cct Pro	acc Thr	tcc Ser	acc Thr	ggt Gly	gca Ala	739		
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gct Ala	aag Lys	gct Ala	gtt Val	gct Ala	ctg Leu	gtt Val	ctc Leu	cca Pro	gag Glu	ctc Leu	aag Lys	ggc Gly	aag Lys	ctt Leu	gac Asp	787		
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ggc tac gca ctt cgc gtt cca gtt atc acc ggt tcc gca acc gac ctg 835  
 Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly Ser Ala Thr Asp Leu  
 230 235 240 245  
  
 acc ttc aac acc aag tct gag gtc acc gtt gag tcc atc aac gct gca 883  
 Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu Ser Ile Asn Ala Ala  
 250 255 260  
  
 atc aag gaa gct gca gtc ggc gag ttc ggc gag acc ctg gct tac tcc 931  
 Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu Thr Leu Ala Tyr Ser  
 265 270 275  
  
 gaa gag cca ctg gtt tcc acc gac atc gtc cac gat tcc cac ggc tcc 979  
 Glu Glu Pro Leu Val Ser Thr Asp Ile Val His Asp Ser His Gly Ser  
 280 285 290  
  
 atc ttc gac gct ggc ctg acc aag gtc tcc ggc aac acc gtc aag gtt 1027  
 Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly Asn Thr Val Lys Val  
 295 300 305  
  
 gtt tcc tgg tac gac aac gag tgg ggc tac acc tgc cag ctc ctg cgt 1075  
 Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr Cys Gln Leu Leu Arg  
 310 315 320 325  
  
 ctg acc gag ctc gta gct tcc aag ctc taattagttc acatcgctaa 1122  
 Leu Thr Glu Leu Val Ala Ser Lys Leu  
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 cgt 1125

&lt;210&gt; 68

&lt;211&gt; 334

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 68

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 Phe Phe Arg Ala Val Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala  
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 Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe  
 35 40 45  
  
 Asp Ser Ile Met Gly Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp  
 50 55 60  
  
 Ser Ile Thr Val Gly Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp  
 65 70 75 80  
  
 Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu  
 85 90 95  
  
 Ser Thr Gly Phe Phe Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu  
 100 105 110  
  
 Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp  
 115 120 125

Ala Thr Phe Val Tyr Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn  
 130 135 140

His Asn Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro  
 145 150 155 160

Met Ala Lys Val Leu Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met  
 165 170 175

Thr Thr Val His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro  
 180 185 190

His Arg Asp Leu Arg Arg Ala Arg Ala Ala Val Asn Ile Val Pro  
 195 200 205

Thr Ser Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu  
 210 215 220

Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly  
 225 230 235 240

Ser Ala Thr Asp Leu Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu  
 245 250 255

Ser Ile Asn Ala Ala Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu  
 260 265 270

Thr Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Thr Asp Ile Val His  
 275 280 285

Asp Ser His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly  
 290 295 300

Asn Thr Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr  
 305 310 315 320

Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu  
 325 330

<210> 69  
 <211> 1338  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1315)  
 <223> RXA02257

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 Met Ala Val Lys Thr  
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ctc aag gac ttg ctc gac gaa ggc gta gac gga cgc cac gtc atc gtt 163  
 Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly Arg His Val Ile Val  
 10 15 20

cga tct gac ttc aat gtt ccc ctc aac gat gac cgc gag atc acc gat	211
Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp Arg Glu Ile Thr Asp	
25 30 35	
aag ggc cga atc att gcc tcc cta cca acc ctt aaa gca ctg agc gaa	259
Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu Lys Ala Leu Ser Glu	
40 45 50	
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Gly Gly Ala Lys Val Ile Val Met Ala His Leu Gly Arg Pro Lys Gly	
55 60 65	
gag gtc aac gag aag tac tcc ctc gca cct gtc gct gag gca ctc tcc	355
Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val Ala Glu Ala Leu Ser	
70 75 80 85	
gat gag ctt ggc cag tac gtt gca ctt gcc gca gac gtt gtt ggc gaa	403
Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala Asp Val Val Gly Glu	
90 95 100	
gac gca cac gag cgc gca aac ggc ctg acc gag ggc gac atc ctg ctc	451
Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu Gly Asp Ile Leu Leu	
105 110 115	
ctg gag aac gtg cgc ttc gac cca cgc gaa acc tcc aag gac gag gca	499
Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr Ser Lys Asp Glu Ala	
120 125 130	
gag cgc acc gct ttc gct cag gag ctc gca gct ctt gca gca gac aac	547
Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala Leu Ala Ala Asp Asn	
135 140 145	
ggc gca ttc gtt tct gac ggc ttc ggt gtt gtc cac cgc gca cag acc	595
Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val His Arg Ala Gln Thr	
150 155 160 165	
tcc gtc tac gac att gca aag ttg ctg cca cac tac gct ggc gga ctg	643
Ser Val Tyr Asp Ile Ala Lys Leu Leu Pro His Tyr Ala Gly Gly Leu	
170 175 180	
gta gag acc gag att tcc gtt ctg gaa aag atc gca gaa tca cca gag	691
Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile Ala Glu Ser Pro Glu	
185 190 195	
gca cca tac gta gtg gtt ctc ggt gga tcc aag gtc tct gac aag atc	739
Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys Val Ser Asp Lys Ile	
200 205 210	
ggt gtt att gag gcg ctg gct gcc aag gct gac aag atc atc gtc ggt	787
Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp Lys Ile Ile Val Gly	
215 220 225	
ggc ggc atg tgc tac acc ttc ctc gca gct cag gga cac aac gtt cag	835
Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln Gly His Asn Val Gln	
230 235 240 245	
cag tcc ctc ctg cag gaa gaa atg aag gct acc tgc acc gac ctg ctc	883
Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr Cys Thr Asp Leu Leu	
250 255 260	
gca cgc ttc ggt gac aag atc gtt ctc cca gtt gac ctg gtt gca gca	931

Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val Asp Leu Val Ala Ala  
 265 270 275

tcc gaa ttt aac aag gac gca gag aag cag atc gtt gac ctg gac tcc 979  
 Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile Val Asp Leu Asp Ser  
 280 285 290

atc cca gaa ggc tgg atg tct ctt gac atc gga cca gag tcc gtc aag 1027  
 Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly Pro Glu Ser Val Lys  
 295 300 305

aac ttc ggt gag gtt ctc agc acc gct aag acc atc ttc tgg aac ggc 1075  
 Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr Ile Phe Trp Asn Gly  
 310 315 320 325

cca atg ggc gtg ttc gag ttc gca gca ttc tct gaa ggc acc cgc ggc 1123  
 Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser Glu Gly Thr Arg Gly  
 330 335 340

atc gcc cag gcc atc atc gat gca act gca ggc aac gac gca ttc tcc 1171  
 Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly Asn Asp Ala Phe Ser  
 345 350 355

gtt gtt ggc ggt ggc gac tcc gca gca tcc gtt cgc gtg ctc ggc ctg 1219  
 Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val Arg Val Leu Gly Leu  
 360 365 370

aac gaa gac ggc ttc tcc cac atc tcc acc ggt ggt ggc gca tcc ctc 1267  
 Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly Gly Gly Ala Ser Leu  
 375 380 385

gag tac ctt gaa ggc aag gaa ctc cca ggc gtt gca att ctc gct cag 1315  
 Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val Ala Ile Leu Ala Gln  
 390 395 400 405

taaatccgac acggcccttt gtt 1338

&lt;210&gt; 70

&lt;211&gt; 405

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 70

Met Ala Val Lys Thr Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly  
 1 5 10 15

Arg His Val Ile Val Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp  
 20 25 30

Arg Glu Ile Thr Asp Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu  
 35 40 45

Lys Ala Leu Ser Glu Gly Gly Ala Lys Val Ile Val Met Ala His Leu  
 50 55 60

Gly Arg Pro Lys Gly Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val  
 65 70 75 80

Ala Glu Ala Leu Ser Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala  
 85 90 95

Asp Val Val Gly Glu Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu  
 100 105 110  
 Gly Asp Ile Leu Leu Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr  
 115 120 125  
 Ser Lys Asp Glu Ala Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala  
 130 135 140  
 Leu Ala Ala Asp Asn Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val  
 145 150 155 160  
 His Arg Ala Gln Thr Ser Val Tyr Asp Ile Ala Lys Leu Leu Pro His  
 165 170 175  
 Tyr Ala Gly Gly Leu Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile  
 180 185 190  
 Ala Glu Ser Pro Glu Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys  
 195 200 205  
 Val Ser Asp Lys Ile Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp  
 210 215 220  
 Lys Ile Ile Val Gly Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln  
 225 230 235 240  
 Gly His Asn Val Gln Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr  
 245 250 255  
 Cys Thr Asp Leu Leu Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val  
 260 265 270  
 Asp Leu Val Ala Ala Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile  
 275 280 285  
 Val Asp Leu Asp Ser Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly  
 290 295 300  
 Pro Glu Ser Val Lys Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr  
 305 310 315 320  
 Ile Phe Trp Asn Gly Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser  
 325 330 335  
 Glu Gly Thr Arg Gly Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly  
 340 345 350  
 Asn Asp Ala Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val  
 355 360 365  
 Arg Val Leu Gly Leu Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly  
 370 375 380  
 Gly Gly Ala Ser Leu Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val  
 385 390 395 400  
 Ala Ile Leu Ala Gln  
 405

<400> 71																	
cgaaacaaga ttcgtgcaac aattgggtgt agacgtgatt gaagacattt gatcacgtga 60																	
ataattctag ttagctccca agttggcata ggaggccaca												gtg	gct	gaa	atc	atg	115
												Val	Ala	Glu	Ile	Met	5
												1					
cac	gta	ttc	gct	cgc	gaa	att	ctc	gac	tcc	cgc	ggg	aac	cca	acc	gtc	163	
His	Val	Phe	Ala	Arg	Glu	Ile	Leu	Asp	Ser	Arg	Gly	Asn	Pro	Thr	Val	20	
				10					15								
gag	gca	gag	gtt	ttc	ctg	gat	gac	ggg	tcc	cac	ggg	gtc	gca	ggg	gtt	211	
Glu	Ala	Glu	Val	Phe	Leu	Asp	Asp	Gly	Ser	His	Gly	Val	Ala	Gly	Val	35	
				25					30								
cca	tcc	ggc	gca	tcc	acc	ggc	gtc	cac	gag	gct	cat	gag	ctg	cgt	gac	259	
Pro	Ser	Gly	Ala	Ser	Thr	Gly	Val	His	Glu	Ala	His	Glu	Leu	Arg	Asp	50	
				40					45								
ggg	ggc	gat	cgc	tac	ctg	ggc	aag	ggc	gtt	ttg	aag	gca	gtt	gaa	aac	307	
Gly	Gly	Asp	Arg	Tyr	Leu	Gly	Lys	Gly	Val	Leu	Lys	Ala	Val	Glu	Asn	65	
									60								
gtc	aac	gaa	gaa	atc	ggc	gac	gag	ctc	gct	ggc	cta	gag	gct	gac	gat	355	
Val	Asn	Glu	Glu	Ile	Gly	Asp	Glu	Leu	Ala	Gly	Leu	Glu	Ala	Asp	Asp	85	
				70					75								
cag	cgc	ctc	atc	gac	gaa	gca	atg	atc	aag	ctt	gat	ggc	acc	gcc	aac	403	
Gln	Arg	Leu	Ile	Asp	Glu	Ala	Met	Ile	Lys	Leu	Asp	Gly	Thr	Ala	Asn	100	
				90					95								
aag	tcc	cgc	ctg	ggg	gca	aac	gca	atc	ctt	ggg	gtt	tcc	atg	gct	gtt	451	
Lys	Ser	Arg	Leu	Gly	Ala	Asn	Ala	Ile	Leu	Gly	Val	Ser	Met	Ala	Val	115	
				105					110								
gca	aag	gct	gct	gct	gat	tcc	gca	ggc	ctc	cca	ctg	ttc	cgc	tac	atc	499	
Ala	Lys	Ala	Ala	Ala	Asp	Ser	Ala	Gly	Leu	Pro	Leu	Phe	Arg	Tyr	Ile	130	
				120					125								
ggg	gga	cca	aac	gca	cac	gtt	ctt	cca	gtt	cca	atg	atg	aac	atc	atc	547	
Gly	Gly	Pro	Asn	Ala	His	Val	Leu	Pro	Val	Pro	Met	Met	Asn	Ile	Ile	145	
				135					140								
acc	ggg	ggc	gct	cac	gct	gac	tcc	ggg	gtt	gac	gtt	cag	gaa	ttc	atg	595	
Thr	Gly	Gly	Ala	His	Ala	Asp	Ser	Gly	Val	Asp	Val	Gln	Glu	Phe	Met	165	
				150					155								
atc	gct	cca	atc	ggg	gca	gag	acc	ttc	tct	gag	gct	ctc	cgc	aac	ggc	643	
Ile	Ala	Pro	Ile	Gly	Ala	Glu	Thr	Phe	Ser	Glu	Ala	Leu	Arg	Asn	Gly	180	
				170					175								

gcg gag gtc tac cac gca ctg aag tcc gtc atc aag gaa aag ggc ctg	691
Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile Lys Glu Lys Gly Leu	
185 190 195	
tcc acc gga ctt ggc gat gag ggc ggc ttc gct cct tcc gtc ggc tcc	739
Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala Pro Ser Val Gly Ser	
200 205 210	
acc cgt gag gct ctt gac ctt atc gtt gag gca atc gag aag gct ggc	787
Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala Ile Glu Lys Ala Gly	
215 220 225	
ttc acc cca ggc aag gac atc gct ctt gct ctg gac gtt gct tcc tct	835
Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu Asp Val Ala Ser Ser	
230 235 240 245	
gag ttc ttc aag gac ggc acc tac cac ttc gaa ggt ggc cag cac tcc	883
Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu Gly Gly Gln His Ser	
250 255 260	
gca gct gag atg gca aac gtt tac gct gag ctg gtt gac gcg tac cca	931
Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu Val Asp Ala Tyr Pro	
265 270 275	
atc gtc tcc atc gag gac cca ctg cag gaa gat gac tgg gag ggt tac	979
Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp Asp Trp Glu Gly Tyr	
280 285 290	
acc aac ctg acc gca acc atc ggc gac aag gtt cag atc gtt ggc gac	1027
Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val Gln Ile Val Gly Asp	
295 300 305	
gac ttc ttc gtc acc aac cct gag cgc ctg aag gag ggc atc gct aag	1075
Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys Glu Gly Ile Ala Lys	
310 315 320 325	
aag gct gcc aac tcc atc ctg gtt aag gtg aac cag atc ggt acc ctg	1123
Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn Gln Ile Gly Thr Leu	
330 335 340	
acc gag acc ttc gac gct gtc gac atg gct cac cgc gca ggc tac acc	1171
Thr Glu Thr Phe Asp Ala Val Asp Met Ala His Arg Ala Gly Tyr Thr	
345 350 355	
tcc atg atg tcc cac cgt tcc ggt gag acc gag gac acc acc att gct	1219
Ser Met Met Ser His Arg Ser Gly Glu Thr Glu Asp Thr Thr Ile Ala	
360 365 370	
gac ctg gca gtt gca ctg aac tgt ggc cag atc aag act ggt gct cca	1267
Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile Lys Thr Gly Ala Pro	
375 380 385	
gca cgt tcc gac cgt gtc gca aag tac aac cag ctt ctg cgc atc gag	1315
Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu	
390 395 400 405	
cag ctg ctt ggc gac gcc ggc gtc tac gca ggt cgc agc gca ttc cca	1363
Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly Arg Ser Ala Phe Pro	
410 415 420	

cgc ttt cag ggc taaataaaaag cgctttttcga cgc  
 Arg Phe Gln Gly  
 425

1398

&lt;210&gt; 72

&lt;211&gt; 425

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 72

Val Ala Glu Ile Met His Val Phe Ala Arg Glu Ile Leu Asp Ser Arg  
 1 5 10 15

Gly Asn Pro Thr Val Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His  
 20 25 30

Gly Val Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala  
 35 40 45

His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu  
 50 55 60

Lys Ala Val Glu Asn Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly  
 65 70 75 80

Leu Glu Ala Asp Asp Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu  
 85 90 95

Asp Gly Thr Ala Asn Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly  
 100 105 110

Val Ser Met Ala Val Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro  
 115 120 125

Leu Phe Arg Tyr Ile Gly Gly Pro Asn Ala His Val Leu Pro Val Pro  
 130 135 140

Met Met Asn Ile Ile Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp  
 145 150 155 160

Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu  
 165 170 175

Ala Leu Arg Asn Gly Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile  
 180 185 190

Lys Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala  
 195 200 205

Pro Ser Val Gly Ser Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala  
 210 215 220

Ile Glu Lys Ala Gly Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu  
 225 230 235 240

Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu  
 245 250 255

Gly Gly Gln His Ser Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu  
 260 265 270



Val Asp Ala Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp  
 275 280 285

Asp Trp Glu Gly Tyr Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val  
 290 295 300

Gln Ile Val Gly Asp Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys  
 305 310 315 320

Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn  
 325 330 335

Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Asp Met Ala His  
 340 345 350

Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu  
 355 360 365

Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile  
 370 375 380

Lys Thr Gly Ala Pro Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln  
 385 390 395 400

Leu Leu Arg Ile Glu Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly  
 405 410 415

Arg Ser Ala Phe Pro Arg Phe Gln Gly  
 420 425

&lt;210&gt; 73

&lt;211&gt; 1554

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1531)

&lt;223&gt; RXA01093

&lt;400&gt; 73

cagaggcgta gaacattgtc.tgttcacact ctgggtcgca agattcatcg agaattaatg 60

gtagtacctg tggcttgagg gggaatgacg tactaggctt atg ggc gtg gat aga 115  
 Met Gly Val Asp Arg  
 1 5

cga act aag att gta tgt acc cta ggc cca gcg gtg gct agt gca gat 163  
 Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Val Ala Ser Ala Asp  
 10 15 20

gga att ctg cgt ttg gta gaa gac ggc atg gat gtt gct cgc ctc aac 211  
 Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn  
 25 30 35

ttc tcc cat ggt gac cac cca gat cat gag caa aac tac aag tgg gtc 259  
 Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val  
 40 45 50

cgc gag gcg gcg gag aag act ggc cgt gca gtc ggt att ctc gca gac	307
Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val Gly Ile Leu Ala Asp	
55 60 65	
ctc caa gga ccg aag atc cgt ctt ggc cgt ttc act gac ggc gca acc	355
Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr	
70 75 80 85	
gtg tgg gaa aac ggc gag acc att cgg atc acc gtt gac gat gta gag	403
Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr Val Asp Asp Val Glu	
90 95 100	
gga acg cac gat cgt gtg tcc acc acc tac aag aat ctg gca aaa gac	451
Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Lys Asp	
105 110 115	
gcg aag cca ggc gac cgc ctg ctc gtt gat gac ggc aag gtt ggc ctc	499
Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu	
120 125 130	
gtc tgc gtt tcc gtc gaa ggt aac gac gtc atc tgt gag gtt gtt gag	547
Val Cys Val Ser Val Glu Gly Asn Asp Val Ile Cys Glu Val Val Glu	
135 140 145	
ggc gga cca gtc tcc aac aac aag ggt gtt tcc ctg cca ggt atg gat	595
Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp	
150 155 160 165	
att tcc gta cct gca ctg tcc gaa aag gat atc cgt gac ctg cgc ttc	643
Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile Arg Asp Leu Arg Phe	
170 175 180	
gcc ctg aag ctc ggc gtg gac ttt att gca ctg tcc ttc gta cgt tcc	691
Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser	
185 190 195	
cca gca gat gct gaa ctc gtt cac aag atc atg gac gaa gaa ggt cgt	739
Pro Ala Asp Ala Glu Leu Val His Lys Ile Met Asp Glu Glu Gly Arg	
200 205 210	
cgt gtt cct gtg atc gcc aag ctg gaa aag cca gag gct gtc acc tcc	787
Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro Glu Ala Val Thr Ser	
215 220 225	
ctc gag cca atc gtg ttg gca ttc gac gcc gtc atg gtt gct cgt ggt	835
Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val Met Val Ala Arg Gly	
230 235 240 245	
gac ctc ggc gtt gag gtt cct ctg gag gag gtt cca ctg gtt cag aag	883
Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val Pro Leu Val Gln Lys	
250 255 260	
cgc gca atc cag att gcc cgt gag aac gca aag cca gtt atc gtg gca	931
Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys Pro Val Ile Val Ala	
265 270 275	
acc cag atg ctg gat tcc atg att gag aac tcc cgc cca acc cgt gcg	979
Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser Arg Pro Thr Arg Ala	
280 285 290	
gaa gct tct gac gtg gca aac gct gtg ctc gat ggc gca gat gct gtc	1027

Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp Gly Ala Asp Ala Val  
 295 300 305  
 atg ctt tct ggt gaa act tca gtg ggc aaa gat ccg cac aac gtt gtg 1075  
 Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp Pro His Asn Val Val  
 310 315 320 325  
 cgc acc atg tct cgc att gtt cgc ttc gct gaa acc gac ggt cgc gtc 1123  
 Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu Thr Asp Gly Arg Val  
 330 335 340  
 cca gac ctg acc cac atc cct cgc act aag cgt ggc gtt att tcc tac 1171  
 Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg Gly Val Ile Ser Tyr  
 345 350 355  
 tct gca cgt gat atc gcc gag cgc ctc aac gct cgt gca ttg gtt gcg 1219  
 Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala Arg Ala Leu Val Ala  
 360 365 370  
 ttc acc acc tct ggt gat acc gca aag cgt gtg gct cgt ctg cac agc 1267  
 Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val Ala Arg Leu His Ser  
 375 380 385  
 cac ctg cca ctg ctc gtg ttc act cca aat gag gca gtt cgc tct gag 1315  
 His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu Ala Val Arg Ser Glu  
 390 395 400 405  
 ctg gcg ctg acc tgg ggt gca acc acc ttc ctg tgt cca cct gtc agc 1363  
 Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu Cys Pro Pro Val Ser  
 410 415 420  
 gat acc gat gac atg atg cgc gaa gtc gac cgt gct ctt tta gca atg 1411  
 Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg Ala Leu Leu Ala Met  
 425 430 435  
 cct gag tac aac aag ggt gac atg atg gtt gtt gtt gca ggt tcc cct 1459  
 Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val Val Ala Gly Ser Pro  
 440 445 450  
 cct ggt gtt acc ggt aac acc aac atg att cac gtc cac ctt ctt ggt 1507  
 Pro Gly Val Thr Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly  
 455 460 465  
 gac gac aca agg att gca aag ctc taatcgctta aatctttcaa aaa 1554  
 Asp Asp Thr Arg Ile Ala Lys Leu  
 470 475

&lt;210&gt; 74

&lt;211&gt; 477

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 74

Met Gly Val Asp Arg Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala  
 1 5 10 15

Val Ala Ser Ala Asp Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp  
 20 25 30

Val Ala Arg Leu Asn Phe Ser His Gly Asp His Pro Asp His Glu Gln

35					40					45					
Asn	Tyr	Lys	Trp	Val	Arg	Glu	Ala	Ala	Glu	Lys	Thr	Gly	Arg	Ala	Val
50					55					60					
Gly	Ile	Leu	Ala	Asp	Leu	Gln	Gly	Pro	Lys	Ile	Arg	Leu	Gly	Arg	Phe
65					70					75					
Thr	Asp	Gly	Ala	Thr	Val	Trp	Glu	Asn	Gly	Glu	Thr	Ile	Arg	Ile	Thr
					85					90					
Val	Asp	Asp	Val	Glu	Gly	Thr	His	Asp	Arg	Val	Ser	Thr	Thr	Tyr	Lys
100					105					110					
Asn	Leu	Ala	Lys	Asp	Ala	Lys	Pro	Gly	Asp	Arg	Leu	Leu	Val	Asp	Asp
115					120					125					
Gly	Lys	Val	Gly	Leu	Val	Cys	Val	Ser	Val	Glu	Gly	Asn	Asp	Val	Ile
130					135					140					
Cys	Glu	Val	Val	Glu	Gly	Gly	Pro	Val	Ser	Asn	Asn	Lys	Gly	Val	Ser
145					150					155					
Leu	Pro	Gly	Met	Asp	Ile	Ser	Val	Pro	Ala	Leu	Ser	Glu	Lys	Asp	Ile
					165					170					
Arg	Asp	Leu	Arg	Phe	Ala	Leu	Lys	Leu	Gly	Val	Asp	Phe	Ile	Ala	Leu
180					185					190					
Ser	Phe	Val	Arg	Ser	Pro	Ala	Asp	Ala	Glu	Leu	Val	His	Lys	Ile	Met
195					200					205					
Asp	Glu	Glu	Gly	Arg	Arg	Val	Pro	Val	Ile	Ala	Lys	Leu	Glu	Lys	Pro
210					215					220					
Glu	Ala	Val	Thr	Ser	Leu	Glu	Pro	Ile	Val	Leu	Ala	Phe	Asp	Ala	Val
225					230					235					
Met	Val	Ala	Arg	Gly	Asp	Leu	Gly	Val	Glu	Val	Pro	Leu	Glu	Glu	Val
					245					250					
Pro	Leu	Val	Gln	Lys	Arg	Ala	Ile	Gln	Ile	Ala	Arg	Glu	Asn	Ala	Lys
260					265					270					
Pro	Val	Ile	Val	Ala	Thr	Gln	Met	Leu	Asp	Ser	Met	Ile	Glu	Asn	Ser
275					280					285					
Arg	Pro	Thr	Arg	Ala	Glu	Ala	Ser	Asp	Val	Ala	Asn	Ala	Val	Leu	Asp
290					295					300					
Gly	Ala	Asp	Ala	Val	Met	Leu	Ser	Gly	Glu	Thr	Ser	Val	Gly	Lys	Asp
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Thr	Asp	Gly	Arg	Val	Pro	Asp	Leu	Thr	His	Ile	Pro	Arg	Thr	Lys	Arg
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Gly	Val	Ile	Ser	Tyr	Ser	Ala	Arg	Asp	Ile	Ala	Glu	Arg	Leu	Asn	Ala
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Arg Ala Leu Val Ala Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val  
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 385 390 395 400  
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 Cys Pro Pro Val Ser Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg  
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 Ala Leu Leu Ala Met Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val  
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 Met Asn Glu Phe Asp  
 1 5  
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 Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu  
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 Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val  
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 Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His  
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 Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln Arg Leu Ser Ser Val  
 55 60 65  
 gga gct acc cgc ttg act acc acc gaa cca gca gtg cag gcc cgc ctc 355  
 Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala Val Gln Ala Arg Leu  
 70 75 80 85  
 aag gcc gcc cgc aat gtt atc gga gct ttc gca ggt gaa ggc cca ctt 403

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Tyr	Pro	Pro	Ser	Asp	Val	Val	Asp	Ala	Phe	Glu	Asp	Ala	Asp	Glu	Ile	
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Glu	Val	Gly	Arg	Ala	Arg	Val	Thr	Arg	Asp	Glu	Thr	Gly	Lys	Val	Leu	
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Asp	Thr	Arg	Gly	Ser	Arg	Arg	Ala	Phe	Thr	Val	Thr	Arg	Val	Phe	Asp	
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Gly	Ala	Val	Leu	Ala	Glu	Gly	Pro	Gln	Lys	Ala	Tyr	Ile	Ser	Asn	Gly	
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Thr	Leu	Leu	Glu	His	Asn	Tyr	Asp	Arg	Ser	Arg	Val	Tyr	Gly	Ile	Pro	
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gcc	gta	gtt	cag	cgc	atc	aac	ctc	aaa	gtc	ggc	gac	cgc	ctc	atc	ctt	1123
Ala	Val	Val	Gln	Arg	Ile	Asn	Leu	Lys	Val	Gly	Asp	Arg	Leu	Ile	Leu	

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acc	gac	gaa	gaa	ctc	acc	tac	gat	cca	tcc	ctc	gga	tcc	ggc	cgc	aca	1171
Thr	Asp	Glu	Glu	Leu	Thr	Tyr	Asp	Pro	Ser	Leu	Gly	Ser	Gly	Arg	Thr	
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Pro	Arg	Ile	Ser	Cys	Thr	Leu	Pro	Gln	Ala	Val	Asp	Ala	Ile	Lys	Val	
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Gly	His	Arg	Val	Leu	Phe	Asp	Asp	Gly	Ala	Ile	Ala	Ala	Val	Cys	Ile	
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gac	aag	acc	tcc	act	gcc	gac	ggc	cac	aac	gac	gta	gaa	ttg	gaa	gtc	1315
Asp	Lys	Thr	Ser	Thr	Ala	Asp	Gly	His	Asn	Asp	Val	Glu	Leu	Glu	Val	
390					395					400					405	
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Asn	Leu	Pro	Asp	Ser	Glu	Leu	Pro	Leu	Pro	Ser	Leu	Thr	Glu	Glu	Asp	
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Leu	Gln	His	Leu	Arg	Phe	Val	Val	Lys	Tyr	Ala	Asp	Ile	Ala	Ala	Ile	
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Ser	Phe	Ile	Arg	Asn	Val	Ala	Asp	Val	Glu	Tyr	Leu	Leu	Gln	Ala	Leu	
			455				460					465				
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Ala	Asp	Ile	Gly	Asp	Pro	Val	Ala	Val	Glu	Arg	Leu	Gly	Leu	Val	Leu	
470					475					480					485	
aaa	atc	gag	acc	atc	cca	ggc	tac	gaa	ggc	ctc	gcc	caa	atc	ctc	ctg	1603
Lys	Ile	Glu	Thr	Ile	Pro	Gly	Tyr	Glu	Gly	Leu	Ala	Gln	Ile	Leu	Leu	
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Thr	Gly	Met	Arg	His	Glu	Asn	Phe	Gly	Ile	Met	Ile	Ala	Arg	Gly	Asp	
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Leu	Ala	Val	Glu	Leu	Gly	Phe	Asp	Arg	Met	Ala	Glu	Val	Pro	Gln	Leu	
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Ile	Met	Ala	Leu	Ala	Glu	Ala	Ala	His	Val	Pro	Thr	Ile	Leu	Ala	Thr	
			535				540					545				
caa	gtc	ctg	gaa	aac	atg	gcc	aaa	aac	gga	ctc	cca	tct	cgc	gca	gaa	1795
Gln	Val	Leu	Glu	Asn	Met	Ala	Lys	Asn	Gly	Leu	Pro	Ser	Arg	Ala	Glu	
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Ile	Thr	Asp	Ala	Ala	Met	Ala	Leu	Arg	Ala	Glu	Cys	Val	Met	Leu	Asn	
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 Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr Glu Met Ser  
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 Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu Leu Arg Lys  
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<213> Corynebacterium glutamicum

<400> 76

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Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu  
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Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln  
                   50                                  55                                  60

Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala  
   65                                  70                                  75                                  80

Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala  
                   85                                  90                                  95

Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu  
                   100                                  105                                  110

Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu  
                   115                                  120                                  125

Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu  
   130                                  135                                  140

Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met  
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Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys  
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Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu  
                   180                                  185                                  190

Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu  
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Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu  
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Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly  
 225 230 235 240  
 Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu  
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 Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser  
 260 265 270  
 Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val  
 275 280 285  
 Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala  
 290 295 300  
 Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg  
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 Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly  
 325 330 335  
 Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu  
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 Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val  
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 Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile  
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 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp  
 385 390 395 400  
 Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala  
 405 410 415  
 Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser  
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 Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala  
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 Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr  
 450 455 460  
 Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg  
 465 470 475 480  
 Leu Gly Leu Val Leu Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu  
 485 490 495  
 Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met  
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 Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala  
 515 520 525  
 Glu Val Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro  
 530 535 540

Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu  
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Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu  
565 570 575

Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val  
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<211> 386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(363)

<223> FRXA02675

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cgc gga gac ctc gcc gtc gaa ctc ggc ttc gac cgc atg gca gaa gtc 96  
Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val  
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ccc caa ctg atc atg gcc ctt gca gaa gcc gcc cac gtc cca acc atc 144  
Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile  
35 40 45

ttg gcc acc caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct 192  
Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser  
50 55 60

cgc gca gaa atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc 240  
Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val  
65 70 75 80

atg ctg aac aag gga cca cac atc aac gac gcc atc aag gtc ctc acc 288  
Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr  
85 90 95

gaa atg agc cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg 336  
Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu  
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Leu Arg Lys Val Lys Ser Trp Glu Glu  
115 120

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 Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile  
           35                  40                  45  
 Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser  
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 Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val  
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 Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr  
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 Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu  
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 Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu  
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 gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc 211  
 Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val  
           25                  30                  35  
 tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat 259  
 Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His  
       40                  45                  50

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Gly	Ala	Thr	Arg	Leu	Thr	Thr	Thr	Glu	Pro	Ala	Val	Gln	Ala	Arg	Leu	
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tat	cca	ccc	tca	gat	gtc	gtc	gat	gcc	ttc	gaa	gat	gcc	gat	gag	att	451
Tyr	Pro	Pro	Ser	Asp	Val	Val	Asp	Ala	Phe	Glu	Asp	Ala	Asp	Glu	Ile	
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Leu	Asp	Glu	His	Ala	Glu	Ile	Leu	Leu	Gly	Glu	Pro	Leu	Pro	Asp	Thr	
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Pro	Ser	Cys	Ile	Met	Val	Thr	Leu	Pro	Thr	Glu	Ala	Ala	Thr	Asp	Ile	
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gaa	ctt	gtc	cgt	ggc	ttc	gcc	aaa	agc	ggc	atg	aat	cta	gct	cgc	atc	595
Glu	Leu	Val	Arg	Gly	Phe	Ala	Lys	Ser	Gly	Met	Asn	Leu	Ala	Arg	Ile	
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Asn	Cys	Ala	His	Asp	Asp	Glu	Thr	Val	Trp	Lys	Gln	Met	Ile	Asp	Asn	
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Val	His	Thr	Val	Ala	Glu	Glu	Val	Gly	Arg	Glu	Ile	Arg	Val	Ser	Met	
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Asp	Leu	Ala	Gly	Pro	Lys	Val	Arg	Thr	Gly	Glu	Ile	Ala	Pro	Gly	Ala	
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gaa	gta	ggt	cgc	gca	cga	gta	acc	cgc	gac	gaa	acc	gga	aaa	gta	ctg	787
Glu	Val	Gly	Arg	Ala	Arg	Val	Thr	Arg	Asp	Glu	Thr	Gly	Lys	Val	Leu	
	215					220					225					
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Thr	Pro	Ala	Lys	Leu	Trp	Ile	Thr	Ala	His	Gly	Ser	Glu	Pro	Val	Pro	
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Ala	Pro	Glu	Ser	Leu	Pro	Gly	Arg	Pro	Ala	Leu	Pro	Ile	Glu	Val	Thr	
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Pro	Glu	Trp	Phe	Asp	Lys	Leu	Glu	Ile	Gly	Ser	Val	Ile	Asn	Val	Pro	
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Asp	Thr	Arg	Gly	Ser	Arg	Arg	Ala	Phe	Thr	Val	Thr	Arg	Val	Phe	Asp	
		280					285					290				
ggc	gcg	gtc	ctc	gcc	gaa	ggc	cca	caa	aaa	gcc	tac	atc	tcc	aac	ggc	1027

Gly	Ala	Val	Leu	Ala	Glu	Gly	Pro	Gln	Lys	Ala	Tyr	Ile	Ser	Asn	Gly	
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Thr	Leu	Leu	Glu	His	Asn	Tyr	Asp	Arg	Ser	Arg	Val	Tyr	Gly	Ile	Pro	
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gcc	gta	gtt	cag	cgc	atc	aac	ctc	aaa	gtc	ggc	gac	cgc	ctc	atc	ctt	1123
Ala	Val	Val	Gln	Arg	Ile	Asn	Leu	Lys	Val	Gly	Asp	Arg	Leu	Ile	Leu	
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acc	gac	gaa	gaa	ctc	acc	tac	gat	cca	tcc	ctc	gga	tcc	ggc	cgc	aca	1171
Thr	Asp	Glu	Glu	Leu	Thr	Tyr	Asp	Pro	Ser	Leu	Gly	Ser	Gly	Arg	Thr	
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cca	cgc	atc	agc	tgc	acc	ctt	cca	caa	gca	gtc	gat	gca	att	aaa	gtc	1219
Pro	Arg	Ile	Ser	Cys	Thr	Leu	Pro	Gln	Ala	Val	Asp	Ala	Ile	Lys	Val	
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Gly	His	Arg	Val	Leu	Phe	Asp	Asp	Gly	Ala	Ile	Ala	Ala	Val	Cys	Ile	
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gac	aag	acc	tcc	act	gcc	gac	ggc	cac	aac	gac	gta	gaa	ttg	gaa	gtc	1315
Asp	Lys	Thr	Ser	Thr	Ala	Asp	Gly	His	Asn	Asp	Val	Glu	Leu	Glu	Val	
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acc	cac	gcc	cgc	cca	caa	ggc	gta	aac	ctg	gcc	gca	tac	aag	gga	atc	1363
Thr	His	Ala	Arg	Pro	Gln	Gly	Val	Asn	Leu	Ala	Ala	Tyr	Lys	Gly	Ile	
				410				415						420		
aac	ctc	cca	gac	tcc	gaa	ctt	cca	ctc	cca	agc	ctc	act	gaa	gaa	gac	1411
Asn	Leu	Pro	Asp	Ser	Glu	Leu	Pro	Leu	Pro	Ser	Leu	Thr	Glu	Glu	Asp	
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ctc	caa	cac	ctg	cgc	ttt	gtc	gtc	aaa	tac	gcc	gac	atc	gca	gcc	atc	1459
Leu	Gln	His	Leu	Arg	Phe	Val	Val	Lys	Tyr	Ala	Asp	Ile	Ala	Ala	Ile	
		440					445					450				
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Ser	Phe	Ile	Arg	Asn	Val	Ala	Asp	Val	Glu	Tyr	Leu	Leu	Gln	Ala	Leu	
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&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

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Asp	Glu	Leu	Ile	Leu	Glu	Leu	Asp	Glu	Val	Thr	Gln	Thr	His	Ser	Glu
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Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu

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Met	His	Tyr	Ala	His	Leu	Arg	Thr	Lys	Asp	Leu	Arg	Gly	Leu	Gln	Gln
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Arg	Leu	Ser	Ser	Val	Gly	Ala	Thr	Arg	Leu	Thr	Thr	Thr	Glu	Pro	Ala
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Val	Gln	Ala	Arg	Leu	Lys	Ala	Ala	Arg	Asn	Val	Ile	Gly	Ala	Phe	Ala
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Gly	Glu	Gly	Pro	Leu	Tyr	Pro	Pro	Ser	Asp	Val	Val	Asp	Ala	Phe	Glu
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Asp	Ala	Asp	Glu	Ile	Leu	Asp	Glu	His	Ala	Glu	Ile	Leu	Leu	Gly	Glu
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Pro	Leu	Pro	Asp	Thr	Pro	Ser	Cys	Ile	Met	Val	Thr	Leu	Pro	Thr	Glu
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Ala	Ala	Thr	Asp	Ile	Glu	Leu	Val	Arg	Gly	Phe	Ala	Lys	Ser	Gly	Met
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Asn	Leu	Ala	Arg	Ile	Asn	Cys	Ala	His	Asp	Asp	Glu	Thr	Val	Trp	Lys
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Gln	Met	Ile	Asp	Asn	Val	His	Thr	Val	Ala	Glu	Glu	Val	Gly	Arg	Glu
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Ile	Arg	Val	Ser	Met	Asp	Leu	Ala	Gly	Pro	Lys	Val	Arg	Thr	Gly	Glu
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Ile	Ala	Pro	Gly	Ala	Glu	Val	Gly	Arg	Ala	Arg	Val	Thr	Arg	Asp	Glu
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Thr	Gly	Lys	Val	Leu	Thr	Pro	Ala	Lys	Leu	Trp	Ile	Thr	Ala	His	Gly
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Ser	Glu	Pro	Val	Pro	Ala	Pro	Glu	Ser	Leu	Pro	Gly	Arg	Pro	Ala	Leu
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Val	Ile	Asn	Val	Pro	Asp	Thr	Arg	Gly	Ser	Arg	Arg	Ala	Phe	Thr	Val
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Thr	Arg	Val	Phe	Asp	Gly	Ala	Val	Leu	Ala	Glu	Gly	Pro	Gln	Lys	Ala
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Tyr	Ile	Ser	Asn	Gly	Thr	Leu	Leu	Glu	His	Asn	Tyr	Asp	Arg	Ser	Arg
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Val	Tyr	Gly	Ile	Pro	Ala	Val	Val	Gln	Arg	Ile	Asn	Leu	Lys	Val	Gly
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Asp	Arg	Leu	Ile	Leu	Thr	Asp	Glu	Glu	Leu	Thr	Tyr	Asp	Pro	Ser	Leu
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Gly	Ser	Gly	Arg	Thr	Pro	Arg	Ile	Ser	Cys	Thr	Leu	Pro	Gln	Ala	Val
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Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile  
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 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp  
 385 390 395 400  
 Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala  
 405 410 415  
 Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser  
 420 425 430  
 Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala  
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 Met Ala Asn Lys Ser  
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 Phe Pro Lys Pro Ser Asp Leu Pro Val Pro Lys Gly Ala Glu Gly Trp  
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 Glu Asp Leu Tyr Pro Tyr Tyr Leu Val Phe Gln Asp Lys Leu Met Asp  
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 Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser Gln His Trp Pro Thr  
 40 45 50  
 gtg ttc aag cct ttt gaa act atc ggt ggt gaa ttc gct gta aag tgc 307  
 Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu Phe Ala Val Lys Cys  
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 Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile Pro Asn Ala Asn Gly  
 70 75 80 85  
 atc gag ttc cgc gtg cat ctg gga tac ctc tat atg tcc cct att cca 403

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Val	Pro	Glu	Asp	Gln	Ile	Ala	Glu	Arg	Val	Pro	Met	Phe	Gln	Glu	Arg		
			105					110					115				
atc	acg	cac	tac	ttc	caa	aac	tgg	gag	cca	atg	ctg	gca	aat	tgg	aag	499	
Ile	Thr	His	Tyr	Phe	Gln	Asn	Trp	Glu	Pro	Met	Leu	Ala	Asn	Trp	Lys		
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gag	cga	gta	tta	gga	acc	atc	aat	gag	ctg	gaa	tct	cta	gaa	ttc	aag	547	
Glu	Arg	Val	Leu	Gly	Thr	Ile	Asn	Glu	Leu	Glu	Ser	Leu	Glu	Phe	Lys		
	135					140					145						
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Lys	Asp	Gly	Thr	Glu	Val	Leu	Met	Glu	Asn	Phe	Asp	Arg	Leu	Ile	Gln		
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Leu	Ala	Tyr	Gln	Asn	Trp	Gln	Tyr	His	Phe	Glu	Phe	Leu	Asn	Leu	Gly		
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tac	atc	gct	tac	cta	gat	ttc	ttc	aat	ttc	tgc	aag	gaa	gtc	ttc	cca	739	
Tyr	Ile	Ala	Tyr	Leu	Asp	Phe	Phe	Asn	Phe	Cys	Lys	Glu	Val	Phe	Pro		
		200					205					210					
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Asp	Ile	Pro	Asp	Gln	Ser	Ile	Ser	Met	Met	Val	Gln	Gly	Val	Asp	Met		
	215					220				225							
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gtc	gac	ctt	ggc	ctg	caa	act	cac	ttt	gcc	aac	ccg	gat	gat	ccg	caa	883	
Val	Asp	Leu	Gly	Leu	Gln	Thr	His	Phe	Ala	Asn	Pro	Asp	Asp	Pro	Gln		
			250					255						260			
gct	acc	ttg	gct	gct	atc	gca	aag	gca	gaa	ggc	ggc	gcg	aca	tgg	ata	931	
Ala	Thr	Leu	Ala	Ala	Ile	Ala	Lys	Ala	Glu	Gly	Gly	Ala	Thr	Trp	Ile		
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gcg	cgc	tgg	gaa	gaa	gca	caa	gat	ccg	tgg	ttc	aac	ttc	acc	gtc	ggt	979	
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aat	ggc	ttc	tac	ggt	cac	gat	aaa	tac	tgg	atc	gag	cac	ctg	gaa	ctt	1027	
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Pro	Leu	Gly	Tyr	Ile	Ala	Asp	Tyr	Ile	Arg	Arg	Leu	Asp	Glu	Gly	Gln		
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acc	atc	tcc	cgc	ccg	aaa	gat	gaa	ctc	atc	gca	gaa	aag	gaa	cgc	gtg	1123	
Thr	Ile	Ser	Arg	Pro	Lys	Asp	Glu	Leu	Ile	Ala	Glu	Lys	Glu	Arg	Val		



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gat	gct	aaa	tgc	ggc	ctc	gct	gct	act	gca	tac	ccc	tat	gtg	gaa	aac		1219		
Asp	Ala	Lys	Cys	Gly	Leu	Ala	Ala	Thr	Ala	Tyr	Pro	Tyr	Val	Glu	Asn				
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cat	aac	ttc	tac	atc	gag	cac	tgg	acc	atg	tca	gta	ttt	tgg	cgc	aaa		1267		
His	Asn	Phe	Tyr	Ile	Glu	His	Trp	Thr	Met	Ser	Val	Phe	Trp	Arg	Lys				
375				380				385											
gta	cgc	gaa	ctt	tcc	cgc	act	ctc	cag	ggc	tac	ggc	ttc	tgg	gag	aac		1315		
Val	Arg	Glu	Leu	Ser	Arg	Thr	Leu	Gln	Gly	Tyr	Gly	Phe	Trp	Glu	Asn				
390				395				400				405							
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Glu	Asp	Asp	Met	Leu	Tyr	Leu	Asn	Arg	Thr	Glu	Val	Arg	Asp	Val	Leu				
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Phe	Asp	Leu	Ala	Thr	Ala	Trp	Gly	Val	Gly	Ala	Pro	Gly	Gly	Pro	Ile				
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Thr	Leu	Lys	Gly	Met	Ala	Ala	Ser	Pro	Gly	Val	Val	Glu	Gly	Tyr	Ala				
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Arg	Val	Ile	Leu	Ser	Ala	Asp	Asp	Leu	Ser	Glu	Ile	Gln	Gln	Asp	Glu				
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Ile	Leu	Val	Ala	Pro	Val	Thr	Ala	Pro	Ser	Trp	Gly	Pro	Ile	Phe	Gly				
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acc aag ggc aag gtt gtc att gtt gat cca gat gcg cca cgc atc gaa 1939  
 Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp Ala Pro Arg Ile Glu  
 600 605 610

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Gln His Trp Pro Thr Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu  
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Phe Ala Val Lys Cys Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile  
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Pro Asn Ala Asn Gly Ile Glu Phe Arg Val His Leu Gly Tyr Leu Tyr  
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Met Ser Pro Ile Pro Val Pro Glu Asp Gln Ile Ala Glu Arg Val Pro  
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Met Phe Gln Glu Arg Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met  
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Leu Ala Asn Trp Lys Glu Arg Val Leu Gly Thr Ile Asn Glu Leu Glu  
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Ser Leu Glu Phe Lys Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile  
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Val Ser Gly Lys Ala Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe  
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Asp Arg Leu Ile Gln Leu Ala Tyr Gln Asn Trp Gln Tyr His Phe Glu  
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Phe Leu Asn Leu Gly Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys

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Asp	Ala	Glu	Glu	Gly	Thr	Leu	Lys	Gly	Met	Ala	Ala	Ser	Pro	Gly	Val	
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Val	Glu	Gly	Tyr	Ala	Arg	Val	Ile	Leu	Ser	Ala	Asp	Asp	Leu	Ser	Glu	
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1 5

aac atc ccg ttt gtc cag cgc ttc gat gaa ggc ctg gat cct gtt cta 163  
Asn Ile Pro Phe Val Gln Arg Phe Asp Glu Gly Leu Asp Pro Val Leu  
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gaa gta ctc ggt ggc aag ggc gct tca cta gtc acc atg aca gat gct 211  
Glu Val Leu Gly Gly Lys Gly Ala Ser Leu Val Thr Met Thr Asp Ala  
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gga atg ccc gtt cca cct gga ttt gtg gtc act act gcc agc ttt gat 259  
Gly Met Pro Val Pro Pro Gly Phe Val Val Thr Thr Ala Ser Phe Asp  
40 45 50

gaa ttc atc cgt gaa gca ggg gtt gct gaa cac atc gat aaa ttc cta 307  
Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His Ile Asp Lys Phe Leu  
55 60 65

aac gat ctc gat gca gaa gat gtt aag gaa gtg gat cga gtt tct gcg 355  
Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val Asp Arg Val Ser Ala  
70 75 80 85

atc atc cgc gat gag ctg tgc agt ctt gac gtt cca gag aat gct cgt 403

Ile	Ile	Arg	Asp	Glu	Leu	Cys	Ser	Leu	Asp	Val	Pro	Glu	Asn	Ala	Arg		
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ttc	gca	gtg	cac	cag	gct	tat	cgc	gat	ctc	atg	gaa	cga	tgc	ggg	ggc	451	
Phe	Ala	Val	His	Gln	Ala	Tyr	Arg	Asp	Leu	Met	Glu	Arg	Cys	Gly	Gly		
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Asp	Val	Pro	Val	Ala	Val	Arg	Ser	Ser	Ala	Thr	Ala	Glu	Asp	Leu	Pro		
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gat	gct	tcc	ttc	gca	ggg	caa	cag	gac	acc	tat	ctg	tgg	caa	gtc	ggg	547	
Asp	Ala	Ser	Phe	Ala	Gly	Gln	Gln	Asp	Thr	Tyr	Leu	Trp	Gln	Val	Gly		
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Leu	Ser	Ala	Val	Thr	Glu	His	Ile	Arg	Lys	Cys	Trp	Ala	Ser	Leu	Phe		
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act	tcc	cgt	gcc	att	atc	tac	cgt	ctg	aaa	aac	aac	atc	ccc	aat	gag	643	
Thr	Ser	Arg	Ala	Ile	Ile	Tyr	Arg	Leu	Lys	Asn	Asn	Ile	Pro	Asn	Glu		
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ggc	ctc	tcc	atg	gcg	gta	gtt	gtt	caa	aaa	atg	gtc	aac	tct	cgt	gtc	691	
Gly	Leu	Ser	Met	Ala	Val	Val	Val	Gln	Lys	Met	Val	Asn	Ser	Arg	Val		
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Ala	Gly	Val	Ala	Ile	Thr	Met	Asn	Pro	Ser	Asn	Gly	Asp	Arg	Ser	Lys		
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atc	acc	atc	gat	tcc	tca	tgg	ggg	gtt	ggg	gaa	atg	gtg	gtc	tca	ggg	787	
Ile	Thr	Ile	Asp	Ser	Ser	Trp	Gly	Val	Gly	Glu	Met	Val	Val	Ser	Gly		
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Glu	Val	Thr	Pro	Asp	Asn	Ile	Leu	Leu	Asp	Lys	Ile	Thr	Leu	Gln	Val		
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Val	Ser	Glu	His	Ile	Gly	Ser	Lys	His	Ala	Glu	Leu	Ile	Pro	Asp	Ala		
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acc	agt	gga	agc	ctc	gtg	gaa	aag	ccc	gtt	gat	gaa	gaa	cgc	gca	aac	931	
Thr	Ser	Gly	Ser	Leu	Val	Glu	Lys	Pro	Val	Asp	Glu	Glu	Arg	Ala	Asn		
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cgc	cgc	agt	ctg	act	gat	gag	gaa	atg	ctc	gct	gtg	gca	caa	atg	gct	979	
Arg	Arg	Ser	Leu	Thr	Asp	Glu	Glu	Met	Leu	Ala	Val	Ala	Gln	Met	Ala		
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Lys	Arg	Ala	Glu	Lys	His	Tyr	Lys	Cys	Pro	Gln	Asp	Ile	Glu	Trp	Ala		
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Leu	Asp	Ala	Asp	Leu	Pro	Asp	Gly	Glu	Asn	Leu	Leu	Leu	Leu	Gln	Ser		
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Arg	Pro	Glu	Thr	Ile	His	Ser	Asn	Gly	Val	Lys	Lys	Glu	Thr	Pro	Thr		

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 ccg cag gct gcc aaa acc ata ggc acc ttc gat ttc agc tca atc acc 1171  
 Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp Phe Ser Ser Ile Thr  
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gtc gca atg acc ggc acg aag taaaaccacc gcacgttttc gtc 1215  
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<211> 364

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

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Thr Met Thr Asp Ala Gly Met Pro Val Pro Pro Gly Phe Val Val Thr  
 35 40 45

Thr Ala Ser Phe Asp Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His  
 50 55 60

Ile Asp Lys Phe Leu Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val  
 65 70 75 80

Asp Arg Val Ser Ala Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val  
 85 90 95

Pro Glu Asn Ala Arg Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met  
 100 105 110

Glu Arg Cys Gly Gly Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr  
 115 120 125

Ala Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr  
 130 135 140

Leu Trp Gln Val Gly Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys  
 145 150 155 160

Trp Ala Ser Leu Phe Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn  
 165 170 175

Asn Ile Pro Asn Glu Gly Leu Ser Met Ala Val Val Val Gln Lys Met  
 180 185 190

Val Asn Ser Arg Val Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn  
 195 200 205

Gly Asp Arg Ser Lys Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu  
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Met Val Val Ser Gly Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys  
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<222> (101)..(1837)
<223> RXN00635
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															Met Ala His Ser Tyr	
															1 5	
gca gaa caa tta att gac act ttg gaa gct caa ggt gtg aag cga att															163	
Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile																
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tat ggt ttg gtg ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc															211	
Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg																
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caa tca gat att gag tgg gtg cac gtt cga aat gag gaa gcg gcg gcg															259	
Gln Ser Asp Ile Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala																
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ttt gca gcc ggt gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt															307	
Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys																
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gct gct tct tgt ggt cct gga aac aca cac ctg att cag ggt ctt tat															355	
Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr																

70	75	80	85	
gat tcg cat cga aat ggt gcg aag gtg ttg gcc atc gct agc cat att Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile	90	95	100	403
ccg agt gcc cag att ggt tcg acg ttc ttc cag gaa acg cat ccg gag Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu	105	110	115	451
att ttg ttt aag gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly	120	125	130	499
gag cag ggt gaa cgc att ttg cat cac gcg att cag tcc acc atg gcg Glu Gln Gly Glu Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala	135	140	145	547
ggt aaa ggt gtg tcg gtg gta gtg att cct ggt gat atc gct aag gaa Gly Lys Gly Val Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu	150	155	160	595
gac gca ggt gac ggt act tat tcc aat tcc act att tct tct ggc act Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr	170	175	180	643
cct gtg gtg ttc ccg gat cct act gag gct gca gcg ctg gtg gag gcg Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala	185	190	195	691
att aac aac gct aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys	200	205	210	739
aat gct cgc gcg cag gtg ttg gag ttg gcg gag aag att aaa tca ccg Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro	215	220	225	787
atc ggg cat gcg ctg ggt ggt aag cag tac atc cag cat gag aat ccg Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro	230	235	240	835
ttt gag gtc ggc atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp	250	255	260	883
gcg tcc aat gag gcg gat ctg ctg att cta ttg ggt acg gat ttc cct Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro	265	270	275	931
tat tct gat ttc ctt cct aaa gac aac gtt gcc cag gtg gat atc aac Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn	280	285	290	979
ggt gcg cac att ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly	295	300	305	1027
gat gtt gct gca aca atc gaa aat att ttg cct cat gtg aag gaa aaa Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys	310	315	320	1075
			325	



aca gat cgt tcc ttc ctt gat cgg atg ctc aag gca cac gag cgt aag	1123
Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys	
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Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val	
345 350 355	
cct att cac cct gaa tac gtt gcc tct att ttg aac gag ctg gcg gat	1219
Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp	
360 365 370	
aag gat gcg gtg ttt act gtg gat acc ggc atg tgc aat gtg tgg cat	1267
Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His	
375 380 385	
gcg agg tac atc gag aat ccg gag gga acg cgc gac ttt gtg ggt tca	1315
Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser	
390 395 400 405	
ttc cgc cac ggc acg atg gct aat gcg ttg cct cat gcg att ggt gcg	1363
Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala	
410 415 420	
caa agt gtt gat cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt	1411
Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly	
425 430 435	
ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa	1459
Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln	
440 445 450	
ctt ccg ctg aag gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg	1507
Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val	
455 460 465	
aag ttg gag atg ctc gtg gag gga cag cca gaa ttt ggt act gac cat	1555
Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His	
470 475 480 485	
gag gaa gtg aat ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg	1603
Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala Gly Ile Lys Ser	
490 495 500	
gta cgc atc acc gat ccg aag aaa gtt cgc gag cag cta gct gag gca	1651
Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala	
505 510 515	
ttg gca tat cct gga cct gta ctg atc gat atc gtc acg gat cct aat	1699
Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn	
520 525 530	
gcg ctg tcg atc cca cca acc atc acg tgg gaa cag gtc atg gga ttc	1747
Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe	
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Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met	
550 555 560 565	

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<213> Corynebacterium glutamicum

<400> 86

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Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile  
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Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn  
 35 40 45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly  
 50 55 60

Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu  
 65 70 75 80

Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala  
 85 90 95

Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln  
 100 105 110

Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu  
 115 120 125

Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile  
 130 135 140

Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly  
 145 150 155 160

Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr  
 165 170 175

Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala  
 180 185 190

Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys  
 195 200 205

Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu  
 210 215 220

Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile  
 225 230 235 240

Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr  
 245 250 255

Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu  
 260 265 270  
 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala  
 275 280 285  
 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys  
 290 295 300  
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro  
 305 310 315 320  
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys  
 325 330 335  
 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn  
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 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu  
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 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met  
 370 375 380  
 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg  
 385 390 395 400  
 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro  
 405 410 415  
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala  
 420 425 430  
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr  
 435 440 445  
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser  
 450 455 460  
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu  
 465 470 475 480  
 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala  
 485 490 495  
 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu  
 500 505 510  
 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile  
 515 520 525  
 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu  
 530 535 540  
 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly  
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<223> FRXA02807
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Met Ala His Ser Tyr Ala Glu Gln Leu																
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Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val																
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30 35 40																
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Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly																
45 50 55																
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Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys																
60 65 70																
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Gly Pro Gly Asn Thr His Leu Ile Gln Gly Leu Tyr Asp Ser His Arg																
75 80 85																
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Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile Pro Ser Ala Gln																
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 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn  
           35                  40                  45  
 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly  
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 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu  
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 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala  
                   85                  90                  95  
 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln  
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 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu  
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 Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile  
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 cag gtg gat atc aac ggt gcg cac att ggt cga cgt acc acg gtg aag 96  
 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys  
           20                  25                  30  
 tat ccg gtg acc ggt gat gtt gct gca aca atc gaa aat att ttg cct 144  
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro  
           35                  40                  45  
 cat gtg aag gaa aaa aca gat cgt tcc ttc ctt gat cgg atg ctc aag 192

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gca	cac	gag	cgt	aag	ttg	agc	tcg	gtg	gta	gag	acg	tac	aca	cat	aac	240	
Ala	His	Glu	Arg	Lys	Leu	Ser	Ser	Val	Val	Glu	Thr	Tyr	Thr	His	Asn		
	65				70					75					80		
gtc	gag	aag	cat	gtg	cct	att	cac	cct	gaa	tac	gtt	gcc	tct	att	ttg	288	
Val	Glu	Lys	His	Val	Pro	Ile	His	Pro	Glu	Tyr	Val	Ala	Ser	Ile	Leu		
				85					90					95			
aac	gag	ctg	gcg	gat	aag	gat	gcg	gtg	ttt	act	gtg	gat	acc	ggc	atg	336	
Asn	Glu	Leu	Ala	Asp	Lys	Asp	Ala	Val	Phe	Thr	Val	Asp	Thr	Gly	Met		
			100				105					110					
tgc	aat	gtg	tgg	cat	gcg	agg	tac	atc	gag	aat	ccg	gag	gga	acg	cgc	384	
Cys	Asn	Val	Trp	His	Ala	Arg	Tyr	Ile	Glu	Asn	Pro	Glu	Gly	Thr	Arg		
	115					120					125						
gac	ttt	gtg	ggt	tca	ttc	cgc	cac	ggc	acg	atg	gct	aat	gcg	ttg	cct	432	
Asp	Phe	Val	Gly	Ser	Phe	Arg	His	Gly	Thr	Met	Ala	Asn	Ala	Leu	Pro		
	130					135					140						
cat	gcg	att	ggt	gcg	caa	agt	gtt	gat	cga	aac	cgc	cag	gtg	atc	gcg	480	
His	Ala	Ile	Gly	Ala	Gln	Ser	Val	Asp	Arg	Asn	Arg	Gln	Val	Ile	Ala		
	145				150					155					160		
atg	tgt	ggc	gat	ggt	ggt	ttg	ggc	atg	ctg	ctg	ggt	gag	ctt	ctg	acc	528	
Met	Cys	Gly	Asp	Gly	Gly	Leu	Gly	Met	Leu	Leu	Gly	Glu	Leu	Leu	Thr		
				165					170					175			
gtt	aag	ctg	cac	caa	ctt	ccg	ctg	aag	gct	gtg	gtg	ttt	aac	aac	agt	576	
Val	Lys	Leu	His	Gln	Leu	Pro	Leu	Lys	Ala	Val	Val	Phe	Asn	Asn	Ser		
			180					185					190				
tct	ttg	ggc	atg	gtg	aag	ttg	gag	atg	ctc	gtg	gag	gga	cag	cca	gaa	624	
Ser	Leu	Gly	Met	Val	Lys	Leu	Glu	Met	Leu	Val	Glu	Gly	Gln	Pro	Glu		
		195					200					205					
ttt	ggt	act	gac	cat	gag	gaa	gtg	aat	ttc	gca	gag	att	gcg	gcg	gct	672	
Phe	Gly	Thr	Asp	His	Glu	Glu	Val	Asn	Phe	Ala	Glu	Ile	Ala	Ala	Ala		
	210					215					220						
gcg	ggt	atc	aaa	tcg	gta	cgc	atc	acc	gat	ccg	aag	aaa	gtt	cgc	gag	720	
Ala	Gly	Ile	Lys	Ser	Val	Arg	Ile	Thr	Asp	Pro	Lys	Lys	Val	Arg	Glu		
	225				230					235					240		
cag	cta	gct	gag	gca	ttg	gca	tat	cct	gga	cct	gta	ctg	atc	gat	atc	768	
Gln	Leu	Ala	Glu	Ala	Leu	Ala	Tyr	Pro	Gly	Pro	Val	Leu	Ile	Asp	Ile		
				245					250					255			
gtc	acg	gat	cct	aat	gcg	ctg	tcg	atc	cca	cca	acc	atc	acg	tgg	gaa	816	
Val	Thr	Asp	Pro	Asn	Ala	Leu	Ser	Ile	Pro	Pro	Thr	Ile	Thr	Trp	Glu		
			260					265					270				
cag	gtc	atg	gga	ttc	agc	aag	gcg	gcc	acc	cga	acc	gtc	ttt	ggt	gga	864	
Gln	Val	Met	Gly	Phe	Ser	Lys	Ala	Ala	Thr	Arg	Thr	Val	Phe	Gly	Gly		
		275					280					285					
gga	gta	gga	gcg	atg	atc	gat	ctg	gcc	cgt	tcg	aac	ata	agg	aat	att	912	
Gly	Val	Gly	Ala	Met	Ile	Asp	Leu	Ala	Arg	Ser	Asn	Ile	Arg	Asn	Ile		

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 Pro Thr Pro  
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 <213> Corynebacterium glutamicum  
  
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 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys  
                     20                      25                      30  
 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro  
                     35                      40                      45  
 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys  
   50                      55                      60  
 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn  
   65                      70                      75                      80  
 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu  
                     85                      90                      95  
 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met  
                     100                      105                      110  
 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg  
   115                      120                      125  
 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro  
   130                      135                      140  
 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala  
   145                      150                      155                      160  
 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr  
                     165                      170                      175  
 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser  
                     180                      185                      190  
 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu  
                     195                      200                      205  
 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala  
   210                      215                      220  
 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu  
   225                      230                      235                      240  
 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile  
                     245                      250                      255

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu  
 260 265 270

Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly  
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Pro Thr Pro  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(931)  
 <223> RXN03044

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 Met Ala Arg Gly Phe  
 1 5

ctc ttg ggc gct acc gca ggt cgc acc acc ctg acc ggt gaa ggc ctc 163  
 Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu  
 10 15 20

cag cac atg gat gga cac tcc cct gtc ttg gct tcc acc aac gag ggt 211  
 Gln His Met Asp Gly His Ser Pro Val Leu Ala Ser Thr Asn Glu Gly  
 25 30 35

gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt 259  
 Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val  
 40 45 50

cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt 307  
 His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val  
 55 60 65

atc tac tac atc acc atc tac aac gag cca acc cca cag cca gct gag 355  
 Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr Pro Gln Pro Ala Glu  
 70 75 80 85

cca gaa gga ctg gac gta gaa ggc ctg cac aag ggc atc tac ctc tac 403  
 Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys Gly Ile Tyr Leu Tyr  
 90 95 100

tcc cgc ggt gaa ggc acc ggc cat gag gca aac atc ttg gct tcc ggt 451  
 Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn Ile Leu Ala Ser Gly  
 105 110 115

gtt ggt atg cag tgg gct ctc aag gct gca tcc atc ctt gag gct gac 499  
 Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser Ile Leu Glu Ala Asp  
 120 125 130



tac gga gtt cgt gcc aac att tac tcc gct act tct tgg gtt aac ttg 547  
 Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr Ser Trp Val Asn Leu  
 135 140 145  
  
 gct cgc gat ggc gct gct cgt aac aag gca cag ctg cgc aac cca ggt 595  
 Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln Leu Arg Asn Pro Gly  
 150 155 160 165  
  
 gca gat gct ggc gag gca ttc gta acc acc cag ctg aag cag acc tcc 643  
 Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln Leu Lys Gln Thr Ser  
 170 175 180  
  
 ggc cca tac gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag 691  
 Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln  
 185 190 195  
  
 atc cgt gaa tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc 739  
 Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly  
 200 205 210  
  
 ttc ggt ttc tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc 787  
 Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile  
 215 220 225  
  
 gac gct gag tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa 835  
 Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu  
 230 235 240 245  
  
 ggc aag atc gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag 883  
 Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys  
 250 255 260  
  
 ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa 931  
 Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu  
 265 270 275  
  
 taaatcacct caaggacag ata 954

&lt;210&gt; 92

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 92

Met Ala Arg Gly Phe Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu  
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Thr Gly Glu Gly Leu Gln His Met Asp Gly His Ser Pro Val Leu Ala  
 20 25 30

Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu  
 35 40 45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly  
 50 55 60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr  
 65 70 75 80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys  
                     85                    90                    95  
 Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn  
                     100                    105                    110  
 Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser  
                     115                    120                    125  
 Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr  
                     130                    135                    140  
 Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln  
 145                    150                    155                    160  
 Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln  
                     165                    170                    175  
 Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr  
                     180                    185                    190  
 Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val  
                     195                    200                    205  
 Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg  
                     210                    215                    220  
 Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn  
 225                    230                    235                    240  
 Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala  
                     245                    250                    255  
 Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro  
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 Asn Ala Pro Glu Glu  
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 <213> Corynebacterium glutamicum

<220>  
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   1                    5                    10                    15  
 tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96  
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe  
                     20                    25                    30  
 tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag 144  
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu

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          35          40          45
tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc 192
Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
      50          55          60

gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat 240
Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
      65          70          75          80

cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
          85          90

caagggacag ata 302

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<210> 94
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<212> PRT
<213> Corynebacterium glutamicum

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<400> 94
Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
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Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
          20          25          30

Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
          35          40          45

Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
      50          55          60

Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
      65          70          75          80

Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
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<210> 95
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(931)
<223> FRXA00268

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ccagcgcacc ggtgactcca tttgggcagc agccgatcag atg gca cgt ggc ttc 115
          Met Ala Arg Gly Phe
          1          5

ttt ttg ggc gct acc gca ggt cgc acc acc ttg acc ggt gaa ggc ctc 163
Phe Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu

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				10				15				20				
cag	cac	atg	gat	gga	cac	tcc	cct	gtt	ttg	gct	tcc	acc	aac	gag	ggt	211
Gln	His	Met	Asp	Gly	His	Ser	Pro	Val	Leu	Ala	Ser	Thr	Asn	Glu	Gly	
25				30				35								
gtc	gag	acc	tac	gac	cca	tcc	ttt	gcg	tac	gag	atc	gca	cac	ctg	gtt	259
Val	Glu	Thr	Tyr	Asp	Pro	Ser	Phe	Ala	Tyr	Glu	Ile	Ala	His	Leu	Val	
40				45				50								
cac	cgt	ggc	atc	gac	cgc	atg	tac	ggc	cca	ggc	aag	ggt	gaa	gat	gtt	307
His	Arg	Gly	Ile	Asp	Arg	Met	Tyr	Gly	Pro	Gly	Lys	Gly	Glu	Asp	Val	
55				60				65								
atc	tac	tac	atc	acc	atc	tac	aac	gag	cca	acc	cca	cag	cca	gct	gag	355
Ile	Tyr	Tyr	Ile	Thr	Ile	Tyr	Asn	Glu	Pro	Thr	Pro	Gln	Pro	Ala	Glu	
70				75				80				85				
cca	gaa	gga	ctg	gac	gta	gaa	ggc	ctg	cac	aag	ggc	atc	tac	ctc	tac	403
Pro	Glu	Gly	Leu	Asp	Val	Glu	Gly	Leu	His	Lys	Gly	Ile	Tyr	Leu	Tyr	
90				95				100								
tcc	cgc	ggt	gaa	ggc	acc	ggc	cat	gag	gca	aac	atc	ttg	gct	tcc	ggt	451
Ser	Arg	Gly	Glu	Gly	Thr	Gly	His	Glu	Ala	Asn	Ile	Leu	Ala	Ser	Gly	
105				110				115								
gtt	ggt	atg	cag	tgg	gct	ctc	aag	gct	gca	tcc	atc	ctt	gag	gct	gac	499
Val	Gly	Met	Gln	Trp	Ala	Leu	Lys	Ala	Ala	Ser	Ile	Leu	Glu	Ala	Asp	
120				125				130								
tac	gga	gtt	cgt	gcc	aac	att	tac	tcc	gct	act	tct	tgg	gtt	aac	ttg	547
Tyr	Gly	Val	Arg	Ala	Asn	Ile	Tyr	Ser	Ala	Thr	Ser	Trp	Val	Asn	Leu	
135				140				145								
gct	cgc	gat	ggc	gct	gct	cgt	aac	aag	gca	cag	ctg	cgc	aac	cca	ggt	595
Ala	Arg	Asp	Gly	Ala	Ala	Arg	Asn	Lys	Ala	Gln	Leu	Arg	Asn	Pro	Gly	
150				155				160				165				
gca	gat	gct	ggc	gag	gca	ttc	gta	acc	acc	cag	ctg	aag	cag	acc	tcc	643
Ala	Asp	Ala	Gly	Glu	Ala	Phe	Val	Thr	Thr	Gln	Leu	Lys	Gln	Thr	Ser	
170				175				180								
ggc	cca	tac	gtt	gca	gtg	tct	gac	ttc	tcc	act	gat	ctg	cca	aac	cag	691
Gly	Pro	Tyr	Val	Ala	Val	Ser	Asp	Phe	Ser	Thr	Asp	Leu	Pro	Asn	Gln	
185				190				195								
atc	cgt	gaa	tgg	gtc	cca	ggc	gac	tac	acc	gtt	ctc	ggt	gca	gat	ggc	739
Ile	Arg	Glu	Trp	Val	Pro	Gly	Asp	Tyr	Thr	Val	Leu	Gly	Ala	Asp	Gly	
200				205				210								
ttc	ggt	ttc	tct	gat	acc	cgc	cca	gct	gct	cgt	cgc	ttc	ttc	aac	atc	787
Phe	Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Ala	Arg	Arg	Phe	Phe	Asn	Ile	
215				220				225								
gac	gct	gag	tcc	att	gtt	gtt	gca	gtg	ctg	aac	tcc	ctg	gca	cgc	gaa	835
Asp	Ala	Glu	Ser	Ile	Val	Val	Ala	Val	Leu	Asn	Ser	Leu	Ala	Arg	Glu	
230				235				240				245				
ggc	aag	atc	gac	gtc	tcc	gtt	g									

ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa 931  
 Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu  
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<211> 277

<212> PRT

<213> *Corynebacterium glutamicum*

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                                   20                                  25                                  30

Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu  
                                   35                                  40                                  45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly  
   50                                  55                                  60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr  
   65                                  70                                  75                                  80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys  
                                   85                                  90                                  95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn  
                                   100                                  105                                  110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser  
   115                                  120                                  125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr  
   130                                  135                                  140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln  
   145                                  150                                  155                                  160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln  
                                   165                                  170                                  175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr  
                                   180                                  185                                  190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val  
                                   195                                  200                                  205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg  
   210                                  215                                  220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn  
   225                                  230                                  235                                  240

Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala  
                                   245                                  250                                  255

Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro  
 260 265 270

Asn Ala Pro Glu Glu  
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<210> 97

<211> 508

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(508)

<223> RXN03086

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 Met Ala Asp Gln Ala  
 1 5

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163  
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg  
 10 15 20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211  
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn  
 25 30 35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259  
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu  
 40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307  
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys  
 55 60 65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355  
 Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile  
 70 75 80 85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403  
 Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys  
 90 95 100

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451  
 Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg  
 105 110 115

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499  
 Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala  
 120 125 130

ggc gca gcc 508  
 Gly Ala Ala  
 135

<210> 98  
 <211> 136  
 <212> PRT  
 <213> Corynebacterium glutamicum

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 Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp  
             20                    25                    30  
 Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln  
             35                    40                    45  
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu  
             50                    55                    60  
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp  
             65                    70                    75                    80  
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp  
                     85                    90                    95  
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala  
             100                    105                    110  
 Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His  
             115                    120                    125  
 Ile Ser Thr Tyr Ala Gly Ala Ala  
             130                    135

<210> 99  
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 <213> Corynebacterium glutamicum

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 <223> FRXA02887

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   Met Ala Asp Gln Ala  
   1                    5  
 aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163  
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg  
                     10                    15                    20  
 gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211  
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn  
                     25                    30                    35  
 gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259

Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu  
           40                          45                          50  
 cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307  
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys  
           55                          60                          65  
 cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355  
 Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile  
           70                          75                          80                          85  
 cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403  
 Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys  
                           90                          95                          100  
 cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451  
 Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg  
                           105                          110                          115  
 gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499  
 Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala  
                           120                          125                          130  
 ggc gca gcc 508  
 Gly Ala Ala  
           135

&lt;210&gt; 100

&lt;211&gt; 136

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 100

Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn  
   1                          5                          10                          15  
 Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp  
           20                          25                          30  
 Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln  
           35                          40                          45  
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu  
           50                          55                          60  
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp  
           65                          70                          75                          80  
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp  
                           85                          90                          95  
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala  
           100                          105                          110  
 Ile Met Val His Arg Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His  
           115                          120                          125  
 Ile Ser Thr Tyr Ala Gly Ala Ala  
           130                          135



<210> 101  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(1362)  
 <223> RXN03043

<400> 101  
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 1 5 10 15  
 ccg tcc tac cct cac cca cac ggt atg aag gac ttc tgg gag ttc cca 96  
 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro  
 20 25 30  
 act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144  
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg  
 35 40 45  
 ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192  
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln  
 50 55 60  
 cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240  
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser  
 65 70 75 80  
 cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288  
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr  
 85 90 95  
 ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336  
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly  
 100 105 110  
 aac acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggc gca ggc 384  
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly  
 115 120 125  
 tgg tct gtg atc aag gtt gtt tgg ggt cgc gag tgg gat gaa ctt ctg 432  
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu  
 130 135 140  
 gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc 480  
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser  
 145 150 155 160  
 gat ggt gac tac cag acc ttc aag gct aac gac ggc gca tat gtt cgt 528  
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg  
 165 170 175  
 gag cac ttc ttc gga cgt gac cca cgc acc gca aag ctc gtt gag aac 576  
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn  
 180 185 190  
 atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac 624

Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr	
		195					200					205				
cgc	aag	gtt	tac	gca	gcc	tac	aag	cga	gct	ctt	gag	acc	aag	gat	cgc	672
Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg	
	210					215					220					
cca	acc	gtc	atc	ctt	gct	cac	acc	att	aag	ggc	tac	gga	ctc	ggc	cac	720
Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His	
225					230					235					240	
aac	ttc	gaa	ggc	cgt	aac	gca	acc	cac	cag	atg	aag	aag	ctg	acg	ctt	768
Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu	
				245					250					255		
gat	gat	ctg	aag	ttg	ttc	cgc	gac	aag	cag	ggc	atc	cca	atc	acc	gat	816
Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Ile	Pro	Ile	Thr	Asp	
		260						265					270			
gag	cag	ctg	gag	aag	gat	cct	tac	ctt	cct	cct	tac	tac	cac	cca	ggt	864
Glu	Gln	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly	
		275					280					285				
gaa	gac	gct	cct	gaa	atc	aag	tac	atg	aag	gaa	cgt	cgc	gca	gcg	ctc	912
Glu	Asp	Ala	Pro	Glu	Ile	Lys	Tyr	Met	Lys	Glu	Arg	Arg	Ala	Ala	Leu	
	290					295					300					
ggt	ggc	tac	ctg	cca	gag	cgt	cgt	gag	aac	tac	gat	cca	att	cag	gtt	960
Gly	Gly	Tyr	Leu	Pro	Glu	Arg	Arg	Glu	Asn	Tyr	Asp	Pro	Ile	Gln	Val	
305					310				315						320	
cca	cca	ctg	gat	aag	ctt	cgc	tct	gtc	cgt	aag	ggc	tcc	ggc	aag	cag	1008
Pro	Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg	Lys	Gly	Ser	Gly	Lys	Gln	
				325					330					335		
cag	atc	gct	acc	acc	atg	gcg	act	gtt	cgt	acc	ttc	aag	gaa	ctg	atg	1056
Gln	Ile	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg	Thr	Phe	Lys	Glu	Leu	Met	
			340					345					350			
cgc	gat	aag	ggc	ttg	gct	gat	cgc	ctt	gtc	cca	atc	att	cct	gat	gag	1104
Arg	Asp	Lys	Gly	Leu	Ala	Asp	Arg	Leu	Val	Pro	Ile	Ile	Pro	Asp	Glu	
		355					360					365				
gca	cgt	acc	ttc	ggt	ctt	gac	tct	tgg	ttc	cca	acc	ttg	aag	atc	tac	1152
Ala	Arg	Thr	Phe	Gly	Leu	Asp	Ser	Trp	Phe	Pro	Thr	Leu	Lys	Ile	Tyr	
	370					375					380					
aac	ccg	cac	ggt	cag	aac	tac	gtg	cct	gtt	gac	cac	gac	ctg	atg	ctc	1200
Asn	Pro	His	Gly	Gln	Asn	Tyr	Val	Pro	Val	Asp	His	Asp	Leu	Met	Leu	
385					390					395				400		
tcc	tac	cgt	gag	gca	cct	gaa	gga	cag	atc	ctg	cac	gaa	ggc	atc	aac	1248
Ser	Tyr	Arg	Glu	Ala	Pro	Glu	Gly	Gln	Ile	Leu	His	Glu	Gly	Ile	Asn	
				405					410					415		
gag	gct	ggt	tcc	gtg	gca	tcg	ttc	atc	gct	gcg	ggt	acc	tcc	tac	gcc	1296
Glu	Ala	Gly	Ser	Val	Ala	Ser	Phe	Ile	Ala	Ala	Gly	Thr	Ser	Tyr	Ala	
			420					425					430			
acc	cac	ggc	aag	gcc	atg	att	ccg	ctg	tac	atc	ttc	tac	tcg	atg	ttc	1344
Thr	His	Gly	Lys	Ala	Met	Ile	Pro	Leu	Tyr	Ile	Phe	Tyr	Ser	Met	Phe	

435 440 445 1385  
 ggg att cca gcg cac cgg tgactccatc tgggcagcag ccg  
 Gly Ile Pro Ala His Arg  
 450

<210> 102  
 <211> 454  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 102  
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 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro  
 20 25 30  
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg  
 35 40 45  
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln  
 50 55 60  
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser  
 65 70 75 80  
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr  
 85 90 95  
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly  
 100 105 110  
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly  
 115 120 125  
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu  
 130 135 140  
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser  
 145 150 155 160  
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg  
 165 170 175  
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn  
 180 185 190  
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr  
 195 200 205  
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg  
 210 215 220  
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His  
 225 230 235 240  
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu  
 245 250 255

Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp  
 260 265 270  
 Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly  
 275 280 285  
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu  
 290 295 300  
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val  
 305 310 315 320  
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln  
 325 330 335  
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met  
 340 345 350  
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu  
 355 360 365  
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr  
 370 375 380  
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu  
 385 390 395 400  
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn  
 405 410 415  
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala  
 420 425 430  
 Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe  
 435 440 445  
 Gly Ile Pro Ala His Arg  
 450

&lt;210&gt; 103

&lt;211&gt; 1287

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1287)

&lt;223&gt; FRXA02897

&lt;400&gt; 103

gat	ctc	gat	ggc	ttc	cgt	cag	gaa	gtt	tcc	cgt	gag	cag	ggt	ggc	att	48
Asp	Leu	Asp	Gly	Phe	Arg	Gln	Glu	Val	Ser	Arg	Glu	Gln	Gly	Gly	Ile	
1				5					10					15		
ccg	tcc	tac	cct	cac	cca	cac	ggt	atg	aag	gac	ttc	tgg	gag	ttc	cca	96
Pro	Ser	Tyr	Pro	His	Pro	His	Gly	Met	Lys	Asp	Phe	Trp	Glu	Phe	Pro	
			20					25					30			
act	gtg	tcc	atg	ggt	ctt	ggc	cca	atg	gat	gcc	att	tac	cag	gca	cgt	144
Thr	Val	Ser	Met	Gly	Leu	Gly	Pro	Met	Asp	Ala	Ile	Tyr	Gln	Ala	Arg	

35					40					45						
ttc	aac	cgc	tac	ctc	gaa	aac	cgt	ggc	atc	aag	gac	acc	tct	gac	cag	192
Phe	Asn	Arg	Tyr	Leu	Glu	Asn	Arg	Gly	Ile	Lys	Asp	Thr	Ser	Asp	Gln	
	50					55					60					
cac	gtc	tgg	gcc	ttc	ctt	ggc	gac	ggc	gaa	atg	gac	gag	cca	gaa	tca	240
His	Val	Trp	Ala	Phe	Leu	Gly	Asp	Gly	Glu	Met	Asp	Glu	Pro	Glu	Ser	
	65				70					75					80	
cgt	ggt	ctc	atc	cag	cag	gct	gca	ctg	aac	aac	ctg	gac	aac	ctg	acc	288
Arg	Gly	Leu	Ile	Gln	Gln	Ala	Ala	Leu	Asn	Asn	Leu	Asp	Asn	Leu	Thr	
				85					90					95		
ttc	gtg	gtt	aac	tgc	aac	ctg	cag	cgt	ctc	gac	gga	cct	gtc	cgc	ggt	336
Phe	Val	Val	Asn	Cys	Asn	Leu	Gln	Arg	Leu	Asp	Gly	Pro	Val	Arg	Gly	
			100					105					110			
aac	acc	aag	atc	atc	cag	gaa	ctc	gag	tcc	ttc	ttc	cgt	ggc	gca	ggc	384
Asn	Thr	Lys	Ile	Ile	Gln	Glu	Leu	Glu	Ser	Phe	Phe	Arg	Gly	Ala	Gly	
		115					120					125				
tgg	tct	gtg	atc	aag	gtt	gtt	tgg	ggt	cgc	gag	tgg	gat	gaa	ctt	ctg	432
Trp	Ser	Val	Ile	Lys	Val	Val	Trp	Gly	Arg	Glu	Trp	Asp	Glu	Leu	Leu	
	130					135					140					
gag	aag	gac	cag	gat	ggt	gca	ctt	gtt	gag	atc	atg	aac	aac	acc	tcc	480
Glu	Lys	Asp	Gln	Asp	Gly	Ala	Leu	Val	Glu	Ile	Met	Asn	Asn	Thr	Ser	
	145				150					155					160	
gat	ggt	gac	tac	cag	acc	ttc	aag	gct	aac	gac	ggc	gca	tat	gtt	cgt	528
Asp	Gly	Asp	Tyr	Gln	Thr	Phe	Lys	Ala	Asn	Asp	Gly	Ala	Tyr	Val	Arg	
				165					170					175		
gag	cac	ttc	ttc	gga	cgt	gac	cca	cgc	acc	gca	aag	ctc	gtt	gag	aac	576
Glu	His	Phe	Phe	Gly	Arg	Asp	Pro	Arg	Thr	Ala	Lys	Leu	Val	Glu	Asn	
			180					185					190			
atg	acc	gac	gaa	gaa	atc	tgg	aag	ctt	cca	cgt	ggc	ggc	cac	gat	tac	624
Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr	
		195					200					205				
cgc	aag	gtt	tac	gca	gcc	tac	aag	cga	gct	ctt	gag	acc	aag	gat	cgc	672
Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg	
	210					215					220					
cca	acc	gtc	atc	ctt	gct	cac	acc	att	aag	ggc	tac	gga	ctc	ggc	cac	720
Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His	
	225				230					235					240	
aac	ttc	gaa	ggc	cgt	aac	gca	acc	cac	cag	atg	aag	aag	ctg	acg	ctt	768
Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu	
				245					250					255		
gat	gat	ctg	aag	ttg	ttc	cgc	gac	aag	cag	ggc	atc	cca	atc	acc	gat	816
Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Ile	Pro	Ile	Thr	Asp	
			260					265					270			
gag	cag	ctg	gag	aag	gat	cct	tac	ctt	cct	cct	tac	tac	cac	cca	ggt	864
Glu	Gln	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly	
		275					280					285				

gaa gac gct cct gaa atc aag tac atg aag gaa cgt cgc gca gcg ctc 912  
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu  
 290 295 300

ggt ggc tac ctg cca gag cgt cgt gag aac tac gat cca att cag gtt 960  
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val  
 305 310 315 320

cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag 1008  
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln  
 325 330 335

cag atc gct acc acc atg gcg act gtt cgt acc ttc aag gaa ctg atg 1056  
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met  
 340 345 350

cgc gat aag ggc ttg gct gat cgc ctt gtc cca atc att cct gat gag 1104  
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu  
 355 360 365

gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac 1152  
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr  
 370 375 380

aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc 1200  
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu  
 385 390 395 400

tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac 1248  
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn  
 405 410 415

gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc 1287  
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr  
 420 425

&lt;210&gt; 104

&lt;211&gt; 429

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 104

Asp Leu Asp Gly Phe Arg Gln Glu Val Ser Arg Glu Gln Gly Gly Ile  
 1 5 10 15

Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro  
 20 25 30

Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg  
 35 40 45

Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln  
 50 55 60

His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser  
 65 70 75 80

Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr  
 85 90 95

Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly  
 100 105 110  
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly  
 115 120 125  
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu  
 130 135 140  
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser  
 145 150 155 160  
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg  
 165 170 175  
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn  
 180 185 190  
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr  
 195 200 205  
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg  
 210 215 220  
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His  
 225 230 235 240  
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu  
 245 250 255  
 Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp  
 260 265 270  
 Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly  
 275 280 285  
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu  
 290 295 300  
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val  
 305 310 315 320  
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln  
 325 330 335  
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met  
 340 345 350  
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu  
 355 360 365  
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr  
 370 375 380  
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu  
 385 390 395 400  
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn  
 405 410 415

Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (88)..(1110)  
 <223> RXN03083

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 Met Ala Lys Arg Ile Val Ile Ile Gly  
 1 5  
 ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 162  
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly  
 10 15 20 25  
 gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 210  
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val  
 30 35 40  
 acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 258  
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile  
 45 50 55  
 aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 306  
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu  
 60 65 70  
 gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 354  
 Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp  
 75 80 85  
 ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca 402  
 Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser  
 90 95 100 105  
 gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc 450  
 Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr  
 110 115 120  
 aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa 498  
 Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu  
 125 130 135  
 gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc 546  
 Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro  
 140 145 150  
 cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg 594  
 Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp  
 155 160 165



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cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt 642
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val
170 175 180 185

ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc 690
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu
190 195 200

ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac 738
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His
205 210 215

gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc 786
Asp Asp Ala Asp Ala Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg
220 225 230

gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc 834
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr
235 240 245

gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac 882
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr
250 255 260 265

ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat 930
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp
270 275 280

ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc 978
Leu Gly Leu Glu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile
285 290 295

aag gtt gac cgg tct ccc gca cca aca tcc ccg gtg tgt acg cag cag 1026
Lys Val Asp Arg Ser Pro Ala Pro Thr Ser Pro Val Cys Thr Gln Gln
300 305 310

gtg act gta ctg acc tat tcc cac tgg cgt ccg ttg cag cga tgc agg 1074
Val Thr Val Leu Thr Tyr Ser His Trp Arg Pro Leu Gln Arg Cys Arg
315 320 325

gcc gta tgc cca tgt atc acg cac tgc gtg aag gcg tgagccccat 1120
Ala Val Ser Pro Cys Ile Thr His Ser Val Lys Ala
330 335 340

ccgtttgaag act 1133

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&lt;210&gt; 106

&lt;211&gt; 341

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 106

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Met Ala Lys Arg Ile Val Ile Ile Gly Gly Gly Pro Ala Gly Tyr Glu
  1           5           10           15

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Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu
      20           25           30

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Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
      35           40           45

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Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala  
 50 55 60  
 Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile  
 65 70 75 80  
 Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu  
 85 90 95  
 Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly  
 100 105 110  
 Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile  
 115 120 125  
 Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu  
 130 135 140  
 Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu  
 145 150 155 160  
 Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu  
 165 170 175  
 Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala  
 180 185 190  
 Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val  
 195 200 205  
 Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp  
 210 215 220  
 Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His  
 225 230 235 240  
 Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val  
 245 250 255  
 Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr  
 260 265 270  
 Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly  
 275 280 285  
 Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Ser Pro Ala  
 290 295 300  
 Pro Thr Ser Pro Val Cys Thr Gln Gln Val Thr Val Leu Thr Tyr Ser  
 305 310 315 320  
 His Trp Arg Pro Leu Gln Arg Cys Arg Ala Val Ser Pro Cys Ile Thr  
 325 330 335  
 His Ser Val Lys Ala  
 340

&lt;210&gt; 107

&lt;211&gt; 1518

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (89)..(1495)

&lt;223&gt; FRXA02853

&lt;400&gt; 107

aattcagcag taatcattta gacttggaaac cgcttaccag tggtttcaac aatgcattca 60

cccagctcac acgtgtggag gtgcctta atg gca aag agg atc gta att atc ggc 115  
Met Ala Lys Arg Ile Val Ile Ile Gly

1

5

ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 163  
Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly  
10 15 20 25gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 211  
Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val  
30 35 40acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 259  
Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile  
45 50 55aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 307  
Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu  
60 65 70gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 355  
Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp  
75 80 85ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca 403  
Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser  
90 95 100 105gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc 451  
Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr  
110 115 120aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa 499  
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu  
125 130 135gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc 547  
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro  
140 145 150cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg 595  
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp  
155 160 165cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt 643  
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val  
170 175 180 185ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc 691  
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu

190								195								200	
ggc	gtc	aaa	gtc	acc	atg	gtg	gca	tcc	cgt	gac	cgc	att	ttg	cct	cac	739	
Gly	Val	Lys	Val	Thr	Met	Val	Ala	Ser	Arg	Asp	Arg	Ile	Leu	Pro	His		
205								210								215	
gat	gac	gca	gat	gcc	gca	gac	gtg	ctg	gaa	acc	gtt	ctg	gct	gag	cgc	787	
Asp	Asp	Ala	Asp	Ala	Ala	Asp	Val	Leu	Glu	Thr	Val	Leu	Ala	Glu	Arg		
220								225								230	
gga	gta	tcc	ctg	gaa	aag	cat	gcc	cgc	gtg	gag	tct	gtc	acc	cgc	acc	835	
Gly	Val	Ser	Leu	Glu	Lys	His	Ala	Arg	Val	Glu	Ser	Val	Thr	Arg	Thr		
235								240								245	
gaa	gac	ggt	ggc	gtg	tgt	gtt	cgc	act	gct	gac	gga	cga	gaa	atc	tac	883	
Glu	Asp	Gly	Gly	Val	Cys	Val	Arg	Thr	Ala	Asp	Gly	Arg	Glu	Ile	Tyr		
250								255								260	
ggt	tct	cac	gcg	ttg	atg	act	gtt	ggt	tcc	att	cca	aac	acg	gca	gat	931	
Gly	Ser	His	Ala	Leu	Met	Thr	Val	Gly	Ser	Ile	Pro	Asn	Thr	Ala	Asp		
270								275								280	
ctt	ggc	ctg	gag	aac	atc	ggt	gtt	gag	ctg	gca	cca	tcc	ggc	cat	atc	979	
Leu	Gly	Leu	Glu	Asn	Ile	Gly	Val	Glu	Leu	Ala	Pro	Ser	Gly	His	Ile		
285								290								295	
aag	gtt	gac	cgn	gtc	tcc	cgc	acc	aac	atc	ccc	ggt	gtg	tac	gca	gca	1027	
Lys	Val	Asp	Arg	Val	Ser	Arg	Thr	Asn	Ile	Pro	Gly	Val	Tyr	Ala	Ala		
300								305								310	
ggt	gac	tgt	act	gac	cta	ttc	cca	ctg	gcg	tcc	gtt	gca	gcg	atg	cag	1075	
Gly	Asp	Cys	Thr	Asp	Leu	Phe	Pro	Leu	Ala	Ser	Val	Ala	Ala	Met	Gln		
315								320								325	
ggc	cgt	atc	gcc	atg	tat	cac	gca	ctc	ggt	gaa	ggc	gtg	agc	ccc	atc	1123	
Gly	Arg	Ile	Ala	Met	Tyr	His	Ala	Leu	Gly	Glu	Gly	Val	Ser	Pro	Ile		
330								335								340	
cgt	ttg	aag	act	gtt	gcc	acc	gca	gtg	ttt	acc	cgc	cca	gag	atc	gca	1171	
Arg	Leu	Lys	Thr	Val	Ala	Thr	Ala	Val	Phe	Thr	Arg	Pro	Glu	Ile	Ala		
350								355								360	
gca	gta	ggt	atc	acc	cat	gca	caa	gtt	gat	tcc	ggc	gaa	gtg	tct	gct	1219	
Ala	Val	Gly	Ile	Thr	His	Ala	Gln	Val	Asp	Ser	Gly	Glu	Val	Ser	Ala		
365								370								375	
cgc	gtg	att	gtg	ctt	cct	ttg	gct	act	aac	cca	cgc	gcc	aag	atg	cgt	1267	
Arg	Val	Ile	Val	Leu	Pro	Leu	Ala	Thr	Asn	Pro	Arg	Ala	Lys	Met	Arg		
380								385								390	
tcc	ctg	cgc	cac	ggt	ttt	gtg	aag	ctg	ttc	tgc	cgc	cgt	aac	tct	ggc	1315	
Ser	Leu	Arg	His	Gly	Phe	Val	Lys	Leu	Phe	Cys	Arg	Arg	Asn	Ser	Gly		
395								400								405	
ctg	atc	atc	ggt	ggt	gtc	gtg	gtg	gca	ccg	acc	gcg	tct	gag	ctg	atc	1363	
Leu	Ile	Ile	Gly	Gly	Val	Val	Val	Ala	Pro	Thr	Ala	Ser	Glu	Leu	Ile		
410								415								420	
cta	ccg	atc	gct	gtg	gca	gtg	acc	aac	cgt	ctg	aca	gtt	gct	gat	ctg	1411	
Leu	Pro	Ile	Ala	Val	Ala	Val	Thr	Asn	Arg	Leu	Thr	Val	Ala	Asp	Leu		
430								435								440	

gct gat acc ttc gcg gtg tac cca tca ttg tca ggt tcg att act gaa 1459  
 Ala Asp Thr Phe Ala Val Tyr Pro Ser Leu Ser Gly Ser Ile Thr Glu  
                   445                                  450                                  455

gca gca cgt cag ctg gtt caa cat gat gat cta ggc taatttttct 1505  
 Ala Ala Arg Gln Leu Val Gln His Asp Asp Leu Gly  
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gagtcttaga ttt 1518

<210> 108

<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Met Ala Lys Arg Ile Val Ile Ile Gly Gly Gly Pro Ala Gly Tyr Glu  
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Ala Ala Leu Ala Gly Ala Lys Tyr Gly Ala Glu Val Thr Val Ile Glu  
                   20                                  25                                  30

Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser  
                   35                                  40                                  45

Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala  
                   50                                  55                                  60

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile  
   65                                  70                                  75                                  80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu  
                   85                                  90                                  95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly  
                   100                                  105                                  110

Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile  
                   115                                  120                                  125

Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu  
   130                                  135                                  140

Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu  
   145                                  150                                  155                                  160

Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu  
                   165                                  170                                  175

Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala  
                   180                                  185                                  190

Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val  
                   195                                  200                                  205

Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp  
   210                                  215                                  220

Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His

225                      230                      235                      240  
 Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val  
                                  245                      250                      255  
 Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr  
                                  260                      265                      270  
 Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly  
                                  275                      280                      285  
 Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Val Ser Arg  
                                  290                      295                      300  
 Thr Asn Ile Pro Gly Val Tyr Ala Ala Gly Asp Cys Thr Asp Leu Phe  
 305                                   310                      315                      320  
 Pro Leu Ala Ser Val Ala Ala Met Gln Gly Arg Ile Ala Met Tyr His  
                                  325                      330                      335  
 Ala Leu Gly Glu Gly Val Ser Pro Ile Arg Leu Lys Thr Val Ala Thr  
                                  340                      345                      350  
 Ala Val Phe Thr Arg Pro Glu Ile Ala Ala Val Gly Ile Thr His Ala  
                                  355                      360                      365  
 Gln Val Asp Ser Gly Glu Val Ser Ala Arg Val Ile Val Leu Pro Leu  
                                  370                      375                      380  
 Ala Thr Asn Pro Arg Ala Lys Met Arg Ser Leu Arg His Gly Phe Val  
 385                                   390                      395                      400  
 Lys Leu Phe Cys Arg Arg Asn Ser Gly Leu Ile Ile Gly Gly Val Val  
                                  405                      410                      415  
 Val Ala Pro Thr Ala Ser Glu Leu Ile Leu Pro Ile Ala Val Ala Val  
                                  420                      425                      430  
 Thr Asn Arg Leu Thr Val Ala Asp Leu Ala Asp Thr Phe Ala Val Tyr  
                                  435                      440                      445  
 Pro Ser Leu Ser Gly Ser Ile Thr Glu Ala Ala Arg Gln Leu Val Gln  
                                  450                      455                      460  
 His Asp Asp Leu Gly  
 465

<210> 109

<211> 2895

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2872)

<223> RXA02259

<400> 109

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ttttttatct catgcacgcc aacaccctca atgtgaaaga	gtg ttt aaa gta gtt	115
	Val Phe Lys Val Val	
	1 5	
atg act gat ttt tta cgc gat gac atc agg ttc ctc ggt caa atc ctc	163	
Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe Leu Gly Gln Ile Leu		
	10 15 20	
ggt gag gta att gcg gaa caa gaa ggc cag gag gtt tat gaa ctg gtc	211	
Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu Val Tyr Glu Leu Val		
	25 30 35	
gaa caa gcg cgc ctg act tct ttt gat atc gcc aag ggc aac gcc gaa	259	
Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala Lys Gly Asn Ala Glu		
	40 45 50	
atg gat agc ctg gtt cag gtt ttc gac ggc att act cca gcc aag gca	307	
Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile Thr Pro Ala Lys Ala		
	55 60 65	
aca ccg att gct cgc gca ttt tcc cac ttc gct ctg ctg gct aac ctg	355	
Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala Leu Leu Ala Asn Leu		
	70 75 80 85	
gcg gaa gac ctc tac gat gaa gag ctt cgt gaa cag gct ctc gat gca	403	
Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu Gln Ala Leu Asp Ala		
	90 95 100	
ggc gac acc cct ccg gac agc act ctt gat gcc acc tgg ctg aaa ctc	451	
Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala Thr Trp Leu Lys Leu		
	105 110 115	
aat gag ggc aat gtt ggc gca gaa gct gtg gcc gat gtg ctg cgc aat	499	
Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala Asp Val Leu Arg Asn		
	120 125 130	
gct gag gtg gcg ccg gtt ctg act gcg cac cca act gag act cgc cgc	547	
Ala Glu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg		
	135 140 145	
cgc act gtt ttt gat gcg caa aag tgg atc acc acc cac atg cgt gaa	595	
Arg Thr Val Phe Asp Ala Gln Lys Trp Ile Thr Thr His Met Arg Glu		
	150 155 160 165	
cgc cac gct ttg cag tct gcg gag cct acc gct cgt acg caa agc aag	643	
Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala Arg Thr Gln Ser Lys		
	170 175 180	
ttg gat gag atc gag aag aac atc cgc cgt cgc atc acc att ttg tgg	691	
Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp		
	185 190 195	
cag acc gcg ttg att cgt gtg gcc cgc cca cgt atc gag gac gag atc	739	
Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Ile		
	200 205 210	
gaa gta ggg ctg cgc tac tac aag ctg agc ctt ttg gaa gag att cca	787	
Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Glu Glu Ile Pro		
	215 220 225	
cgt atc aac cgt gat gtg gct gtt gag ctt cgt gag cgt ttc ggc gag	835	

Arg 230	Ile	Asn	Arg	Asp	Val 235	Ala	Val	Glu	Leu	Arg 240	Glu	Arg	Phe	Gly	Glu 245	
ggc	gtt	cct	ttg	aag	ccc	gtg	gtc	aag	cca	ggc	tcc	tgg	att	ggc	gga	883
Gly	Val	Pro	Leu	Lys 250	Pro	Val	Val	Lys	Pro 255	Gly	Ser	Trp	Ile	Gly	Gly	
gac	cac	gac	ggc	aac	cct	tat	gtc	acc	gcg	gaa	aca	ggt	gag	tat	tcc	931
Asp	His	Asp	Gly 265	Asn	Pro	Tyr	Val	Thr 270	Ala	Glu	Thr	Val	Glu	Tyr	Ser	
act	cac	cg	gct	gcg	gaa	acc	gtg	ctc	aag	tac	tat	gca	cg	cag	ctg	979
Thr	His	Arg	Ala 280	Ala	Glu	Thr	Val	Leu 285	Lys	Tyr	Tyr	Ala	Arg	Gln	Leu	
cat	tcc	ctc	gag	cat	gag	ctc	agc	ctg	tcg	gac	cg	atg	aat	aag	gtc	1027
His	Ser	Leu	Glu	His	Glu	Leu	Ser	Leu	Ser	Asp 305	Arg	Met	Asn	Lys	Val	
acc	ccg	cag	ctg	ctt	gcg	ctg	gca	gat	gca	ggg	cac	aac	gac	gtg	cca	1075
Thr	Pro	Gln	Leu	Leu	Ala	Leu	Ala	Asp	Ala	Gly	His	Asn	Asp	Val	Pro 325	
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agc	cg	gtg	gat	gag	cct	tat	cga	cg	gcc	gtc	cat	ggc	gtt	cg	gga	1123
Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Val	His	Gly	Val	Arg	Gly 340	
330									335							
cgt	atc	ctc	gcg	acg	acg	gcc	gag	ctg	atc	ggc	gag	gac	gcc	gtt	gag	1171
Arg	Ile	Leu	Ala 345	Thr	Thr	Ala	Glu	Leu	Ile	Gly	Glu	Asp	Ala	Val	Glu 355	
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Gly	Val	Trp	Phe	Lys	Val	Phe	Thr 365	Pro	Tyr	Ala	Ser	Pro	Glu	Glu	Phe	
360												370				
tta	aac	gat	gcg	ttg	acc	att	gat	cat	tct	ctg	cgt	gaa	tcc	aag	gac	1267
Leu	Asn	Asp	Ala	Leu	Thr	Ile	Asp	His	Ser	Leu	Arg	Glu	Ser	Lys	Asp 385	
375						380										
gtt	ctc	att	gcc	gat	gat	cgt	ttg	tct	gtg	ctg	att	tct	gcc	atc	gag	1315
Val	Leu	Ile	Ala	Asp	Asp	Arg	Leu	Ser	Val	Leu	Ile	Ser	Ala	Ile	Glu 405	
390					395					400						
agc	ttt	gga	ttc	aac	ctt	tac	gca	ctg	gat	ctg	cg	caa	aac	tcc	gaa	1363
Ser	Phe	Gly	Phe	Asn	Leu	Tyr	Ala	Leu	Asp 415	Leu	Arg	Gln	Asn	Ser	Glu 420	
410																
agc	tac	gag	gac	gtc	ctc	acc	gag	ctt	ttc	gaa	cg	gcc	caa	gtc	acc	1411
Ser	Tyr	Glu	Asp	Val	Leu	Thr	Glu	Leu	Phe	Glu	Arg	Ala	Gln	Val	Thr 435	
425								430								
gca	aac	tac	cg	gag	ctg	tct	gaa	gca	gag	aag	ctt	gag	gtg	ctg	ctg	1459
Ala	Asn	Tyr	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Lys	Leu	Glu	Val	Leu	Leu	
440							445					450				
aag	gaa	ctg	cg	agc	cct	cgt	ccg	ctg	atc	ccg	cac	ggc	tca	gat	gaa	1507
Lys	Glu	Leu	Arg	Ser	Pro	Arg	Pro	Leu	Ile	Pro	His	Gly	Ser	Asp	Glu 465	
455						460										
tac	agc	gag	gtc	acc	gac	cg	gag	ctc	ggc	atc	ttc	cg	acc	gcg	tcg	1555
Tyr	Ser	Glu	Val	Thr	Asp	Arg	Glu	Leu	Gly	Ile	Phe	Arg	Thr	Ala	Ser	



470	475	480	485	
gag gct gtt aag aaa ttc ggg cca cgg atg gtg cct cac tgc atc atc				1603
Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val Pro His Cys Ile Ile				
	490	495	500	
tcc atg gca tca tgc gtc acc gat gtg ctc gag ccg atg gtg ttg ctc				1651
Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu Pro Met Val Leu Leu				
	505	510	515	
aag gaa ttc gga ctc atc gca gcc aac ggc gac aac cca cgc ggc acc				1699
Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp Asn Pro Arg Gly Thr				
	520	525	530	
gtc gat gtc atc cca ctg ttc gaa acc atc gaa gat ctc cag gcc ggc				1747
Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu Asp Leu Gln Ala Gly				
	535	540	545	
gcc gga atc ctc gac gaa ctg tgg aaa att gat ctc tac cgc aac tac				1795
Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp Leu Tyr Arg Asn Tyr				
	550	555	560	565
ctc ctg cag cgc gac aac gtc cag gaa gtc atg ctc ggt tac tcc gat				1843
Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp				
	570	575	580	
tcc aac aag gat ggc gga tat ttc tcc gca aac tgg gcg ctt tac gac				1891
Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn Trp Ala Leu Tyr Asp				
	585	590	595	
gcg gaa ctg cag ctc gtc gaa cta tgc cga tca gcc ggg gtc aag ctt				1939
Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser Ala Gly Val Lys Leu				
	600	605	610	
cgc ctg ttc cac ggc cgt ggt ggc acc gtc ggc cgc ggt ggc gga cct				1987
Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro				
	615	620	625	
tcc tac gac gcg att ctt gcc cag ccc agg ggg gct gtc caa ggt tcc				2035
Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly Ala Val Gln Gly Ser				
	630	635	640	645
gtg cgc atc acc gag cag ggc gag atc atc tcc gct aag tac ggc aac				2083
Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn				
	650	655	660	
ccc gaa acc gcg cgc cga aac ctc gaa gcc ctg gtc tca gcc acg ctt				2131
Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu				
	665	670	675	
gag gca tgc ctt ctc gac gtc tcc gaa ctc acc gat cac caa cgc gcg				2179
Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr Asp His Gln Arg Ala				
	680	685	690	
tac gac atc atg agt gag atc tct gag ctc agc ttg aag aag tac gcc				2227
Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala				
	695	700	705	
tcc ttg gtg cac gag gat caa ggc ttc atc gat tac ttc acc cag tcc				2275
Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp Tyr Phe Thr Gln Ser				
	710	715	720	725

acg ccg ctg cag gag att gga tcc ctc aac atc gga tcc agg cct tcc	2323
Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser	
730 735 740	
tca cgc aag cag acc tcc tcg gtg gaa gat ttg cga gcc atc cca tgg	2371
Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu Arg Ala Ile Pro Trp	
745 750 755	
gtg ctc agc tgg tca cag tct cgt gtc atg ctg cca ggc tgg ttt ggt	2419
Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly	
760 765 770	
gtc gga acc gca tta gag cag tgg att ggc gaa ggg gag cag gcc acc	2467
Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu Gly Glu Gln Ala Thr	
775 780 785	
caa cgc att gcc gag ctg caa aca ctc aat gag tcc tgg cca ttt ttc	2515
Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu Ser Trp Pro Phe Phe	
790 795 800 805	
acc tca gtg ttg gat aac atg gct cag gtg atg tcc aag gca gag ctg	2563
Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu	
810 815 820	
cgt ttg gca aag ctc tac gca gac ctg atc cca gat acg gaa gta gcc	2611
Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro Asp Thr Glu Val Ala	
825 830 835	
gag cga gtc tat tcc gtc atc cgc gag gag tac ttc ctg acc aag aag	2659
Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys	
840 845 850	
atg ttc tgc gta atc acc ggc tct gat gat ctg ctt gat gac aac cca	2707
Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu Leu Asp Asp Asn Pro	
855 860 865	
ctt etc gca cgc tct gtc cag cgc cga tac ccc tac ctg ctt cca ctc	2755
Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro Tyr Leu Leu Pro Leu	
870 875 880 885	
aac gtg atc cag gta gag atg atg cga cgc tac cga aaa ggc gac caa	2803
Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Lys Gly Asp Gln	
890 895 900	
agc gag caa gtg tcc cgc aac att cag ctg acc atg aac ggt ctt tcc	2851
Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr Met Asn Gly Leu Ser	
905 910 915	
act gcg ctg cgc aac tcc ggc tagtccagcc ggctgggtag tac	2895
Thr Ala Leu Arg Asn Ser Gly	
920	

&lt;210&gt; 110

&lt;211&gt; 924

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 110

Val Phe Lys Val Val Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe

1	5	10	15
Leu Gly Gln Ile	Leu Gly Glu Val	Ile Ala Glu Gln	Glu Gly Gln Glu
20		25	30
Val Tyr Glu Leu	Val Glu Gln Ala	Arg Leu Thr Ser	Phe Asp Ile Ala
35	40	45	
Lys Gly Asn Ala	Glu Met Asp Ser	Leu Val Gln Val	Phe Asp Gly Ile
50	55	60	
Thr Pro Ala Lys	Ala Thr Pro Ile	Ala Arg Ala Phe	Ser His Phe Ala
65	70	75	80
Leu Leu Ala Asn	Leu Ala Glu Asp	Leu Tyr Asp Glu	Glu Leu Arg Glu
85	90	95	
Gln Ala Leu Asp	Ala Gly Asp Thr	Pro Pro Asp Ser	Thr Leu Asp Ala
100	105	110	
Thr Trp Leu Lys	Leu Asn Glu Gly	Asn Val Gly Ala	Glu Ala Val Ala
115	120	125	
Asp Val Leu Arg	Asn Ala Glu Val	Ala Pro Val Leu	Thr Ala His Pro
130	135	140	
Thr Glu Thr Arg	Arg Arg Thr Val	Phe Asp Ala Gln	Lys Trp Ile Thr
145	150	155	160
Thr His Met Arg	Glu Arg His Ala	Leu Gln Ser Ala	Glu Pro Thr Ala
165	170	175	
Arg Thr Gln Ser	Lys Leu Asp Glu	Ile Glu Lys Asn	Ile Arg Arg Arg
180	185	190	
Ile Thr Ile Leu	Trp Gln Thr Ala	Leu Ile Arg Val	Ala Arg Pro Arg
195	200	205	
Ile Glu Asp Glu	Ile Glu Val Gly	Leu Arg Tyr Tyr	Lys Leu Ser Leu
210	215	220	
Leu Glu Glu Ile	Pro Arg Ile Asn	Arg Asp Val Ala	Val Glu Leu Arg
225	230	235	240
Glu Arg Phe Gly	Glu Gly Val Pro	Leu Lys Pro Val	Val Lys Pro Gly
245	250	255	
Ser Trp Ile Gly	Gly Asp His Asp	Gly Asn Pro Tyr	Val Thr Ala Glu
260	265	270	
Thr Val Glu Tyr	Ser Thr His Arg	Ala Ala Glu Thr	Val Leu Lys Tyr
275	280	285	
Tyr Ala Arg Gln	Leu His Ser Leu	Glu His Glu Leu	Ser Leu Ser Asp
290	295	300	
Arg Met Asn Lys	Val Thr Pro Gln	Leu Leu Ala Leu	Ala Asp Ala Gly
305	310	315	320
His Asn Asp Val	Pro Ser Arg Val	Asp Glu Pro Tyr	Arg Arg Ala Val
325	330	335	

His Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Glu Leu Ile Gly  
 340 345 350  
 Glu Asp Ala Val Glu Gly Val Trp Phe Lys Val Phe Thr Pro Tyr Ala  
 355 360 365  
 Ser Pro Glu Glu Phe Leu Asn Asp Ala Leu Thr Ile Asp His Ser Leu  
 370 375 380  
 Arg Glu Ser Lys Asp Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu  
 385 390 395 400  
 Ile Ser Ala Ile Glu Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu  
 405 410 415  
 Arg Gln Asn Ser Glu Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu  
 420 425 430  
 Arg Ala Gln Val Thr Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys  
 435 440 445  
 Leu Glu Val Leu Leu Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro  
 450 455 460  
 His Gly Ser Asp Glu Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile  
 465 470 475 480  
 Phe Arg Thr Ala Ser Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val  
 485 490 495  
 Pro His Cys Ile Ile Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu  
 500 505 510  
 Pro Met Val Leu Leu Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp  
 515 520 525  
 Asn Pro Arg Gly Thr Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu  
 530 535 540  
 Asp Leu Gln Ala Gly Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp  
 545 550 555 560  
 Leu Tyr Arg Asn Tyr Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met  
 565 570 575  
 Leu Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn  
 580 585 590  
 Trp Ala Leu Tyr Asp Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser  
 595 600 605  
 Ala Gly Val Lys Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly  
 610 615 620  
 Arg Gly Gly Gly Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly  
 625 630 635 640  
 Ala Val Gln Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser  
 645 650 655

Ala Lys Tyr Gly Asn Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu  
 660 665 670  
 Val Ser Ala Thr Leu Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr  
 675 680 685  
 Asp His Gln Arg Ala Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser  
 690 695 700  
 Leu Lys Lys Tyr Ala Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp  
 705 710 715 720  
 Tyr Phe Thr Gln Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile  
 725 730 735  
 Gly Ser Arg Pro Ser Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu  
 740 745 750  
 Arg Ala Ile Pro Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu  
 755 760 765  
 Pro Gly Trp Phe Gly Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu  
 770 775 780  
 Gly Glu Gln Ala Thr Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu  
 785 790 795 800  
 Ser Trp Pro Phe Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met  
 805 810 815  
 Ser Lys Ala Glu Leu Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro  
 820 825 830  
 Asp Thr Glu Val Ala Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr  
 835 840 845  
 Phe Leu Thr Lys Lys Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu  
 850 855 860  
 Leu Asp Asp Asn Pro Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro  
 865 870 875 880  
 Tyr Leu Leu Pro Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr  
 885 890 895  
 Arg Lys Gly Asp Gln Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr  
 900 905 910  
 Met Asn Gly Leu Ser Thr Ala Leu Arg Asn Ser Gly  
 915 920

&lt;210&gt; 111

&lt;211&gt; 939

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(916')

&lt;223&gt; RXN02326

&lt;400&gt; 111

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ccaggcggac agttgtccaa cctgcgtgca caggccaccg cactgggcct tgcggatcgt 60

ttcgaactca tcgaagacaa ctacgcaagc cgттаатgag atg ctg gga cgc cca 115
                                         Met Leu Gly Arg Pro
                                         1           5

acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac 163
Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His
                        10                        15                        20

ctc gtt ggt gcg ggt gtg gat cca gca gac ttt gct gcc gat cca caa 211
Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln
                        25                        30                        35

aag tac gac atc cca gac tct gtc atc gcg ttc ctg cgc ggc gag ctt 259
Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu
                        40                        45                        50

ggt aac cct cca ggt ggc tgg cca gag cca ctg cgc acc cgc gca ctg 307
Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu
                        55                        60                        65

gaa ggc cgc tcc gaa ggc aag gca cct ctg acg gaa gtt cct gag gaa 355
Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr Glu Val Pro Glu Glu
                        70                        75                        80                        85

gag cag gcg cac ctc gac gct gat gat tcc aag gaa cgt cgc aat agc 403
Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser
                        90                        95                        100

ctc aac cgc ctg ctg ttc ccg aag cca acc gaa gag ttc ctc gag cac 451
Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His
                        105                        110                        115

cgt cgc cgc ttc ggc aac acc tct gcg ctg gat gat cgt gaa ttc ttc 499
Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe
                        120                        125                        130

tac ggc ctg gtc gaa ggc cgc gag act ttg atc cgc ctg cca gat gtg 547
Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val
                        135                        140                        145

cgc acc cca ctg ctt gtt cgc ctg gat gcg atc tct gag cca gac gat 595
Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp
                        150                        155                        160                        165

aag ggt atg cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca 643
Lys Gly Met Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro
                        170                        175                        180

atg cgt gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa 691
Met Arg Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu
                        185                        190                        195

aag gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt 739
Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly
                        200                        205                        210

gtt gtc acc gtg act gtt gct gaa ggt gat gag gtc aag gct gga gat 787

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Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly Asp  
 215 220 225

gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc act gct 835  
 Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala  
 230 235 240 245

tct gtt gac ggc aaa atc gat cgc gtt gtg gtt cct gct gca acg aag 883  
 Ser Val Asp Gly Lys Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys  
 250 255 260

gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936  
 Val Glu Gly Gly Asp Leu Ile Val Val Val Ser  
 265 270

ccc 939

<210> 112  
 <211> 272  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 112  
 Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly  
 1 5 10 15

Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe  
 20 25 30

Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe  
 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu  
 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr  
 65 70 75 80

Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys  
 85 90 95

Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu  
 100 105 110

Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp  
 115 120 125

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile  
 130 135 140

Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile  
 145 150 155 160

Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn  
 165 170 175

Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val  
 180 185 190

Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala

195	200	205
Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu		
210	215	220
Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu		
225	230	235
Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val		
245	250	255
Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser		
260	265	270

<210> 113  
 <211> 939  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(916)  
 <223> FRXA02326

<400> 113  
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 Met Leu Gly Arg Pro  
 1 5  
 acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac 163  
 Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His  
 10 15 20  
 ctc gtt ggt gcg ggt gtg gat cca gca gac ttt gct gcc gat cca caa 211  
 Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln  
 25 30 35  
 aag tac gac atc cca gac tct gtc atc gcg ttc ctg cgc ggc gag ctt 259  
 Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu  
 40 45 50  
 ggt aac cct cca ggt ggc tgg cca gag cca ctg cgc acc cgc gca ctg 307  
 Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu  
 55 60 65  
 gaa ggc cgc tcc gaa ggc aag gca cct ctg acg gaa gtt cct gag gaa 355  
 Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr Glu Val Pro Glu Glu  
 70 75 80 85  
 gag cag gcg cac ctc gac gct gat gat tcc aag gaa cgt cgc aat agc 403  
 Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser  
 90 95 100  
 ctc aac cgc ctg ctg ttc ccg aag cca acc gaa gag ttc ctc gag cac 451  
 Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His



105										110					115					
cgt	cgc	cgc	ttc	ggc	aac	acc	tct	gcg	ctg	gat	gat	cgt	gaa	ttc	ttc	499				
Arg	Arg	Arg	Phe	Gly	Asn	Thr	Ser	Ala	Leu	Asp	Asp	Arg	Glu	Phe	Phe					
120						125						130								
tac	ggc	ctg	gtc	gaa	ggc	cgc	gag	act	ttg	atc	cgc	ctg	cca	gat	gtg	547				
Tyr	Gly	Leu	Val	Glu	Gly	Arg	Glu	Thr	Leu	Ile	Arg	Leu	Pro	Asp	Val					
135						140						145								
cgc	acc	cca	ctg	ctt	gtt	cgc	ctg	gat	gcg	atc	tct	gag	cca	gac	gat	595				
Arg	Thr	Pro	Leu	Leu	Val	Arg	Leu	Asp	Ala	Ile	Ser	Glu	Pro	Asp	Asp					
150			155						160			165								
aag	ggt	atg	cgc	aat	gtt	gtg	gcc	aac	gtc	aac	ggc	cag	atc	cgc	cca	643				
Lys	Gly	Met	Arg	Asn	Val	Val	Ala	Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro					
			170						175			180								
atg	cgt	gtg	cgt	gac	cgc	tcc	gtt	gag	tct	gtc	acc	gca	acc	gca	gaa	691				
Met	Arg	Val	Arg	Asp	Arg	Ser	Val	Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu					
			185						190			195								
aag	gca	gat	tcc	tcc	aac	aag	ggc	cat	gtt	gct	gca	cca	ttc	gct	ggt	739				
Lys	Ala	Asp	Ser	Ser	Asn	Lys	Gly	His	Val	Ala	Ala	Pro	Phe	Ala	Gly					
200						205						210								
gtt	gtc	acc	gtg	act	gtt	gct	gaa	ggt	gat	gag	gtc	aag	gct	gga	gat	787				
Val	Val	Thr	Val	Thr	Val	Ala	Glu	Gly	Asp	Glu	Val	Lys	Ala	Gly	Asp					
215						220						225								
gca	gtc	gca	atc	atc	gag	gct	atg	aag	atg	gaa	gca	aca	atc	act	gct	835				
Ala	Val	Ala	Ile	Ile	Glu	Ala	Met	Lys	Met	Glu	Ala	Thr	Ile	Thr	Ala					
230			235						240			245								
tct	gtt	gac	ggc	aaa	atc	gat	cgc	gtt	gtg	gtt	cct	gct	gca	acg	aag	883				
Ser	Val	Asp	Gly	Lys	Ile	Asp	Arg	Val	Val	Val	Pro	Ala	Ala	Thr	Lys					
			250						255			260								
gtg	gaa	ggt	ggc	gac	ttg	atc	gtc	gtc	gtt	tcc	taa	ac	ctt	ttc	tg	936				
Val	Glu	Gly	Gly	Asp	Leu	Ile	Val	Val	Val	Ser										
			265			270														
ccc															939					

&lt;210&gt; 114

&lt;211&gt; 272

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 114

Met	Leu	Gly	Arg	Pro	Thr	Lys	Val	Thr	Pro	Ser	Ser	Lys	Val	Val	Gly
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Asp	Leu	Ala	Leu	His	Leu	Val	Gly	Ala	Gly	Val	Asp	Pro	Ala	Asp	Phe
		20						25					30		

Ala	Ala	Asp	Pro	Gln	Lys	Tyr	Asp	Ile	Pro	Asp	Ser	Val	Ile	Ala	Phe
		35					40					45			

Leu	Arg	Gly	Glu	Leu	Gly	Asn	Pro	Pro	Gly	Gly	Trp	Pro	Glu	Pro	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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      50              55              60
Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
 65              70              75              80
Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
      85              90              95
Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
      100              105              110
Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
      115              120              125
Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
      130              135              140
Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
      145              150              155              160
Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
      165              170              175
Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
      180              185              190
Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
      195              200              205
Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
      210              215              220
Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
      225              230              235              240
Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
      245              250              255
Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
      260              265              270

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<210> 115

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXN02327

<400> 115

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 Leu Leu Ala Thr Arg  
 1 5

gtc	cgc	tca	ttc	gca	ctg	aag	cct	gcg	gca	gag	gcc	gtc	gca	aag	ctg	163
Val	Arg	Ser	Phe	Ala	Leu	Lys	Pro	Ala	Ala	Glu	Ala	Val	Ala	Lys	Leu	
				10					15					20		
act	cct	gag	ctt	ttg	tcc	gtg	gag	gcc	tgg	ggc	ggc	gcg	acc	tac	gat	211
Thr	Pro	Glu	Leu	Leu	Ser	Val	Glu	Ala	Trp	Gly	Gly	Ala	Thr	Tyr	Asp	
			25					30					35			
gtg	gcg	atg	cgt	ttc	ctc	ttt	gag	gat	ccg	tgg	gac	agg	ctc	gac	gag	259
Val	Ala	Met	Arg	Phe	Leu	Phe	Glu	Asp	Pro	Trp	Asp	Arg	Leu	Asp	Glu	
		40					45					50				
ctg	cgc	gag	gcg	atg	ccg	aat	gta	aac	att	cag	atg	ctg	ctt	cgc	ggc	307
Leu	Arg	Glu	Ala	Met	Pro	Asn	Val	Asn	Ile	Gln	Met	Leu	Leu	Arg	Gly	
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cgc	aac	acc	gtg	gga	tac	acc	ccg	tac	cca	gac	tcc	gtc	tgc	cgc	gcg	355
Arg	Asn	Thr	Val	Gly	Tyr	Thr	Pro	Tyr	Pro	Asp	Ser	Val	Cys	Arg	Ala	
	70				75					80					85	
ttt	gtt	aag	gaa	gct	gcc	agc	tcc	ggc	gtg	gac	atc	ttc	cgc	atc	ttc	403
Phe	Val	Lys	Glu	Ala	Ala	Ser	Ser	Gly	Val	Asp	Ile	Phe	Arg	Ile	Phe	
			90					95						100		
gac	gcg	ctt	aac	gac	gtc	tcc	cag	atg	cgt	cca	gca	atc	gac	gca	gtc	451
Asp	Ala	Leu	Asn	Asp	Val	Ser	Gln	Met	Arg	Pro	Ala	Ile	Asp	Ala	Val	
			105					110					115			
ctg	gag	acc	aac	acc	gcg	gta	gcc	gag	gtg	gct	atg	gct	tat	tct	ggc	499
Leu	Glu	Thr	Asn	Thr	Ala	Val	Ala	Glu	Val	Ala	Met	Ala	Tyr	Ser	Gly	
		120					125					130				
gat	ctc	tct	gat	cca	aat	gaa	aag	ctc	tac	acc	ctg	gat	tac	tac	cta	547
Asp	Leu	Ser	Asp	Pro	Asn	Glu	Lys	Leu	Tyr	Thr	Leu	Asp	Tyr	Tyr	Leu	
	135					140					145					
aag	atg	gca	gag	gag	atc	gtc	aag	tct	ggc	gct	cac	atc	ttg	gcc	att	595
Lys	Met	Ala	Glu	Glu	Ile	Val	Lys	Ser	Gly	Ala	His	Ile	Leu	Ala	Ile	
	150				155				160					165		
aag	gat	atg	gct	ggc	ctg	ctt	cgc	cca	gct	gcg	gta	acc	aag	ctg	gtc	643
Lys	Asp	Met	Ala	Gly	Leu	Leu	Arg	Pro	Ala	Ala	Val	Thr	Lys	Leu	Val	
			170					175						180		
acc	gca	ctg	cgc	cgt	gaa	ttc	gat	ctg	cca	gtg	cac	gtg	cac	acc	cac	691
Thr	Ala	Leu	Arg	Arg	Glu	Phe	Asp	Leu	Pro	Val	His	Val	His	Thr	His	
			185					190					195			
gac	act	gcg	ggc	ggc	cag	ctg	gca	acc	tac	ttt	gct	gca	gct	caa	gct	739
Asp	Thr	Ala	Gly	Gly	Gln	Leu	Ala	Thr	Tyr	Phe	Ala	Ala	Ala	Gln	Ala	
		200					205					210				
ggc	gca	gat	gct	gtt	gac	ggc	gct	tcc	ggc	acc	act	gtc	tgg	cac	cac	787
Gly	Ala	Asp	Ala	Val	Asp	Gly	Ala	Ser	Gly	Thr	Thr	Val	Trp	His	His	
	215					220					225					
ctc	cca	agc	cat	ccc	ttg	tct	gcc	att	gtt	gct	gca	ttc	gcg	cac	acc	835
Leu	Pro	Ser	His	Pro	Leu	Ser	Ala	Ile	Val	Ala	Ala	Phe	Ala	His	Thr	
	230				235					240					245	

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 Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro  
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 tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc 931  
 Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr  
 265 270 275  
  
 cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag 979  
 Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln  
 280 285 290  
  
 ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt 1027  
 Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg  
 295 300 305  
  
 ttc gaa ctc atc gaa gac aac tac gca agc cgt taatgagatg ctgggacgcc 1080  
 Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg  
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 caa 1083

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 <213> Corynebacterium glutamicum

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 Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp  
 35 40 45  
  
 Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln  
 50 55 60  
  
 Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp  
 65 70 75 80  
  
 Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp  
 85 90 95  
  
 Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro  
 100 105 110  
  
 Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala  
 115 120 125  
  
 Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr  
 130 135 140  
  
 Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala  
 145 150 155 160  
  
 His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala  
 165 170 175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val  
 180 185 190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe  
 195 200 205

Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr  
 210 215 220

Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala  
 225 230 235 240

Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val  
 245 250 255

Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro  
 260 265 270

Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu  
 275 280 285

Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu  
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Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg  
 305 310 315 320

&lt;210&gt; 117

&lt;211&gt; 1083

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1060)

&lt;223&gt; FRXA02327

&lt;400&gt; 117

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ggcagttact gataccacct tccgcgatgc acaccagtct ttg ctt gcg acc cga 115  
 Leu Leu Ala Thr Arg  
 1 5

gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg 163  
 Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu  
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act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc gcg acc tac gat 211  
 Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp  
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gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag 259  
 Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu  
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Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly	
55 60 65	
cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg	355
Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala	
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Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe	
90 95 100	
gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc	451
Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val	
105 110 115	
ctg gag acc aac acc gcg gta gcc gag gtg gct atg gct tat tct ggt	499
Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly	
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gat ctc tct gat cca aat gaa aag ctc tac acc ctg gat tac tac cta	547
Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu	
135 140 145	
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Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile	
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aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc	643
Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val	
170 175 180	
acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac gtg cac acc cac	691
Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His Val His Thr His	
185 190 195	
gac act gcg ggt ggc cag ctg gca acc tac ttt gct gca gct caa gct	739
Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala Ala Ala Gln Ala	
200 205 210	
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Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His	
215 220 225	
ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc	835
Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr	
230 235 240 245	
cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg	883
Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro	
250 255 260	
tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag tct gga acc	931
Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr	
265 270 275	
cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca ggc gga cag	979
Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln	
280 285 290	
ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt gcg gat cgt	1027

Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu Ala Asp Arg  
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caa 1083

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<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 118

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Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp  
 35 40 45

Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln  
 50 55 60

Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp  
 65 70 75 80

Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp  
 85 90 95

Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro  
 100 105 110

Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala  
 115 120 125

Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr  
 130 135 140

Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala  
 145 150 155 160

His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala  
 165 170 175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val  
 180 185 190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe  
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Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr  
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Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala  
 225 230 235 240

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Val Thr Ala Ile Thr																15
1																5
ctt ggc ggt ctc ttg ttg aaa gga ata att act cta gtg tcg act cac																163
Leu Gly Gly Leu Leu Leu Lys Gly Ile Ile Thr Leu Val Ser Thr His																10
15																20
aca tct tca acg ctt cca gca ttc aaa aag atc ttg gta gca aac cgc																211
Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu Val Ala Asn Arg																25
30																35
ggc gaa atc gcg gtc cgt gct ttc cgt gca gca ctc gaa acc ggt gca																259
Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu Glu Thr Gly Ala																40
45																50
gcc acg gta gct att tac ccc cgt gaa gat cgg gga tca ttc cac cgc																307
Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly Ser Phe His Arg																55
60																65
tct ttt gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc																355
Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val																70
75																80
aag gcg tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt																403
Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val																90
95																100
aaa gca gat gcc att tac ccg gga tac qgc ttc ctg tct qaa aat gcc																451



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Gln	Leu	Ala	Arg	Glu	Cys	Ala	Glu	Asn	Gly	Ile	Thr	Phe	Ile	Gly	Pro		
		120					125					130					
acc	cca	gag	gtt	ctt	gat	ctc	acc	ggg	gat	aag	tct	cgc	gcg	gta	acc	547	
Thr	Pro	Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser	Arg	Ala	Val	Thr		
	135					140					145						
gcc	gcg	aag	aag	gct	ggg	ctg	cca	gtt	ttg	gcg	gaa	tcc	acc	ccg	agc	595	
Ala	Ala	Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu	Ser	Thr	Pro	Ser		
150					155					160					165		
aaa	aac	atc	gat	gag	atc	gtt	aaa	agc	gct	gaa	ggc	cag	act	tac	ccc	643	
Lys	Asn	Ile	Asp	Glu	Ile	Val	Lys	Ser	Ala	Glu	Gly	Gln	Thr	Tyr	Pro		
				170					175					180			
atc	ttt	gtg	aag	gca	gtt	gcc	ggg	ggg	ggc	gga	cgc	ggg	atg	cgt	ttt	691	
Ile	Phe	Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg	Gly	Met	Arg	Phe		
			185					190					195				
gtt	gct	tca	cct	gat	gag	ctt	cgc	aaa	tta	gca	aca	gaa	gca	tct	cgt	739	
Val	Ala	Ser	Pro	Asp	Glu	Leu	Arg	Lys	Leu	Ala	Thr	Glu	Ala	Ser	Arg		
		200					205					210					
gaa	gct	gaa	gcg	gct	ttc	ggc	gat	ggc	gcg	gta	tat	gtc	gaa	cgt	gct	787	
Glu	Ala	Glu	Ala	Ala	Phe	Gly	Asp	Gly	Ala	Val	Tyr	Val	Glu	Arg	Ala		
	215					220					225						
gtg	att	aac	cct	cag	cat	att	gaa	gtg	cag	atc	ctt	ggc	gat	cac	act	835	
Val	Ile	Asn	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu	Gly	Asp	His	Thr		
230					235					240					245		
gga	gaa	gtt	gta	cac	ctt	tat	gaa	cgt	gac	tgc	tca	ctg	cag	cgt	cgt	883	
Gly	Glu	Val	Val	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser	Leu	Gln	Arg	Arg		
				250					255					260			
cac	caa	aaa	gtt	gtc	gaa	att	gcg	cca	gca	cag	cat	ttg	gat	cca	gaa	931	
His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His	Leu	Asp	Pro	Glu		
			265					270					275				
ctg	cgt	gat	cgc	att	tgt	gcg	gat	gca	gta	aag	ttc	tgc	cgc	tcc	att	979	
Leu	Arg	Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe	Cys	Arg	Ser	Ile		
		280					285					290					
ggg	tac	cag	ggc	gcg	gga	acc	gtg	gaa	ttc	ttg	gtc	gat	gaa	aag	ggc	1027	
Gly	Tyr	Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val	Asp	Glu	Lys	Gly		
	295					300					305						
aac	cac	gtc	ttc	atc	gaa	atg	aac	cca	cgt	atc	cag	gtt	gag	cac	acc	1075	
Asn	His	Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln	Val	Glu	His	Thr		
310					315					320					325		
gtg	act	gaa	gaa	gtc	acc	gag	gtg	gac	ctg	gtg	aag	gcg	cag	atg	cgc	1123	
Val	Thr	Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys	Ala	Gln	Met	Arg		
				330					335					340			
ttg	gct	gct	ggg	gca	acc	ttg	aag	gaa	ttg	ggg	ctg	acc	caa	gat	aag	1171	
Leu	Ala	Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu	Thr	Gln	Asp	Lys		

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cca aac aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg 375 380 385			1267
tca cca ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly 390 395 400 405			1315
ggc gaa atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys 410 415 420			1363
cgt ggt tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu 425 430 435			1411
gct gag ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg 440 445 450			1459
gcg ttg ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly 455 460 465			1507
ttc att gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp 470 475 480 485			1555
gag cag gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys 490 495 500			1603
cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu 505 510 515			1651
cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg 520 525 530			1696
tgaagcagct tggcccagcc gcg			1719

&lt;210&gt; 120

&lt;211&gt; 532

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 120

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Leu Val Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile
20 25 30

Leu Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala  
                   35                                  40                                  45  
 Leu Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg  
           50                                  55                                  60  
 Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr  
   65                                  70                                  75                                  80  
 Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly  
                                   85                                  90                                  95  
 Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe  
                                   100                                  105                                  110  
 Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile  
           115                                  120                                  125  
 Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys  
           130                                  135                                  140  
 Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala  
   145                                  150                                  155                                  160  
 Glu Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu  
                                   165                                  170                                  175  
 Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly  
                                   180                                  185                                  190  
 Arg Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala  
           195                                  200                                  205  
 Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val  
   210                                  215                                  220  
 Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile  
   225                                  230                                  235                                  240  
 Leu Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys  
                                   245                                  250                                  255  
 Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln  
                                   260                                  265                                  270  
 His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys  
           275                                  280                                  285  
 Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu  
   290                                  295                                  300  
 Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile  
   305                                  310                                  315                                  320  
 Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val  
                                   325                                  330                                  335  
 Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly  
                                   340                                  345                                  350  
 Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg

355                      360                      365  
 Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr  
 370                      375                      380  
 Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly  
 385                      390                      395                      400  
 Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu  
 405                      410                      415  
 Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg  
 420                      425                      430  
 Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn  
 435                      440                      445  
 Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys  
 450                      455                      460  
 Arg Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala  
 465                      470                      475                      480  
 Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp  
 485                      490                      495  
 Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala  
 500                      505                      510  
 Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly  
 515                      520                      525  
 Ser Arg Asp Arg  
 530

<210> 121  
 <211> 1406  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1383)  
 <223> FRXA02328

<400> 121  
 gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc aag gcg 48  
 Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala  
 1                      5                      10                      15  
 tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt aaa gca 96  
 Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala  
 20                      25                      30  
 gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc cag ctt 144  
 Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu  
 35                      40                      45  
 gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca acc cca 192  
 Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro

50	55	60	
gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc gcc gcg Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala 65 70 75 80			240
aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc aaa aac Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn 85 90 95			288
atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc atc ttt Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe 100 105 110			336
gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt gtt gct Val Lys Ala Val Ala Gly Gly Gly Arg Gly Met Arg Phe Val Ala 115 120 125			384
tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt gaa gct Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala 130 135 140			432
gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct gtg att Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile 145 150 155 160			480
aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act gga gaa Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu 165 170 175			528
gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt cac caa Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln 180 185 190			576
aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa ctg cgt Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg 195 200 205			624
gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att ggt tac Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr 210 215 220			672
cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc aac cac Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His 225 230 235 240			720
gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc gtg act Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr 245 250 255			768
gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc ttg gct Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala 260 265 270			816
gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag atc aag Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys 275 280 285			864
acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat cca aac Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn 290 295 300			912

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aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc tca cca 960
Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro
305                      310                      315                      320

ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt ggc gaa 1008
Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu
                      325                      330                      335

atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc cgt ggt 1056
Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly
                      340                      345                      350

tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg gct gag 1104
Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu
                      355                      360                      365

ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt gcg ttg 1152
Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu
                      370                      375                      380

ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga ttc att 1200
Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile
385                      390                      395                      400

gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat gag cag 1248
Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln
                      405                      410                      415

gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag cct cat 1296
Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His
                      420                      425                      430

ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg cct aac 1344
Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn
                      435                      440                      445

atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc tgaagcagct 1393
Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
                      450                      455                      460

tggcccagcc gcg 1406

```

&lt;210&gt; 122

&lt;211&gt; 461

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 122

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Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala
  1                      5                      10                      15

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Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
      20                      25                      30

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Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
      35                      40                      45

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```

Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
      50                      55                      60

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Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser	Arg	Ala	Val	Thr	Ala	Ala	
65					70					75					80	
Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu	Ser	Thr	Pro	Ser	Lys	Asn	
				85					90					95		
Ile	Asp	Glu	Ile	Val	Lys	Ser	Ala	Glu	Gly	Gln	Thr	Tyr	Pro	Ile	Phe	
			100					105					110			
Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg	Gly	Met	Arg	Phe	Val	Ala	
		115					120					125				
Ser	Pro	Asp	Glu	Leu	Arg	Lys	Leu	Ala	Thr	Glu	Ala	Ser	Arg	Glu	Ala	
	130					135					140					
Glu	Ala	Ala	Phe	Gly	Asp	Gly	Ala	Val	Tyr	Val	Glu	Arg	Ala	Val	Ile	
145					150					155					160	
Asn	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu	Gly	Asp	His	Thr	Gly	Glu	
				165					170					175		
Val	Val	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser	Leu	Gln	Arg	Arg	His	Gln	
			180					185					190			
Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His	Leu	Asp	Pro	Glu	Leu	Arg	
		195					200					205				
Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe	Cys	Arg	Ser	Ile	Gly	Tyr	
	210					215					220					
Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val	Asp	Glu	Lys	Gly	Asn	His	
225					230					235					240	
Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln	Val	Glu	His	Thr	Val	Thr	
				245					250					255		
Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys	Ala	Gln	Met	Arg	Leu	Ala	
			260					265					270			
Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu	Thr	Gln	Asp	Lys	Ile	Lys	
		275					280					285				
Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile	Thr	Thr	Glu	Asp	Pro	Asn	
	290					295					300					
Asn	Gly	Phe	Arg	Pro	Asp	Thr	Gly	Thr	Ile	Thr	Ala	Tyr	Arg	Ser	Pro	
305					310					315					320	
Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala	Ala	Gln	Leu	Gly	Gly	Glu	
				325					330					335		
Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	Val	Lys	Met	Thr	Cys	Arg	Gly	
			340					345					350			
Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg	Ala	Gln	Arg	Ala	Leu	Ala	Glu	
		355					360					365				
Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn	Ile	Gly	Phe	Leu	Arg	Ala	Leu	
	370					375					380					

Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile  
 385 390 395 400  
 Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln  
 405 410 415  
 Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His  
 420 425 430  
 Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn  
 435 440 445  
 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg  
 450 455 460

<210> 123  
 <211> 1347  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1324)  
 <223> RXN01048

<400> 123  
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 gagcttccccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115  
 Met Thr Ile Asp Leu  
 1 5  
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163  
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His  
 10 15 20  
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211  
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met  
 25 30 35  
 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259  
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu  
 40 45 50  
 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307  
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly  
 55 60 65  
 aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355  
 Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly  
 70 75 80 85  
 gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403  
 Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln  
 90 95 100  
 ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451  
 Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp  
 105 110 115



gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc	883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly	
250 255 260	
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct	931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala	
265 270 275	
ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca	979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro	
280 285 290	
acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc	1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val	
295 300 305	
gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg	1075
Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala	
310 315 320 325	
ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc	1123
Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile	
330 335 340	
acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag	1171
Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln	
345 350 355	
ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc	1219

Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro  
 360 365 370  
 gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267  
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg  
 375 380 385  
 aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315  
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala  
 390 395 400 405  
 cca ata ttt taagagcaaa cttgaggccc aca 1347  
 Pro Ile Phe

<210> 124  
 <211> 408  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 124  
 Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu  
 1 5 10 15  
 Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg  
 20 25 30  
 Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val  
 35 40 45  
 Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr  
 50 55 60  
 His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala  
 65 70 75 80  
 Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met  
 85 90 95  
 Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile  
 100 105 110  
 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile  
 115 120 125  
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser  
 130 135 140  
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp  
 145 150 155 160  
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu  
 165 170 175  
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp  
 180 185 190  
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val  
 195 200 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser  
 210 215 220  
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala  
 225 230 235 240  
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn  
 245 250 255  
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn  
 260 265 270  
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe  
 275 280 285  
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys  
 290 295 300  
 Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile  
 305 310 315 320  
 Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala  
 325 330 335  
 Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln  
 340 345 350  
 Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu  
 355 360 365  
 Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg  
 370 375 380  
 Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser  
 385 390 395 400  
 Leu Pro Val Glu Ala Pro Ile Phe  
 405

&lt;210&gt; 125

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(288)

&lt;223&gt; FRXA01048

&lt;400&gt; 125

cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga 48  
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly  
 1 5 10 15

att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96  
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu  
 20 25 30

atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144  
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr

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          35              40              45
tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192
Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
      50              55              60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240
Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
      65              70              75              80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288
Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
              85              90              95

taagagcaaa cttgaggccc aca 311

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<210> 126  
 <211> 96  
 <212> PRT  
 <213> Corynebacterium glutamicum

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<400> 126
Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
      1              5              10              15

Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
              20              25              30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
              35              40              45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
      50              55              60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
      65              70              75              80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
              85              90              95

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<210> 127  
 <211> 1063  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1063)  
 <223> FRXA00290

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<400> 127
agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccc caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
              Met Thr Ile Asp Leu
              1              5

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cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac	163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His	
10 15 20	
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883  
 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly  
                   250                  255                  260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931  
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala  
                   265                  270                  275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979  
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro  
                   280                  285                  290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027  
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val  
                   295                  300                  305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063  
 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser  
                   310                  315                  320

&lt;210&gt; 128

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 128

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu  
   1                  5                  10                  15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg  
                   20                  25                  30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val  
                   35                  40                  45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr  
                   50                  55                  60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala  
   65                  70                  75                  80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met  
                   85                  90                  95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile  
                   100                  105                  110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile  
                   115                  120                  125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser  
                   130                  135                  140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp  
   145                  150                  155                  160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu  
                   165                  170                  175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp

	180		185		190
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val	195		200		205
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser	210		215		220
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala	225		230		235
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn	245		250		255
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn	260		265		270
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe	275		280		285
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys	290		295		300
Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg	305		310		315
					320

Ser

<210> 129  
 <211> 1065  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1042)  
 <223> RXA02694

<400> 129  
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 tgggttggtcc ggtaggggaa atcaggaagt gggatcgaaa atg aaa gaa acc gtc 115  
 Met Lys Glu Thr Val 1 5  
 ggt aac aag att gtc ctc att ggc gca gga gat gtt gga gtt gca tac 163  
 Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp Val Gly Val Ala Tyr 10 15 20  
 gca tac gca ctg atc aac cag ggc atg gca gat cac ctt gcg atc atc 211  
 Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp His Leu Ala Ile Ile 25 30 35  
 gac atc gat gaa aag aaa ctc gaa ggc aac gtc atg gac tta aac cat 259  
 Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val Met Asp Leu Asn His 40 45 50  
 ggt gtt gtg tgg gcc gat tcc cgc acc cgc gtc acc aag ggc acc tac 307  
 Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val Thr Lys Gly Thr Tyr

55	60	65	
gct gac tgc gaa gac gca gcc atg gtt gtc att tgt gcc ggc gca gcc Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile Cys Ala Gly Ala Ala 70 75 80 85			355
caa aag cca ggc gag acc cgc ctc cag ctg gtg gac aaa aac gtc aag Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val Asp Lys Asn Val Lys 90 95 100			403
att atg aaa tcc atc gtc ggc gat gtc atg gac agc gga ttc gac ggc Ile Met Lys Ser Ile Val Gly Asp Val Met Asp Ser Gly Phe Asp Gly 105 110 115			451
atc ttc ctc gtg gcg tcc aac cca gtg gat atc ctg acc tac gca gtg Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile Leu Thr Tyr Ala Val 120 125 130			499
tgg aaa ttc tcc ggc ttg gaa tgg aac cgc gtg atc ggc tcc gga act Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val Ile Gly Ser Gly Thr 135 140 145			547
gtc ctg gac tcc gct cga ttc cgc tac atg ctg ggc gaa ctc tac gaa Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu Gly Glu Leu Tyr Glu 150 155 160 165			595
gtg gca cca agc tcc gtc cac gcc tac atc atc ggc gaa cac ggc gac Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile Gly Glu His Gly Asp 170 175 180			643
act gaa ctt cca gtc ctg tcc tcc gcg acc atc gca ggc gta tcg ctt Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile Ala Gly Val Ser Leu 185 190 195			691
agc cga atg ctg gac aaa gac cca gag ctt gag ggc cgt cta gag aaa Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu Gly Arg Leu Glu Lys 200 205 210			739
att ttc gaa gac acc cgc gac gct gcc tat cac att atc gac gcc aag Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His Ile Ile Asp Ala Lys 215 220 225			787
ggc tcc act tcc tac ggc atc ggc atg ggt ctt gct cgc atc acc cgc Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu Ala Arg Ile Thr Arg 230 235 240 245			835
gca atc cta cag aac caa gac gtt gca gtc cca gtc tct gca ctg ctc Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu 250 255 260			883
cac ggt gaa tac ggt gag gaa gac atc tac atc ggc acc cca gct gtg His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val 265 270 275			931
gtg aac cgc cga ggc atc cgc cgc gtt gtc gaa cta gaa atc acc gac Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp 280 285 290			979
cac gag atg gaa cgc ttc aag cat tcc gca aat acc ctg cgc gaa att His Glu Met Glu Arg Phe Lys His Ser Ala Asn Thr Leu Arg Glu Ile 295 300 305			1027



cag aag cag ttc ttc taaatctttg gcgcctagtt ggc  
 Gln Lys Gln Phe Phe  
 310

1065

&lt;210&gt; 130

&lt;211&gt; 314

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 130

Met Lys Glu Thr Val Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp  
 1 5 10 15

Val Gly Val Ala Tyr Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp  
 20 25 30

His Leu Ala Ile Ile Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val  
 35 40 45

Met Asp Leu Asn His Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val  
 50 55 60

Thr Lys Gly Thr Tyr Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile  
 65 70 75 80

Cys Ala Gly Ala Ala Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val  
 85 90 95

Asp Lys Asn Val Lys Ile Met Lys Ser Ile Val Gly Asp Val Met Asp  
 100 105 110

Ser Gly Phe Asp Gly Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile  
 115 120 125

Leu Thr Tyr Ala Val Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val  
 130 135 140

Ile Gly Ser Gly Thr Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu  
 145 150 155 160

Gly Glu Leu Tyr Glu Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile  
 165 170 175

Gly Glu His Gly Asp Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile  
 180 185 190

Ala Gly Val Ser Leu Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu  
 195 200 205

Gly Arg Leu Glu Lys Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His  
 210 215 220

Ile Ile Asp Ala Lys Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu  
 225 230 235 240

Ala Arg Ile Thr Arg Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro  
 245 250 255

Val Ser Ala Leu Leu His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile

	260		265		270
Gly Thr Pro Ala Val Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu					
275		280		285	
Leu Glu Ile Thr Asp His Glu Met Glu Arg Phe Lys His Ser Ala Asn					
290	295	300			
Thr Leu Arg Glu Ile Gln Lys Gln Phe Phe					
305	310				

<210> 131  
 <211> 2967  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2944)  
 <223> RXN00296

<400> 131  
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 tcaaagcccg cttggatcga atttcacaaa aggaccaccc atg act cac acc atc 115  
 Met Thr His Thr Ile 5  
 1  
 aaa ttc aac aga ctc gac cca gaa gta ttt agc cag cat tct cgc gcg 163  
 Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser Arg Ala 20  
 10 15  
 aag ctg cgc acg gat atg aca acc cgt gca gca tat tct tct gat gca 211  
 Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser Asp Ala 35  
 25 30  
 gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa aat gtg 259  
 Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu Asn Val 50  
 40 45  
 gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg tgg tct 307  
 Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly Trp Ser 65  
 55 60  
 gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg atc ggt 355  
 Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala Ile Gly 85  
 70 75 80  
 gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att tta gat 403  
 Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile Leu Asp 100  
 90 95  
 att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg gtg tgt 451  
 Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val Val Cys 115  
 105 110  
 gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac ggc ccg 499  
 Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr Gly Pro 130  
 120 125

gat	cct	tcc	acg	cat	tcc	cgg	tgc	acg	atc	ggt	ggc	atg	ggt	gcc	aac	547
Asp	Pro	Ser	Thr	His	Ser	Arg	Cys	Thr	Ile	Gly	Gly	Met	Val	Ala	Asn	
	135					140					145					
aat	gcg	tgt	ggt	tca	cac	tcg	ggt	gca	ttc	ggt	aca	gct	gcg	gaa	aat	595
Asn	Ala	Cys	Gly	Ser	His	Ser	Val	Ala	Phe	Gly	Thr	Ala	Ala	Glu	Asn	
150					155				160						165	
ctc	gtg	gat	gtc	acg	ctc	atg	ctc	agc	gat	ggc	cga	gaa	gtc	act	gtg	643
Leu	Val	Asp	Val	Thr	Leu	Met	Leu	Ser	Asp	Gly	Arg	Glu	Val	Thr	Val	
				170					175					180		
aca	aaa	gat	ggc	tgc	gat	gat	gct	gag	atc	aat	cag	aag	ctc	acc	gac	691
Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn	Gln	Lys	Leu	Thr	Asp	
			185					190					195			
tta	gcg	tcc	aag	aat	cag	gac	ctt	att	agt	aaa	gaa	ctg	ggt	cgt	ttc	739
Leu	Ala	Ser	Lys	Asn	Gln	Asp	Leu	Ile	Ser	Lys	Glu	Leu	Gly	Arg	Phe	
	200						205					210				
cct	cgc	caa	gtg	tcg	ggc	tac	ggt	ttg	cat	tat	ctt	gcc	cac	gac	atg	787
Pro	Arg	Gln	Val	Ser	Gly	Tyr	Gly	Leu	His	Tyr	Leu	Ala	His	Asp	Met	
	215					220					225					
gcc	aaa	gca	atg	gcg	ggc	acc	gag	gga	acc	att	gga	atc	att	act	cgg	835
Ala	Lys	Ala	Met	Ala	Gly	Thr	Glu	Gly	Thr	Ile	Gly	Ile	Ile	Thr	Arg	
230					235					240					245	
ttg	acg	gtg	aag	ttg	ggt	cca	aca	ccc	aaa	gtg	aaa	gcg	ctt	gct	gtc	883
Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val	Lys	Ala	Leu	Ala	Val	
			250						255					260		
ctg	gct	ttc	gac	acg	ggt	ttt	gac	gcc	gcc	cga	gca	gcc	gcc	aaa	ttg	931
Leu	Ala	Phe	Asp	Thr	Val	Phe	Asp	Ala	Ala	Arg	Ala	Ala	Ala	Lys	Leu	
			265					270					275			
cga	ctg	cct	ggg	gta	gca	acc	att	gaa	ggc	atg	ggc	gga	gat	ctc	ctc	979
Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	Gly	Gly	Asp	Leu	Leu	
		280					285					290				
gct	gcg	ctg	cgc	agt	aaa	cag	gga	caa	tca	gaa	gct	ggg	cag	aat	ctt	1027
Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu	Ala	Gly	Gln	Asn	Leu	
	295					300					305					
cca	gga	aac	cgc	atc	ggc	att	gaa	gcc	ggc	gga	tgg	ttg	tac	tgc	gag	1075
Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly	Trp	Leu	Tyr	Cys	Glu	
310					315					320					325	
aca	gga	agt	gac	acc	ctg	cag	gcc	gcg	gta	caa	gcc	gcc	gag	gaa	gtc	1123
Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu	Glu	Val	
				330					335					340		
gca	acc	gcc	ggt	gac	acc	att	gat	tac	gtg	gtc	gtg	tct	gag	cct	tct	1171
Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val	Val	Ser	Glu	Pro	Ser	
			345					350					355			
gaa	atg	cgg	gaa	ttg	tgg	cgc	atc	cgt	gaa	tcc	tcg	gcg	ggc	att	gtc	1219
Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser	Ser	Ala	Gly	Ile	Val	
	360						365					370				
acg	cgc	tta	gct	gat	ggt	ggg	gaa	gcg	tgg	ccg	aat	tgg	gaa	gac	tcg	1267

Thr	Arg	Leu	Ala	Asp	Gly	Gly	Glu	Ala	Trp	Pro	Asn	Trp	Glu	Asp	Ser	
	375					380					385					
gcg	gtg	cct	cca	gag	aat	tta	gct	gat	tat	ctc	cgc	gat	ctt	tat	gcg	1315
Ala	Val	Pro	Pro	Glu	Asn	Leu	Ala	Asp	Tyr	Leu	Arg	Asp	Leu	Tyr	Ala	
390					395					400					405	
ctg	atg	gat	aag	ttc	gat	tac	cag	ggt	att	cca	ttt	gga	cac	ttt	gga	1363
Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His	Phe	Gly	
				410					415					420		
gaa	ggc	tgc	gtc	cac	gtt	cgc	atc	agt	ttt	gat	ttc	tct	acc	aag	gaa	1411
Glu	Gly	Cys	Val	His	Val	Arg	Ile	Ser	Phe	Asp	Phe	Ser	Thr	Lys	Glu	
			425					430					435			
ggc	ctg	aag	aaa	ttc	gag	gcg	ttc	atg	aat	gaa	gcc	tcc	acc	ttg	gtg	1459
Gly	Leu	Lys	Lys	Phe	Glu	Ala	Phe	Met	Asn	Glu	Ala	Ser	Thr	Leu	Val	
		440					445					450				
gcg	tct	tat	ggt	ggc	agc	ctc	tcg	ggc	gag	cat	gga	gac	ggt	cgc	gcc	1507
Ala	Ser	Tyr	Gly	Gly	Ser	Leu	Ser	Gly	Glu	His	Gly	Asp	Gly	Arg	Ala	
	455					460					465					
cgc	tca	tcc	ttc	ctt	gac	cgc	atg	tat	tca	gca	gaa	atg	cgt	gca	ctc	1555
Arg	Ser	Ser	Phe	Leu	Asp	Arg	Met	Tyr	Ser	Ala	Glu	Met	Arg	Ala	Leu	
470					475					480					485	
ttc	gaa	gaa	ttc	aag	ctg	att	ttc	gat	ccc	cag	cgc	atc	ttc	aat	ccg	1603
Phe	Glu	Glu	Phe	Lys	Leu	Ile	Phe	Asp	Pro	Gln	Arg	Ile	Phe	Asn	Pro	
				490					495					500		
gga	gtg	ttg	gtc	tgg	gca	gat	cct	gtc	atg	caa	gga	ctt	cgc	atg	gac	1651
Gly	Val	Leu	Val	Trp	Ala	Asp	Pro	Val	Met	Gln	Gly	Leu	Arg	Met	Asp	
			505					510					515			
ccg	ggc	cag	cgc	gcc	ctc	gac	atc	acg	ccc	gta	cac	aaa	ttc	tct	aaa	1699
Pro	Gly	Gln	Arg	Ala	Leu	Asp	Ile	Thr	Pro	Val	His	Lys	Phe	Ser	Lys	
		520					525					530				
gac	aaa	ggt	tcc	atg	atc	aac	gcg	gtg	aat	cgc	tgc	gtg	ggt	gta	tcc	1747
Asp	Lys	Gly	Ser	Met	Ile	Asn	Ala	Val	Asn	Arg	Cys	Val	Gly	Val	Ser	
	535					540					545					
gca	tgc	cgc	tca	gaa	tcc	gac	gcg	atg	tgc	ccg	tcc	ttc	caa	atc	acc	1795
Ala	Cys	Arg	Ser	Glu	Ser	Asp	Ala	Met	Cys	Pro	Ser	Phe	Gln	Ile	Thr	
550					555					560					565	
ggc	gac	gaa	gta	cat	tcc	acc	aga	ggc	cgc	gcc	cgc	ttg	ctc	tct	gag	1843
Gly	Asp	Glu	Val	His	Ser	Thr	Arg	Gly	Arg	Ala	Arg	Leu	Leu	Ser	Glu	
				570					575					580		
atg	ttc	cgc	ggt	gaa	tcc	atc	gcc	gac	ggc	tac	cgc	agc	gaa	gaa	gtc	1891
Met	Phe	Arg	Gly	Glu	Ser	Ile	Ala	Asp	Gly	Tyr	Arg	Ser	Glu	Glu	Val	
			585					590					595			
aat	gaa	gcc	ctt	gac	ctg	tgc	ctt	tcc	tgc	aaa	gca	tgc	gca	tcg	gaa	1939
Asn	Glu	Ala	Leu	Asp	Leu	Cys	Leu	Ser	Cys	Lys	Ala	Cys	Ala	Ser	Glu	
		600					605					610				
tgt	cca	gtc	aac	gtc	gac	atg	tcc	acc	tac	aaa	gcc	gaa	ttc	ctg	gac	1987
Cys	Pro	Val	Asn	Val	Asp	Met	Ser	Thr	Tyr	Lys	Ala	Glu	Phe	Leu	Asp	

615	620	625	
aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc atg ggc Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val Met Gly 630 635 640 645			2035
tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt ctt cct Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu Leu Pro 650 655 660			2083
acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca gtg gtg Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro Val Val 665 670 675			2131
cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc gcc cac Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe Ala His 680 685 690			2179
cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa acg gtg Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu Thr Val 695 700 705			2227
gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga cca gct Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly Pro Ala 710 715 720 725			2275
cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg gtc atc His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val Val Ile 730 735 740			2323
cca gat ggc ttc gtc tgc tgt gga ctc acc tgg cat tcc acc ggc caa Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr Gly Gln 745 750 755			2371
ttg agc atg aca aag aaa gtc cta gaa caa acg gcg aaa gtg atg aaa Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val Met Lys 760 765 770			2419
ccc tac ctg gac caa ggt cta aca gtc gtt ggt ttg gaa cct tcg tgc Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro Ser Cys 775 780 785			2467
acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac cct gat Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn Pro Asp 790 795 800 805			2515
ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc atc gca Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val Ile Ala 810 815 820			2563
cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta aca gaa Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu Thr Glu 825 830 835			2611
tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta ggc gac Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu Gly Asp 840 845 850			2659
cca caa caa tcg gca ctc gtt ctt gaa gct ttg ggt gta aaa gat gaa Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys Asp Glu 855 860 865			2707

caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc ttt gaa 2755  
 Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly Phe Glu  
 870 875 880 885

aaa gac cac gct gaa atg tcc ttc gca ctt ggt gaa cga gag ctg ttc 2803  
 Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu Leu Phe  
 890 895 900

ccc aag gtc aga aaa gca gaa gga cat gtg att gct gac ggt ttc tcc 2851  
 Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly Phe Ser  
 905 910 915

tgc cgc acc cag atc gaa caa ggc acc gga aaa caa gca acg cac ctt 2899  
 Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr His Leu  
 920 925 930

gca gag gtg gtc tta agc atc ttg gag caa aac aac atg gca caa 2944  
 Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala Gln  
 935 940 945

taacgatcat gcaacaggtg ctg 2967

<210> 132

<211> 948

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

Met Thr His Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser  
 1 5 10 15

Gln His Ser Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala  
 20 25 30

Tyr Ser Ser Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala  
 35 40 45

Glu Pro Glu Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val  
 50 55 60

Ala Arg Gly Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala  
 65 70 75 80

Gly Asn Ala Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe  
 85 90 95

Asn Arg Ile Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu  
 100 105 110

Pro Gly Val Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly  
 115 120 125

Leu Thr Tyr Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly  
 130 135 140

Gly Met Val Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly  
 145 150 155 160

Thr Ala Ala Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly

165										170					175				
Arg	Glu	Val	Thr	Val	Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn				
			180					185					190						
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 Ser Phe Gln Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala  
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 Tyr Asn Val Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp  
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 Ser Asp Asn Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe  
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Ala Glu Val Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser  
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Leu Gln Leu Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu  
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Arg Ser Leu Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu  
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Gly Val Lys Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly  
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Asn Trp Gly Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly  
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Ala Asp Gly Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys  
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 Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu  
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Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu																																	
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gaa gtc gca acc gcc gtt gac acc att gat tac gtg gtc gtg tct gag	1056
Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu	
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Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly	
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Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu	
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Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr	
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Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr	
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Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe	
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Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg	
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Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe	
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Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly	
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Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu	
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Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu	
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Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro	
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Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu	
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Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly	
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Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr	
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755 760 765	
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785 790 795 800	
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Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val	
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Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu  
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865 870 875 880

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885 890 895

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900 905 910

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915 920 925

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Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val

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Thr	Val	Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn	Gln	Lys	Leu
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Thr	Arg	Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val	Lys	Ala	Leu
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Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	Gly	Gly	Asp
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Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu
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Tyr	Ala	Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His
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 Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val  
 625 630 635 640  
 Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu  
 645 650 655  
 Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro  
 660 665 670  
 Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe  
 675 680 685  
 Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu  
 690 695 700  
 Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly  
 705 710 715 720  
 Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val  
 725 730 735  
 Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr  
 740 745 750

Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val  
755 760 765

Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro  
770 775 780

Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn  
785 790 795 800

Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val  
805 810 815

Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu  
820 825 830

Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu  
835 840 845

Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys  
850 855 860

Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly  
865 870 875 880

Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu  
885 890 895

Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly  
900 905 910

Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr  
915 920 925

His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala  
930 935 940

Gln  
945

<210> 135

<211> 1383

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1360)

<223> RXA01901

<400> 135

gcattgttgc ttctctctgt gatcgctcgt ttcttcatcc aacgcgtcgc gcaccaagag 60

aactaaaatc taagtaaaac ccctccgaaa ggaaccaccc atg gtg aaa cgt caa 115  
Met Val Lys Arg Gln  
1 5

ctg ccc aac ccc gca gaa cta ctc gaa ctc atg aag ttc aaa aag cca 163  
Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met Lys Phe Lys Lys Pro  
10 15 20



gag ctc aac ggc aag aaa cga cgc cta gac tcc gcg ctc acc atc tac	211
Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser Ala Leu Thr Ile Tyr	
25 30 35	
gac ctg cgt aaa att gct aaa cga cgc acc cca gct gcc gcg ttc gac	259
Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro Ala Ala Phe Asp	
40 45 50	
tac acc gac ggc gca gcc gag gcc gaa ctc tca atc aca cgc gca cgt	307
Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser Ile Thr Arg Ala Arg	
55 60 65	
gaa gca ttc gaa aac atc gaa ttc cac cca gac atc ctc aag cct gca	355
Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp Ile Leu Lys Pro Ala	
70 75 80 85	
gaa cac gta gac acc acc acc caa atc ctg ggc gga acc tcc tcc atg	403
Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly Gly Thr Ser Ser Met	
90 95 100	
cca ttc ggc atc gca cca acc ggc ttc acc cgc ctc atg cag acc gaa	451
Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg Leu Met Gln Thr Glu	
105 110 115	
ggt gaa atc gca ggt gcc gga gct gca ggc gct gca gga att cct ttc	499
Gly Glu Ile Ala Gly Ala Gly Ala Gly Ala Ala Gly Ile Pro Phe	
120 125 130	
acc ctg tcc acc ctg ggc act acc tcc atc gaa gac gtc aag gcc acc	547
Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu Asp Val Lys Ala Thr	
135 140 145	
aac ccc aac ggc cga aac tgg ttc cag ctc tac gtc atg cgc gac cgc	595
Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr Val Met Arg Asp Arg	
150 155 160 165	
gaa atc tcc tac ggc ctc gtc gaa cgc gca gcc aaa gca gga ttc gac	643
Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala Lys Ala Gly Phe Asp	
170 175 180	
acc ctg atg ttc acc gtg gat acc ccc atc gcc ggc tac cgc atc cgc	691
Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala Gly Tyr Arg Ile Arg	
185 190 195	
gat tcc cgc aac gga ttc tcc atc ccg cca cag ctg acc cca tcc acc	739
Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln Leu Thr Pro Ser Thr	
200 205 210	
gtg ctc aat gca atc cca cgc cca tgg tgg tgg atc gac ttc ctg acc	787
Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp Ile Asp Phe Leu Thr	
215 220 225	
acc cca acc ctt gag ttc gca tcc ctt tcc tcg acc ggc gga acc gtg	835
Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser Thr Gly Gly Thr Val	
230 235 240 245	
ggc gac ctc ctc aac tcc gcg atg gat ccc acc att tct tac gaa gac	883
Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr Ile Ser Tyr Glu Asp	
250 255 260	
ctc aag gtc atc cgt gaa atg tgg cca ggc aag ctc gta gtc aag ggt	931

Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys Leu Val Val Lys Gly  
 265 270 275  
 gtc cag aac gtt gaa gac tcc gtc aaa ctc ctc gac caa ggc gtc gac 979  
 Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu Asp Gln Gly Val Asp  
 280 285 290  
 ggc ctc atc ctc tcc aac cac ggt ggc cgt caa ctc gac cgc gca cca 1027  
 Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln Leu Asp Arg Ala Pro  
 295 300 305  
 gtc cca ttc cac ctc ctg cca cag gta cgc aag gaa gtc gga tct gaa 1075  
 Val Pro Phe His Leu Leu Pro Gln Val Arg Lys Glu Val Gly Ser Glu  
 310 315 320 325  
 cca acc atc atg atc gac acc ggc atc atg aac ggc gcc gac atc gtc 1123  
 Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn Gly Ala Asp Ile Val  
 330 335 340  
 gca gcc gta gcc atg ggc gct gac ttc acc ctc atc ggt cgt gcc tac 1171  
 Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu Ile Gly Arg Ala Tyr  
 345 350 355  
 ctc tac gga ctc atg gcc gga ggc cgc gaa ggc gtc gac cgc acc atc 1219  
 Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly Val Asp Arg Thr Ile  
 360 365 370  
 gcc att ctc cgc agc gag atc acc cgc acc atg gct ctc ctc ggt gtt 1267  
 Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met Ala Leu Leu Gly Val  
 375 380 385  
 tcc tcc ctc gaa gaa ctc gag cca cgc cac gtc acc cag ctg gcc aag 1315  
 Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val Thr Gln Leu Ala Lys  
 390 395 400 405  
 atg gtt cca gtt tct gac gca act cgt tct gca gcg gcg gag att 1360  
 Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala Ala Ala Glu Ile  
 410 415 420  
 taaaagtttc tctccttagc tat 1383

&lt;210&gt; 136

&lt;211&gt; 420

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 136

Met Val Lys Arg Gln Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met  
 1 5 10 15

Lys Phe Lys Lys Pro Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser  
 20 25 30

Ala Leu Thr Ile Tyr Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro  
 35 40 45

Ala Ala Ala Phe Asp Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser  
 50 55 60

Ile Thr Arg Ala Arg Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp

65	70	75	80
Ile Leu Lys Pro Ala Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly	85	90	95
Gly Thr Ser Ser Met Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg	100	105	110
Leu Met Gln Thr Glu Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala	115	120	125
Ala Gly Ile Pro Phe Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu	130	135	140
Asp Val Lys Ala Thr Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr	145	150	155
Val Met Arg Asp Arg Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala	165	170	175
Lys Ala Gly Phe Asp Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala	180	185	190
Gly Tyr Arg Ile Arg Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln	195	200	205
Leu Thr Pro Ser Thr Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp	210	215	220
Ile Asp Phe Leu Thr Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser	225	230	235
Thr Gly Gly Thr Val Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr	245	250	255
Ile Ser Tyr Glu Asp Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys	260	265	270
Leu Val Val Lys Gly Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu	275	280	285
Asp Gln Gly Val Asp Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln	290	295	300
Leu Asp Arg Ala Pro Val Pro Phe His Leu Leu Pro Gln Val Arg Lys	305	310	315
Glu Val Gly Ser Glu Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn	325	330	335
Gly Ala Asp Ile Val Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu	340	345	350
Ile Gly Arg Ala Tyr Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly	355	360	365
Val Asp Arg Thr Ile Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met	370	375	380
Ala Leu Leu Gly Val Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val	385	390	395
			400

Thr Gln Leu Ala Lys Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala  
 405 410 415

Ala Ala Glu Ile  
 420

<210> 137

<211> 1836

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1813)

<223> RXN01952

<400> 137

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tgacgcgctt gtgatgcaac tgaatatagg aagcttagag atg acg caa cca gga 115  
 Met Thr Gln Pro Gly  
 1 5

cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163  
 Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile  
 10 15 20

gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211  
 Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe  
 25 30 35

agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259  
 Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg  
 40 45 50

ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac 307  
 Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp  
 55 60 65

aac aac ctc atc gtc atc ccg cag gca tcg aac acg ggc ctg act ggt 355  
 Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly  
 70 75 80 85

gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc 403  
 Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile  
 90 95 100

tcg act cac cgc atc gat gag gtg cac ctc atc aac gac gcg cgc gag 451  
 Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu  
 105 110 115

gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc 499  
 Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu  
 120 125 130

gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc 547  
 Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile  
 135 140 145

ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag	595
Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln	
150 155 160 165	
att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc	643
Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val	
170 175 180	
aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc	691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu	
185 190 195	
gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg	739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp	
200 205 210	
tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag	787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
215 220 225	
tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat	835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
230 235 240 245	
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg	883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
250 255 260	
atg gtg ttc gcg gtg cgc acc cgc acc ttc cct cgc gaa gtg cac ccg	931
Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
265 270 275	
acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc	979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
280 285 290	
cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag	1027
Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu Pro Ile Ser Gly Glu	
295 300 305	
tac atg ggc cgc agt gcc ttc gac ttg gcc gag aag tac ggc aaa gac	1075
Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu Lys Tyr Gly Lys Asp	
310 315 320 325	
acc ttc gtc ttc ctg aag ttc atg agt cca gcg ctg cag acg cgc atg	1123
Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala Leu Gln Thr Arg Met	
330 335 340	
ttc tcg ttc aag acg tgg gcc aac ggc ttg ttc tcg aag att ccc ggc	1171
Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe Ser Lys Ile Pro Gly	
345 350 355	
att ggt ccg acc ttc gcc gac acg gta tcg caa gcc atg ttc agc gtg	1219
Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln Ala Met Phe Ser Val	
360 365 370	
ctg ccc aac cag ctg ccc aag cgc atg atg gag tac cgc aac cgt ttc	1267
Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu Tyr Arg Asn Arg Phe	
375 380 385	
gag cat cac ctg ctg ctc acc gtc agc gag tcg cag aag gcc gcg agc	1315

Glu His His Leu Leu Leu Thr Val Ser Glu Ser Gln Lys Ala Ala Ser  
 390 395 400 405  
 gag aag atg ctc aag gag ttc ttc gca gag ccc gag cac act ggt gag 1363  
 Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro Glu His Thr Gly Glu  
 410 415 420  
 ttc ttc atc tgc acg tct gat gaa gaa aag agc gcg tcg ctc aac cgg 1411  
 Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser Ala Ser Leu Asn Arg  
 425 430 435  
 ttc ggc gcg gcc agt gcc gcc act cgc tac gcc gcg ttg aag cgc cgg 1459  
 Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala Ala Leu Lys Arg Arg  
 440 445 450  
 cac atc gca ggg ctc atc ccc atc gat gtg gcc ctg cgt cgc gac gat 1507  
 His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala Leu Arg Arg Asp Asp  
 455 460 465  
 tgg aac tgg ctc gag gtg ctg ccg gag gag atc gac gac cag ctt gag 1555  
 Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile Asp Asp Gln Leu Glu  
 470 475 480 485  
 gtc aag gcg tat tac ggg cac ttc ttc tgc cat gtg atg cac cag gac 1603  
 Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His Val Met His Gln Asp  
 490 495 500  
 tat gtc gcc aag cag ggc gtg gat ctc gag gcg ctg cac gac cgc atc 1651  
 Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala Leu His Asp Arg Ile  
 505 510 515  
 cag cac ctg ctg gag gag cgc ggc gcg aag ctg ccc gcc gag cac aac 1699  
 Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu Pro Ala Glu His Asn  
 520 525 530  
 tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac ttc aag 1747  
 Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His Phe Lys  
 535 540 545  
 gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc acg tcg 1795  
 Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly Thr Ser  
 550 555 560 565  
 ccg cac aag gac tgg gcc taagtcccca aggtagcgcg acg 1836  
 Pro His Lys Asp Trp Ala  
 570

&lt;210&gt; 138

&lt;211&gt; 571

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 138

Met Thr Gln Pro Gly Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp  
 1 5 10 15

Ala Phe Lys Arg Ile Val Gly Asp Glu His Val Leu Thr Ser Glu Arg  
 20 25 30

Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val

35					40					45					
Phe	Ala	Val	Val	Arg	Pro	Gly	Thr	Leu	Val	Glu	Met	Trp	Arg	Ala	Leu
50						55					60				
Gln	Val	Ser	Val	Asp	Asn	Asn	Leu	Ile	Val	Ile	Pro	Gln	Ala	Ser	Asn
65					70					75					80
Thr	Gly	Leu	Thr	Gly	Gly	Ser	Gly	Pro	Gly	Phe	Gln	Asp	Tyr	Asp	Arg
				85					90					95	
Pro	Ile	Val	Ile	Ile	Ser	Thr	His	Arg	Ile	Asp	Glu	Val	His	Leu	Ile
			100					105					110		
Asn	Asp	Ala	Arg	Glu	Ala	Ile	Ser	Leu	Ala	Gly	Thr	Pro	Leu	Thr	His
		115					120					125			
Leu	Thr	Asp	Ala	Leu	Ala	Lys	His	Gln	Arg	Glu	Pro	His	Ser	Val	Ile
130					135					140					
Gly	Ser	Thr	Ser	Ile	Gly	Ala	Ser	Val	Ile	Gly	Gly	Ile	Ala	Asn	Asn
145					150					155					160
Ser	Gly	Gly	Ser	Gln	Ile	Arg	Lys	Gly	Pro	Ala	Phe	Thr	Arg	Glu	Ala
				165					170					175	
Ile	Phe	Ala	Arg	Val	Asn	Asp	Asp	Gly	Lys	Val	Glu	Leu	Val	Asn	His
			180					185						190	
Leu	Gly	Ile	Ser	Leu	Gly	Asp	Asp	Pro	Glu	Val	Ala	Leu	Asp	Arg	Leu
		195					200					205			
Gln	Arg	Gly	Glu	Trp	Ser	Pro	Glu	Asp	Val	Thr	Pro	Ala	Pro	Glu	Asp
	210					215					220				
Ser	Asn	Glu	Thr	Glu	Tyr	Ala	Glu	His	Leu	Arg	Lys	Ile	Val	Pro	Ser
225					230					235					240
Pro	Ala	Arg	Tyr	Asn	Ala	Asn	Pro	Glu	Tyr	Leu	Phe	Glu	Ala	Ser	Gly
				245					250					255	
Ser	Ala	Gly	Lys	Leu	Met	Val	Phe	Ala	Val	Arg	Thr	Arg	Thr	Phe	Pro
			260					265					270		
Arg	Glu	Val	His	Pro	Thr	Val	Phe	Tyr	Ile	Gly	Thr	Asn	Asn	Thr	His
		275					280					285			
Glu	Leu	Glu	Glu	Ile	Arg	Arg	Leu	Phe	Leu	Glu	Ala	Asp	Met	Pro	Leu
	290					295					300				
Pro	Ile	Ser	Gly	Glu	Tyr	Met	Gly	Arg	Ser	Ala	Phe	Asp	Leu	Ala	Glu
305					310					315					320
Lys	Tyr	Gly	Lys	Asp	Thr	Phe	Val	Phe	Leu	Lys	Phe	Met	Ser	Pro	Ala
				325					330					335	
Leu	Gln	Thr	Arg	Met	Phe	Ser	Phe	Lys	Thr	Trp	Ala	Asn	Gly	Leu	Phe
			340					345					350		
Ser	Lys	Ile	Pro	Gly	Ile	Gly	Pro	Thr	Phe	Ala	Asp	Thr	Val	Ser	Gln
		355					360					365			

Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu  
370 375 380

Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser  
385 390 395 400

Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro  
405 410 415

Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser  
420 425 430

Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala  
435 440 445

Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala  
450 455 460

Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile  
465 470 475 480

Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His  
485 490 495

Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala  
500 505 510

Leu His Asp Arg Ile Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu  
515 520 525

Pro Ala Glu His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met  
530 535 540

Glu Glu His Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly  
545 550 555 560

Ile Gly Gly Thr Ser Pro His Lys Asp Trp Ala  
565 570

<210> 139

<211> 239

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(216)

<223> FRXA01952

<400> 139

cca gga cta tgt cgc caa gca ggg cgt gga tct caa ggc gct gac gac 48  
Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp  
1 5 10 15

cgc atc cag cac ttg ctg gag gag cac ggc aag aag ctg ccc gcc gag 96  
Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu  
20 25 30

cac aac tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac 144



His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His  
                   35                                  40                                  45

ttc aag gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc 192  
 Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly  
           50                                  55                                  60

acg tcg ccg cac aag gac tgg gcc taagtcccca aggtagcgcg acg 239  
 Thr Ser Pro His Lys Asp Trp Ala  
           65                                  70

<210> 140

<211> 72

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp  
       1                                  5                                  10                                  15

Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu  
                   20                                  25                                  30

His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His  
                   35                                  40                                  45

Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly  
           50                                  55                                  60

Thr Ser Pro His Lys Asp Trp Ala  
       65                                  70

<210> 141

<211> 1699

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1699)

<223> FRXA01955

<400> 141

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tgacgcgctt gtgatgcaac tgaatatagg aagcttagag atg acg caa cca gga 115  
   Met Thr Gln Pro Gly  
   1                                  5

cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163  
 Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile  
                                   10                                  15                                  20

gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211  
 Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe  
                   25                                  30                                  35

agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259  
 Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg

40	45	50	
ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp 55 60 65			307
aac aac ctc atc gtc atc ccg cag gca tcg aac acg ggc ctg act ggt Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly 70 75 80 85			355
gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile 90 95 100			403
tcg act cac cgc atc gat gag gtg cac ctc atc aac gac gcg cgc gag Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu 105 110 115			451
gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu 120 125 130			499
gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile 135 140 145			547
ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln 150 155 160 165			595
att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val 170 175 180			643
aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu 185 190 195			691
gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp 200 205 210			739
tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu 215 220 225			787
tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn 230 235 240 245			835
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu 250 255 260			883
atg gtg ttc gcg gtg cgc acc cgc acc ttc cct cgc gaa gtg cac ccg Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro 265 270 275			931
acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile 280 285 290			979

cgt	cgg	ttg	ttc	ctc	gaa	gcc	gac	atg	ccg	ctg	cct	atc	tct	ggg	gag	1027
Arg	Arg	Leu	Phe	Leu	Glu	Ala	Asp	Met	Pro	Leu	Pro	Ile	Ser	Gly	Glu	
	295					300					305					
tac	atg	ggc	cgc	agt	gcc	ttc	gac	ttg	gcc	gag	aag	tac	ggc	aaa	gac	1075
Tyr	Met	Gly	Arg	Ser	Ala	Phe	Asp	Leu	Ala	Glu	Lys	Tyr	Gly	Lys	Asp	
310					315					320					325	
acc	ttc	gtc	ttc	ctg	aag	ttc	atg	agt	cca	gcg	ctg	cag	acg	cgc	atg	1123
Thr	Phe	Val	Phe	Leu	Lys	Phe	Met	Ser	Pro	Ala	Leu	Gln	Thr	Arg	Met	
				330					335					340		
ttc	tcg	ttc	aag	acg	tgg	gcc	aac	ggc	ttg	ttc	tcg	aag	att	ccc	ggc	1171
Phe	Ser	Phe	Lys	Thr	Trp	Ala	Asn	Gly	Leu	Phe	Ser	Lys	Ile	Pro	Gly	
			345					350					355			
att	ggg	ccg	acc	ttc	gcc	gac	acg	gta	tcg	caa	gcc	atg	ttc	agc	gtg	1219
Ile	Gly	Pro	Thr	Phe	Ala	Asp	Thr	Val	Ser	Gln	Ala	Met	Phe	Ser	Val	
		360					365					370				
ctg	ccc	aac	cag	ctg	ccc	aag	cgc	atg	atg	gag	tac	cgc	aac	cgt	ttc	1267
Leu	Pro	Asn	Gln	Leu	Pro	Lys	Arg	Met	Met	Glu	Tyr	Arg	Asn	Arg	Phe	
	375					380					385					
gag	cat	cac	ctg	ctg	ctc	acc	gtc	agc	gag	tcg	cag	aag	gcc	gcg	agc	1315
Glu	His	His	Leu	Leu	Leu	Thr	Val	Ser	Glu	Ser	Gln	Lys	Ala	Ala	Ser	
390					395					400					405	
gag	aag	atg	ctc	aag	gag	ttc	ttc	gca	gag	ccc	gag	cac	act	ggg	gag	1363
Glu	Lys	Met	Leu	Lys	Glu	Phe	Phe	Ala	Glu	Pro	Glu	His	Thr	Gly	Glu	
			410					415					420			
ttc	ttc	atc	tgc	acg	tct	gat	gaa	gaa	aag	agc	gcg	tcg	ctc	aac	cgg	1411
Phe	Phe	Ile	Cys	Thr	Ser	Asp	Glu	Glu	Lys	Ser	Ala	Ser	Leu	Asn	Arg	
			425					430					435			
ttc	ggc	gcg	gcc	agt	gcc	gcc	act	cgc	tac	gcc	gcg	ttg	aag	cgc	cgg	1459
Phe	Gly	Ala	Ala	Ser	Ala	Ala	Thr	Arg	Tyr	Ala	Ala	Leu	Lys	Arg	Arg	
		440					445					450				
cac	atc	gca	ggg	ctc	atc	ccc	atc	gat	gtg	gcc	ctg	cgt	cgc	gac	gat	1507
His	Ile	Ala	Gly	Leu	Ile	Pro	Ile	Asp	Val	Ala	Leu	Arg	Arg	Asp	Asp	
	455					460					465					
tgg	aac	tgg	ctc	gag	gtg	ctg	ccg	gag	gag	atc	gac	gac	cag	ctt	gag	1555
Trp	Asn	Trp	Leu	Glu	Val	Leu	Pro	Glu	Glu	Ile	Asp	Asp	Gln	Leu	Glu	
470					475					480					485	
gtc	aag	gcg	tat	tac	ggg	cac	ttc	ttc	tgc	cat	gtg	atg	cac	cag	gac	1603
Val	Lys	Ala	Tyr	Tyr	Gly	His	Phe	Phe	Cys	His	Val	Met	His	Gln	Asp	
			490						495					500		
tat	gtc	gcc	aag	cag	ggc	gtg	gat	ctc	gag	gcg	ctg	cac	gac	cgc	atc	1651
Tyr	Val	Ala	Lys	Gln	Gly	Val	Asp	Leu	Glu	Ala	Leu	His	Asp	Arg	Ile	
			505					510					515			
cag	cac	ctg	ctg	gag	gag	cgc	ggc	gcg	aag	ctg	ccc	gcc	gag	cac	aac	1699
Gln	His	Leu	Leu	Glu	Glu	Arg	Gly	Ala	Lys	Leu	Pro	Ala	Glu	His	Asn	
		520					525					530				

<210> 142  
 <211> 533  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 142

Met	Thr	Gln	Pro	Gly	Gln	Thr	Thr	Thr	Thr	Ser	His	Glu	Ala	Ile	Asp
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Ala	Phe	Lys	Arg	Ile	Val	Gly	Asp	Glu	His	Val	Leu	Thr	Ser	Glu	Arg
			20					25					30		
Ala	Thr	Met	Pro	Phe	Ser	Lys	Gly	Tyr	Arg	Phe	Gly	Gly	Gly	Pro	Val
		35					40					45			
Phe	Ala	Val	Val	Arg	Pro	Gly	Thr	Leu	Val	Glu	Met	Trp	Arg	Ala	Leu
	50					55					60				
Gln	Val	Ser	Val	Asp	Asn	Asn	Leu	Ile	Val	Ile	Pro	Gln	Ala	Ser	Asn
	65				70					75					80
Thr	Gly	Leu	Thr	Gly	Gly	Ser	Gly	Pro	Gly	Phe	Gln	Asp	Tyr	Asp	Arg
				85					90					95	
Pro	Ile	Val	Ile	Ile	Ser	Thr	His	Arg	Ile	Asp	Glu	Val	His	Leu	Ile
			100					105					110		
Asn	Asp	Ala	Arg	Glu	Ala	Ile	Ser	Leu	Ala	Gly	Thr	Pro	Leu	Thr	His
		115					120					125			
Leu	Thr	Asp	Ala	Leu	Ala	Lys	His	Gln	Arg	Glu	Pro	His	Ser	Val	Ile
	130					135					140				
Gly	Ser	Thr	Ser	Ile	Gly	Ala	Ser	Val	Ile	Gly	Gly	Ile	Ala	Asn	Asn
145					150					155					160
Ser	Gly	Gly	Ser	Gln	Ile	Arg	Lys	Gly	Pro	Ala	Phe	Thr	Arg	Glu	Ala
				165					170					175	
Ile	Phe	Ala	Arg	Val	Asn	Asp	Asp	Gly	Lys	Val	Glu	Leu	Val	Asn	His
			180					185					190		
Leu	Gly	Ile	Ser	Leu	Gly	Asp	Asp	Pro	Glu	Val	Ala	Leu	Asp	Arg	Leu
	195						200					205			
Gln	Arg	Gly	Glu	Trp	Ser	Pro	Glu	Asp	Val	Thr	Pro	Ala	Pro	Glu	Asp
	210					215					220				
Ser	Asn	Glu	Thr	Glu	Tyr	Ala	Glu	His	Leu	Arg	Lys	Ile	Val	Pro	Ser
225					230					235				240	
Pro	Ala	Arg	Tyr	Asn	Ala	Asn	Pro	Glu	Tyr	Leu	Phe	Glu	Ala	Ser	Gly
				245					250					255	
Ser	Ala	Gly	Lys	Leu	Met	Val	Phe	Ala	Val	Arg	Thr	Arg	Thr	Phe	Pro
			260					265					270		
Arg	Glu	Val	His	Pro	Thr	Val	Phe	Tyr	Ile	Gly	Thr	Asn	Asn	Thr	His
		275					280					285			

Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu  
 290 295 300  
 Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu  
 305 310 315 320  
 Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala  
 325 330 335  
 Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe  
 340 345 350  
 Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln  
 355 360 365  
 Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu  
 370 375 380  
 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser  
 385 390 395 400  
 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro  
 405 410 415  
 Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser  
 420 425 430  
 Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala  
 435 440 445  
 Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala  
 450 455 460  
 Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile  
 465 470 475 480  
 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His  
 485 490 495  
 Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala  
 500 505 510  
 Leu His Asp Arg Ile Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu  
 515 520 525  
 Pro Ala Glu His Asn  
 530

&lt;210&gt; 143

&lt;211&gt; 1035

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1012)

&lt;223&gt; RXA00293

&lt;400&gt; 143

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acaaaaccca	acctcacacc	aacaacctat	cctggagccc	atg	aaa	atc	ttt	gtt	115							
				Met	Lys	Ile	Phe	Val								
				1				5								
ggt	ttt	ggc	gat	tat	cca	ctc	acc	acc	aag	gcc	ctt	aag	gag	gca	ggc	163
Gly	Phe	Gly	Asp	Tyr	Pro	Leu	Thr	Thr	Lys	Ala	Leu	Lys	Glu	Ala	Gly	
				10					15					20		
gca	gaa	ata	gtg	gac	tcc	ctc	gaa	aaa	gcc	gag	ggg	ttt	gtc	ttc	act	211
Ala	Glu	Ile	Val	Asp	Ser	Leu	Glu	Lys	Ala	Glu	Gly	Phe	Val	Phe	Thr	
			25					30					35			
caa	aca	cca	ggc	aca	gaa	ttt	ccc	cta	ctt	ccc	gac	gga	gtg	agg	tgg	259
Gln	Thr	Pro	Gly	Thr	Glu	Phe	Pro	Leu	Leu	Pro	Asp	Gly	Val	Arg	Trp	
		40					45					50				
gtg	caa	ttt	ccc	aat	gcg	ggg	ctc	aac	gca	tat	ttc	aca	gct	ggg	cag	307
Val	Gln	Phe	Pro	Asn	Ala	Gly	Leu	Asn	Ala	Tyr	Phe	Thr	Ala	Gly	Gln	
	55					60					65					
att	gat	gac	aaa	cgc	cgg	tgg	tca	aat	gca	tca	ggg	gtg	tat	ggc	caa	355
Ile	Asp	Asp	Lys	Arg	Arg	Trp	Ser	Asn	Ala	Ser	Gly	Val	Tyr	Gly	Gln	
	70				75				80						85	
cag	gta	gcc	gaa	gca	gca	atg	gct	ctt	ttg	ctg	gga	ctg	att	cat	atg	403
Gln	Val	Ala	Glu	Ala	Ala	Met	Ala	Leu	Leu	Leu	Gly	Leu	Ile	His	Met	
				90					95					100		
cac	ccc	acc	atg	gtg	cgt	gcc	gat	agt	tgg	gca	cca	agc	act	caa	ata	451
His	Pro	Thr	Met	Val	Arg	Ala	Asp	Ser	Trp	Ala	Pro	Ser	Thr	Gln	Ile	
			105					110					115			
gat	cag	cag	acc	aga	tgg	ctt	gat	ggt	gca	aca	gtt	gcc	att	gtg	gga	499
Asp	Gln	Gln	Thr	Arg	Trp	Leu	Asp	Gly	Ala	Thr	Val	Ala	Ile	Val	Gly	
			120				125					130				
gct	ggt	gga	atc	ggt	aaa	cat	ctg	gca	gcc	atg	ttg	aaa	cct	ttt	ggc	547
Ala	Gly	Gly	Ile	Gly	Lys	His	Leu	Ala	Ala	Met	Leu	Lys	Pro	Phe	Gly	
	135				140						145					
gca	aag	tct	tta	gca	gta	agc	agg	acc	ggt	aca	ccc	acc	caa	gat	ttt	595
Ala	Lys	Ser	Leu	Ala	Val	Ser	Arg	Thr	Gly	Thr	Pro	Thr	Gln	Asp	Phe	
	150				155					160					165	
gat	gca	acg	gaa	cct	ata	tcc	aac	ctg	cac	caa	gta	ctt	gcc	gac	gcc	643
Asp	Ala	Thr	Glu	Pro	Ile	Ser	Asn	Leu	His	Gln	Val	Leu	Ala	Asp	Ala	
			170						175					180		
gac	cat	gtg	gtg	ttg	tgc	gta	cgc	ctt	acc	gca	gac	acc	tat	cat	ctg	691
Asp	His	Val	Val	Leu	Cys	Val	Pro	Leu	Thr	Ala	Asp	Thr	Tyr	His	Leu	
			185					190					195			
atc	gga	aaa	gca	gag	ctt	aaa	gca	atg	cag	tcc	act	gca	att	ttg	atc	739
Ile	Gly	Lys	Ala	Glu	Leu	Lys	Ala	Met	Gln	Ser	Thr	Ala	Ile	Leu	Ile	
		200					205					210				
aac	gtg	gct	cgc	gga	gaa	gta	gta	gat	aca	gaa	gca	tta	gtt	gac	gcc	787
Asn	Val	Ala	Arg	Gly	Glu	Val	Val	Asp	Thr	Glu	Ala	Leu	Val	Asp	Ala	
	215					220					225					

tta gat gcc caa gaa ata tcc ggg gca ggc tta gat gtc acc gat cct 835  
 Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu Asp Val Thr Asp Pro  
 230 235 240 245  
  
 gaa cca ttg ccg gac gat cat cca ctg tgg ggg cgc agc aat gtg atc 883  
 Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly Arg Ser Asn Val Ile  
 250 255 260  
  
 att acc ccg cac gta gcc aac acg ttg acc tcg atg gat cgc atg ctt 931  
 Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser Met Asp Arg Met Leu  
 265 270 275  
  
 gcc cca gtg gtg gca gaa aac tac cga cgg ttt ctc gct gga gaa aag 979  
 Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe Leu Ala Gly Glu Lys  
 280 285 290  
  
 atg ctg acc gag gtg gac atc cac aaa ggt tac tagagcagtg gctttgaata 1032  
 Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr  
 295 300  
  
 tag 1035

&lt;210&gt; 144

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 144

Met Lys Ile Phe Val Gly Phe Gly Asp Tyr Pro Leu Thr Thr Lys Ala  
 1 5 10 15  
  
 Leu Lys Glu Ala Gly Ala Glu Ile Val Asp Ser Leu Glu Lys Ala Glu  
 20 25 30  
  
 Gly Phe Val Phe Thr Gln Thr Pro Gly Thr Glu Phe Pro Leu Leu Pro  
 35 40 45  
  
 Asp Gly Val Arg Trp Val Gln Phe Pro Asn Ala Gly Leu Asn Ala Tyr  
 50 55 60  
  
 Phe Thr Ala Gly Gln Ile Asp Asp Lys Arg Arg Trp Ser Asn Ala Ser  
 65 70 75 80  
  
 Gly Val Tyr Gly Gln Gln Val Ala Glu Ala Ala Met Ala Leu Leu Leu  
 85 90 95  
  
 Gly Leu Ile His Met His Pro Thr Met Val Arg Ala Asp Ser Trp Ala  
 100 105 110  
  
 Pro Ser Thr Gln Ile Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr  
 115 120 125  
  
 Val Ala Ile Val Gly Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met  
 130 135 140  
  
 Leu Lys Pro Phe Gly Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr  
 145 150 155 160  
  
 Pro Thr Gln Asp Phe Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln  
 165 170 175

Val Leu Ala Asp Ala Asp His Val Val Leu Cys Val Pro Leu Thr Ala  
 180 185 190

Asp Thr Tyr His Leu Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser  
 195 200 205

Thr Ala Ile Leu Ile Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu  
 210 215 220

Ala Leu Val Asp Ala Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu  
 225 230 235 240

Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly  
 245 250 255

Arg Ser Asn Val Ile Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser  
 260 265 270

Met Asp Arg Met Leu Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe  
 275 280 285

Leu Ala Gly Glu Lys Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr  
 290 295 300

<210> 145  
 <211> 687  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (62)..(664)  
 <223> RXN01130

<400> 145  
 agttcgtggc ggatgctgtg aacgtttccg gtggtcgcgt gggcgaagag gttctgtgtg 60

g atg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109  
 Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp  
 1 5 10 15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157  
 Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser  
 20 25 30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205  
 Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser  
 35 40 45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253  
 Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala  
 50 55 60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301  
 Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val  
 65 70 75 80



act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349  
 Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala  
                     85                    90                    95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397  
 Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys  
                     100                    105                    110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445  
 Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu  
                     115                    120                    125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493  
 Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val  
                     130                    135                    140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541  
 Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu  
                     145                    150                    155                    160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589  
 Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu  
                     165                    170                    175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637  
 Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly  
                     180                    185                    190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct tga 687  
 Ala Thr Ser Phe Gln Val Asp Leu Asp  
                     195                    200

&lt;210&gt; 146

&lt;211&gt; 201

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 146

Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp  
   1                    5                    10                    15

Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser  
                     20                    25                    30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser  
                     35                    40                    45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala  
                     50                    55                    60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val  
                     65                    70                    75                    80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala  
                     85                    90                    95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys  
                     100                    105                    110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu  
 115 120 125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val  
 130 135 140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu  
 145 150 155 160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu  
 165 170 175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly  
 180 185 190

Ala Thr Ser Phe Gln Val Asp Leu Asp  
 195 200

&lt;210&gt; 147

&lt;211&gt; 326

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(303)

&lt;223&gt; FRXA01130

&lt;400&gt; 147

ggt ggt gcc ctg act ggt ctt gag cgc gtt gag aag atc acc cgc atc	48
Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile	
1 5 10 15	
aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg aac ctc ttc ctg	96
Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu	
20 25 30	
cag tac act gac gct cct ggt gca ctg ggt acc gtt ggt acc aag ctg	144
Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu	
35 40 45	
ggt gct gct ggc atc aac atc gag gct gct gcg ttg act cag gct gag	192
Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu	
50 55 60	
aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag tcc gct gtc tct	240
Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser	
65 70 75 80	
gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt gct act tcc ttc	288
Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe	
85 90 95	
cag gtt gat ctt gac taattagaga tccatttgct tga	326
Gln Val Asp Leu Asp	
100	

&lt;210&gt; 148

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 148

Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile  
 1 5 10 15

Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu  
 20 25 30

Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu  
 35 40 45

Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu  
 50 55 60

Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser  
 65 70 75 80

Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe  
 85 90 95

Gln Val Asp Leu Asp  
 100

&lt;210&gt; 149

&lt;211&gt; 604

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(604)

&lt;223&gt; RXN03112

&lt;400&gt; 149

gtgagcacgc aatttctttg ctgctgtcta ctgctcgcca gatcctgctg ctgatgcgac 60

gctgctgag ggcgagtga agcgggtcttc tttcaacggt gtg gaa att ttc gga 115  
 Val Glu Ile Phe Gly  
 1 5

aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163  
 Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala  
 10 15 20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211  
 Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr  
 25 30 35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259  
 Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu  
 40 45 50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307  
 Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys  
 55 60 65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355  
 Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser

70	75	80	85	
aag aag ggc cag atc atc atc aac gct gct cgt ggt ggc ctt gtt gat				403
Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp	90	95	100	
gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct				451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala	105	110	115	
ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc				499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe	120	125	130	
aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa				547
Lys Leu Pro Gln Val Val Thr Pro His Leu Gly Ala Ser Thr Glu	135	140	145	
gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag				595
Glu Ala Gln Asp Arg Ala Gly Thr Asp Ile Ala Asp Ser Val Leu Lys	150	155	160	165
gcg ctg gct				604
Ala Leu Ala				

&lt;210&gt; 150

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 150

Val	Glu	Ile	Phe	Gly	Lys	Thr	Val	Gly	Ile	Val	Gly	Phe	Gly	His	Ile
1				5					10					15	

Gly	Gln	Leu	Phe	Ala	Gln	Arg	Leu	Ala	Ala	Phe	Glu	Thr	Thr	Ile	Val
		20						25						30	

Ala	Tyr	Asp	Pro	Tyr	Ala	Asn	Pro	Ala	Arg	Ala	Ala	Gln	Leu	Asn	Val
		35					40					45			

Glu	Leu	Val	Glu	Leu	Asp	Glu	Leu	Met	Ser	Arg	Ser	Asp	Phe	Val	Thr
	50					55					60				

Ile	His	Leu	Pro	Lys	Thr	Lys	Glu	Thr	Ala	Gly	Met	Phe	Asp	Ala	His
65					70					75				80	

Leu	Leu	Ala	Lys	Ser	Lys	Lys	Gly	Gln	Ile	Ile	Ile	Asn	Ala	Ala	Arg
				85					90					95	

Gly	Gly	Leu	Val	Asp	Glu	Gln	Ala	Leu	Ala	Asp	Ala	Ile	Glu	Ser	Gly
		100						105					110		

His	Ile	Arg	Gly	Ala	Gly	Phe	Asp	Val	Tyr	Ser	Thr	Glu	Pro	Cys	Thr
		115					120					125			

Asp	Ser	Pro	Leu	Phe	Lys	Leu	Pro	Gln	Val	Val	Val	Thr	Pro	His	Leu
	130					135					140				

Gly	Ala	Ser	Thr	Glu	Glu	Ala	Gln	Asp	Arg	Ala	Gly	Thr	Asp	Ile	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145	150	155	160
Asp Ser Val Leu Lys Ala Leu Ala			
165			
<210> 151 <211> 649 <212> DNA <213> Corynebacterium glutamicum  <220> <221> CDS <222> (101)..(649) <223> FRXA01133  <400> 151			
tgttttctagtc cgcacgccaa aacccggcgt ggacacgtct gcagccgacg cggtcgtgcc 60			
tgttgtagac ggacattcct agttttttcca ggagtaactt gtg agc cag aat ggc 115			
Val Ser Gln Asn Gly 5			
cgt ccg gta gtc ctc atc gcc gat aag ctt gcg cag tcc act gtt gac 163			
Arg Pro Val Val Ile Ala Asp Lys Leu Ala Gln Ser Thr Val Asp 20			
gcg ctt gga gat gca gta gaa gtc cgt tgg gtt gac gga cct aac cgc 211			
Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro Asn Arg 35			
cca gaa ctg ctt gat gca gtt aag gaa gcg gac gca ctg ctc gtg cgt 259			
Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp Ala Leu Leu Val Arg 50			
tct gct acc act gtc gat gct gaa gtc atc gcc gct gcc cct aac ttg 307			
Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala Ala Pro Asn Leu 65			
aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac gtt gac atc cct 355			
Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp Ile Pro 85			
gct gcc act gaa gct ggc gtc atg gtt gct aac gca ccg acc tct aat 403			
Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala Pro Thr Ser Asn 100			
att cac tcc gct tgt gag cac gca att tct ttg ctg ctg tct act gct 451			
Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu Leu Ser Thr Ala 115			
cgc cag atc ctg ctg ctg atg cga cgc tgc gtg agg gcg agt gga agc 499			
Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val Arg Ala Ser Gly Ser 130			
ggt ctt ctt tca acg gtg tgg aaa ttt tcg gaa aaa ctg tcg gta tcg 547			
Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu Lys Leu Ser Val Ser 145			
tcg gtt ttg gcc aca ttg gtc agt tgt ttg ctc agc gtc ttg ctg cgt 595			
Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu Ser Val Leu Leu Arg			

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<210> 152
<211> 183
<212> PRT
<213> Corynebacterium glutamicum
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<210> 153
<211> 1011
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS

&lt;222&gt; (101)..(988)

&lt;223&gt; RXN00871

&lt;400&gt; 153

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gggaaaaggc gatcaccagc cgttggctcg acccagcaac ccacggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
                                         Met Arg Trp Phe His
                                         1           5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
              10              15              20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
              25              30              35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
              40              45              50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
              55              60              65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355
His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu
              70              75              80              85

tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403
Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val
              90              95              100

gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc 451
Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile
              105              110              115

gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc 499
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser
              120              125              130

cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga 547
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg
              135              140              145

cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac 595
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr
              150              155              160              165

cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg 643
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu
              170              175              180

gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg 691
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg
              185              190              195

gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser
              200              205              210

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cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc 787  
 Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile  
 215 220 225

gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc 835  
 Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly  
 230 235 240 245

tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga 883  
 Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg  
 250 255 260

atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca 931  
 Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr  
 265 270 275

tgg acc ggg caa gca ttt gat gat cgc ttg cca tat gag aac gca aac 979  
 Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro Tyr Glu Asn Ala Asn  
 280 285 290

aag gag gga taaaatttca tggctgaaac gaa 1011  
 Lys Glu Gly  
 295

<210> 154  
 <211> 296  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 154  
 Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln  
 1 5 10 15

Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg  
 20 25 30

Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly  
 35 40 45

Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His  
 50 55 60

His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly  
 65 70 75 80

Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser  
 85 90 95

Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys  
 100 105 110

Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly  
 115 120 125

Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala  
 130 135 140

Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu  
 145 150 155 160



Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly  
 165 170 175  
 His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser  
 180 185 190  
 Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe  
 195 200 205  
 Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val  
 210 215 220  
 Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala  
 225 230 235 240  
 Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly  
 245 250 255  
 Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala  
 260 265 270  
 Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro  
 275 280 285  
 Tyr Glu Asn Ala Asn Lys Glu Gly  
 290 295

&lt;210&gt; 155

&lt;211&gt; 964

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(964)

&lt;223&gt; FRXA00871

&lt;400&gt; 155

gggaaaaggc gatcaccagc cggttggtcg acccagcaac ccacggtggc attaacctcg 60

gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115  
 Met Arg Trp Phe His  
 1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163  
 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala  
 10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211  
 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly  
 25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259  
 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe  
 40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307  
 Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr  
 55 60 65

cat	ctt	cac	gga	aga	aag	tca	gtc	ttt	gat	gga	cca	acc	gat	gtg	ctc	355
His	Leu	His	Gly	Arg	Lys	Ser	Val	Phe	Asp	Gly	Pro	Thr	Asp	Val	Leu	
70					75					80					85	
tac	ctc	ccc	act	gga	caa	aca	gca	acg	ctc	agt	ggt	cag	gga	cga	gtc	403
Tyr	Leu	Pro	Thr	Gly	Gln	Thr	Ala	Thr	Leu	Ser	Gly	Gln	Gly	Arg	Val	
				90					95						100	
gcc	gtg	gcg	gaa	gct	ccc	act	cag	gaa	ccc	aag	gag	tgg	aag	tac	atc	451
Ala	Val	Ala	Glu	Ala	Pro	Thr	Gln	Glu	Pro	Lys	Glu	Trp	Lys	Tyr	Ile	
			105					110					115			
gct	cca	gca	gaa	act	cct	gtg	gag	ttg	cgt	gga	gct	ggc	cgc	tcg	agc	499
Ala	Pro	Ala	Glu	Thr	Pro	Val	Glu	Leu	Arg	Gly	Ala	Gly	Arg	Ser	Ser	
			120				125					130				
cga	caa	gtc	cac	aac	ttt	ggc	acc	ccg	gaa	gct	ctc	gat	gct	gct	cga	547
Arg	Gln	Val	His	Asn	Phe	Gly	Thr	Pro	Glu	Ala	Leu	Asp	Ala	Ala	Arg	
	135					140					145					
cta	atc	gtg	tgt	gaa	gta	atc	acc	cca	ggt	gaa	aac	tgg	agc	tct	tac	595
Leu	Ile	Val	Cys	Glu	Val	Ile	Thr	Pro	Gly	Glu	Asn	Trp	Ser	Ser	Tyr	
150					155					160					165	
cct	cca	cac	aag	cat	gat	gag	cac	atc	cca	gga	cac	gag	tcc	aag	ctg	643
Pro	Pro	His	Lys	His	Asp	Glu	His	Ile	Pro	Gly	His	Glu	Ser	Lys	Leu	
				170					175					180		
gag	gaa	atc	tac	tac	ttc	gaa	agc	gcc	cca	tcg	cga	gtt	ggt	ggc	agg	691
Glu	Glu	Ile	Tyr	Tyr	Phe	Glu	Ser	Ala	Pro	Ser	Arg	Val	Gly	Gly	Arg	
			185					190					195			
gcc	gaa	gca	gca	gaa	gga	gct	ttc	gga	atg	ttt	tcc	acc	tac	tcc	tca	739
Ala	Glu	Ala	Ala	Glu	Gly	Ala	Phe	Gly	Met	Phe	Ser	Thr	Tyr	Ser	Ser	
			200				205					210				
cca	gcg	ggg	gag	atc	gat	atc	aac	gcc	atg	gtg	tac	agc	ggc	gat	atc	787
Pro	Ala	Gly	Glu	Ile	Asp	Ile	Asn	Ala	Met	Val	Tyr	Ser	Gly	Asp	Ile	
			215			220					225					
gcg	cta	gtt	cct	ttc	gga	tac	cac	ggc	cct	gcc	gtg	gca	gca	cct	ggc	835
Ala	Leu	Val	Pro	Phe	Gly	Tyr	His	Gly	Pro	Ala	Val	Ala	Ala	Pro	Gly	
230				235					240						245	
tat	gac	ttg	tac	tac	ctc	aac	gtc	atg	gca	gga	cct	gat	ccg	gag	aga	883
Tyr	Asp	Leu	Tyr	Tyr	Leu	Asn	Val	Met	Ala	Gly	Pro	Asp	Pro	Glu	Arg	
				250					255					260		
atc	tgg	ctg	att	aac	gat	gac	cca	gcg	cac	gcc	tgg	gtt	cga	gat	aca	931
Ile	Trp	Leu	Ile	Asn	Asp	Asp	Pro	Ala	His	Ala	Trp	Val	Arg	Asp	Thr	
			265					270					275			
tgg	acc	ggg	caa	gca	ttt	gat	gat	cgc	ttg	cca						964
Trp	Thr	Gly	Gln	Ala	Phe	Asp	Asp	Arg	Leu	Pro						
			280				285									

&lt;210&gt; 156

&lt;211&gt; 288

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 156

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Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln
 1              5              10              15

Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg
      20              25              30

Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
      35              40              45

Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His
      50              55              60

His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly
      65              70              75              80

Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser
      85              90              95

Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys
      100              105              110

Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
      115              120              125

Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala
      130              135              140

Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu
      145              150              155              160

Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
      165              170              175

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
      180              185              190

Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
      195              200              205

Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
      210              215              220

Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
      225              230              235              240

Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
      245              250              255

Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
      260              265              270

Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
      275              280              285

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<220>  
<221> CDS  
<222> (101)..(373)  
<223> RXN02829
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<210> 158
<211> 91
<212> PRT
<213> Corynebacterium glutamicum
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<400> 158

Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly  
1 5 10 15

Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile  
20 25 30

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp  
35 40 45

Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys  
50 55 60

Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn

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65              70              75              80
Arg Leu Thr Asp Asp Gly His Met Thr Trp Asp
      85              90

<210> 159
<211> 376
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(376)
<223> FRXA02829

<400> 159
tttttcgttt aatctcatat ttaaacacgt tccttttaat tggttttata aattgataaa 60

ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115
              Met Gln Lys Asn Ile
              1              5

cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163
Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
              10              15              20

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211
Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
              25              30              35

gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259
Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
              40              45              50

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
              55              60              65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp
              70              75              80              85

gga cat atg acg tgg gga tcc 376
Gly His Met Thr Trp Gly Ser
              90

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<210> 160
<211> 92
<212> PRT
<213> Corynebacterium glutamicum

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<400> 160
Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
  1              5              10              15

Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
      20              25              30

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp

```

35	40	45
Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys		
50	55	60
Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn		
65	70	75
Arg Leu Thr Asp Asp Gly His Met Thr Trp Gly Ser		
	85	90

<210> 161  
 <211> 948  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(925)  
 <223> RXN01468

<400> 161  
 tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa aatttcgccc aaaacaggga caatggtgtt atg aca gtg aac att 115  
 Met Thr Val Asn Ile  
 1 5

tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163  
 Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile  
 10 15 20

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211  
 Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val  
 25 30 35

gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt 259  
 Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu  
 40 45 50

tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att 307  
 Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile  
 55 60 65

tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag 355  
 Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys  
 70 75 80 85

gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg 403  
 Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu  
 90 95 100

cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc 451  
 His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val  
 105 110 115

ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata 499  
 Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile  
 120 125 130

aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc 547  
 Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val  
 135 140 145  
 act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc 595  
 Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala  
 150 155 160 165  
 gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag 643  
 Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys  
 170 175 180  
 cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat 691  
 Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His  
 185 190 195  
 tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa 739  
 Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys  
 200 205 210  
 tct ggt ttg gaa gcc ggc ctg agc acc gtg ctg gtt cga agc gga att 787  
 Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile  
 215 220 225  
 tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg 835  
 Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val  
 230 235 240 245  
 atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt 883  
 Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly  
 250 255 260  
 gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac 925  
 Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp  
 265 270 275  
 tagtattctg taggtcatgg cat 948

&lt;210&gt; 162

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 162

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile  
 1 5 10 15

Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu  
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe  
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile  
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu  
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly

85					90					95					
Leu	Thr	Thr	Ala	Leu	His	Thr	Ala	Gly	Trp	Ile	Leu	Thr	Asp	Ala	Asn
			100					105					110		
Pro	Glu	Phe	Val	Val	Leu	Gly	Glu	Thr	Arg	Thr	Tyr	Ser	Phe	Glu	Ala
		115					120					125			
Ile	Thr	Thr	Ala	Ile	Asn	Leu	Ile	Leu	Gly	Gly	Ala	Arg	Phe	Ile	Cys
		130					135					140			
Thr	Asn	Pro	Asp	Val	Thr	Gly	Pro	Ser	Pro	Ser	Gly	Ile	Leu	Pro	Ala
145							150					155			160
Thr	Gly	Ser	Val	Ala	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Gly	Ala	Glu	Pro
				165					170					175	
Tyr	Tyr	Ile	Gly	Lys	Pro	Asn	Pro	Val	Met	Met	Arg	Ser	Ala	Leu	Asn
			180					185					190		
Thr	Ile	Gly	Ala	His	Ser	Glu	His	Thr	Val	Met	Ile	Gly	Asp	Arg	Met
		195					200						205		
Asp	Thr	Asp	Val	Lys	Ser	Gly	Leu	Glu	Ala	Gly	Leu	Ser	Thr	Val	Leu
		210					215					220			
Val	Arg	Ser	Gly	Ile	Ser	Asp	Asp	Ala	Glu	Ile	Arg	Arg	Tyr	Pro	Phe
225							230					235			240
Arg	Pro	Thr	His	Val	Ile	Asn	Ser	Ile	Ala	Asp	Leu	Ala	Asp	Cys	Trp
				245					250					255	
Asp	Asp	Pro	Phe	Gly	Asp	Gly	Ala	Phe	His	Val	Pro	Asp	Glu	Gln	Gln
			260					265					270		
Phe	Thr	Asp													
		275													

&lt;210&gt; 163

&lt;211&gt; 948

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(925)

&lt;223&gt; FRXA01468

&lt;400&gt; 163

tgccaaggat ttgaccaccg tgcaggattt gattgacttt attaacacca ataaggctga 60

ttagcgggaa	aatttcgccc	aaaacaggga	caatggtgtt	atg	aca	gtg	aac	att	115
				Met	Thr	Val	Asn	Ile	
				1				5	

tca	tat	ctg	acc	gac	atg	gac	ggc	gtc	ctc	atc	aaa	gag	ggc	gag	ata	163
Ser	Tyr	Leu	Thr	Asp	Met	Asp	Gly	Val	Leu	Ile	Lys	Glu	Gly	Glu	Ile	
				10				15						20		

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211



Ile	Pro	Gly	Ala	Asp	Arg	Phe	Leu	Gln	Ser	Leu	Thr	Asp	Asn	Asn	Val		
			25					30					35				
gag	ttt	atg	gtt	ttg	acc	aac	aac	tcc	att	ttc	acc	ccg	agg	gat	ctt	259	
Glu	Phe	Met	Val	Leu	Thr	Asn	Asn	Ser	Ile	Phe	Thr	Pro	Arg	Asp	Leu		
		40					45					50					
tct	gca	cgt	ctt	aag	act	tcc	ggg	ttg	gat	atc	ccg	ccg	gag	cgt	att	307	
Ser	Ala	Arg	Leu	Lys	Thr	Ser	Gly	Leu	Asp	Ile	Pro	Pro	Glu	Arg	Ile		
		55				60					65						
tgg	act	tct	gca	acc	gcc	act	gct	cac	ttc	ctg	aaa	tcc	cag	gtc	aag	355	
Trp	Thr	Ser	Ala	Thr	Ala	Thr	Ala	His	Phe	Leu	Lys	Ser	Gln	Val	Lys		
		70			75				80						85		
gag	ggc	aca	gcc	tat	gtt	gtt	ggc	gag	tcc	ggg	ctg	acc	act	gcg	ttg	403	
Glu	Gly	Thr	Ala	Tyr	Val	Val	Gly	Glu	Ser	Gly	Leu	Thr	Thr	Ala	Leu		
			90						95					100			
cat	acc	gcg	ggg	tgg	att	ttg	acg	gat	gca	aat	cct	gag	ttt	gtt	gtc	451	
His	Thr	Ala	Gly	Trp	Ile	Leu	Thr	Asp	Ala	Asn	Pro	Glu	Phe	Val	Val		
			105					110					115				
ctg	ggc	gaa	acc	cgc	aca	tat	tcc	ttc	gag	gca	atc	act	act	gcg	ata	499	
Leu	Gly	Glu	Thr	Arg	Thr	Tyr	Ser	Phe	Glu	Ala	Ile	Thr	Thr	Ala	Ile		
		120					125					130					
aat	ctg	att	ttg	ggg	ggc	gct	cgc	ttt	att	tgc	acc	aac	ccg	gat	gtc	547	
Asn	Leu	Ile	Leu	Gly	Gly	Ala	Arg	Phe	Ile	Cys	Thr	Asn	Pro	Asp	Val		
		135				140					145						
act	gga	cct	tca	cca	agt	ggc	att	ttg	cct	gct	act	ggc	tct	gtc	gcc	595	
Thr	Gly	Pro	Ser	Pro	Ser	Gly	Ile	Leu	Pro	Ala	Thr	Gly	Ser	Val	Ala		
		150			155					160					165		
gca	ctt	att	acc	gca	gct	act	ggc	gct	gag	cct	tat	tac	atc	ggc	aag	643	
Ala	Leu	Ile	Thr	Ala	Ala	Thr	Gly	Ala	Glu	Pro	Tyr	Tyr	Ile	Gly	Lys		
				170					175					180			
cca	aac	cct	gtg	atg	atg	cgc	agt	gcg	ctg	aac	acc	atc	ggg	gcg	cat	691	
Pro	Asn	Pro	Val	Met	Met	Arg	Ser	Ala	Leu	Asn	Thr	Ile	Gly	Ala	His		
			185					190					195				
tcc	gag	cac	act	gtc	atg	atc	ggc	gac	cgc	atg	gac	acc	gac	gtg	aaa	739	
Ser	Glu	His	Thr	Val	Met	Ile	Gly	Asp	Arg	Met	Asp	Thr	Asp	Val	Lys		
		200					205					210					
tct	ggg	ttg	gaa	gcc	ggc	ctg	agc	acc	gtg	ctg	gtt	cga	agc	gga	att	787	
Ser	Gly	Leu	Glu	Ala	Gly	Leu	Ser	Thr	Val	Leu	Val	Arg	Ser	Gly	Ile		
		215				220					225						
tcc	gac	gac	gcc	gag	atc	cgc	cgc	tac	ccc	ttc	cgc	cca	act	cac	gtg	835	
Ser	Asp	Asp	Ala	Glu	Ile	Arg	Arg	Tyr	Pro	Phe	Arg	Pro	Thr	His	Val		
					235				240						245		
atc	aat	tcc	atc	gcc	gat	ctt	gcc	gat	tgc	tgg	gac	gat	cct	ttc	ggg	883	
Ile	Asn	Ser	Ile	Ala	Asp	Leu	Ala	Asp	Cys	Trp	Asp	Asp	Pro	Phe	Gly		
				250					255					260			
gac	ggg	gca	ttt	cac	gta	cca	gat	gag	cag	cag	ttc	act	gac			925	
Asp	Gly	Ala	Phe	His	Val	Pro	Asp	Glu	Gln	Gln	Phe	Thr	Asp				

265

270

275

tagtattctg taggtcatgg cat

948

&lt;210&gt; 164

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 164

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile  
 1 5 10 15

Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu  
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe  
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile  
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu  
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly  
 85 90 95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn  
 100 105 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala  
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys  
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala  
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro  
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn  
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met  
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu  
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe  
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp  
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln  
 260 265 270

Phe Thr Asp  
275

<210> 165  
<211> 1128  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1105)  
<223> RXA00794

<400> 165  
gcgggttgat acagcccaag cgccgataca tttataatgc gcctagatac gtgcaaccca 60  
  
cgtaaccagg tcagatcaag tgccccagga ggcccttcag atg aac cta aag aac 115  
Met Asn Leu Lys Asn  
1 5  
  
ccc gaa acg cca gac cgt aac ctt gct atg gag ctg gtg cga gtt acg 163  
Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr  
10 15 20  
  
gaa gca gct gca ctg gct tct gga cgt tgg gtt gga cgt ggc atg aag 211  
Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys  
25 30 35  
  
aat gaa ggc gac ggt gcc gct gtt gac gcc atg cgc cag ctc atc aac 259  
Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn  
40 45 50  
  
tca gtg acc atg aag ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac 307  
Ser Val Thr Met Lys Gly Val Val Val Ile Gly Glu Gly Glu Lys Asp  
55 60 65  
  
gaa gct cca atg ctg tac aac ggc gaa gag gtc gga acc ggc ttt gga 355  
Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val Gly Thr Gly Phe Gly  
70 75 80 85  
  
cct gag gtt gat atc gca gtt gac cca gtt gac ggc acc acc ctg atg 403  
Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp Gly Thr Thr Leu Met  
90 95 100  
  
gct gag ggt cgc ccc aac gca att tcc att ctc gca gct gca gag cgt 451  
Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu Ala Ala Ala Glu Arg  
105 110 115  
  
ggc acc atg tac gat cca tcc tcc gtc ttc tac atg aag aag atc gcc 499  
Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr Met Lys Lys Ile Ala  
120 125 130  
  
gtg gga cct gag gcc gca ggc aag atc gac atc gaa gct cca gtt gcc 547  
Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile Glu Ala Pro Val Ala  
135 140 145  
  
cac aac atc aac gcg gtg gca aag tcc aag gga atc aac cct tcc gac 595  
His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly Ile Asn Pro Ser Asp  
150 155 160 165

gtc acc gtt gtc gtg ctt gac cgt cct cgc cac atc gaa ctg atc gca 643  
 Val Thr Val Val Val Leu Asp Arg Pro Arg His Ile Glu Leu Ile Ala  
 170 175 180

gac att cgt cgt gca ggc gca aag gtt cgt ctc atc tcc gac ggc gac 691  
 Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu Ile Ser Asp Gly Asp  
 185 190 195

gtt gca ggt gca gtt gca gca gct cag gat tcc aac tcc gtg gac atc 739  
 Val Ala Gly Ala Val Ala Ala Ala Gln Asp Ser Asn Ser Val Asp Ile  
 200 205 210

atg atg ggc acc ggc gga acc cca gaa ggc atc atc act gcg tgc gcc 787  
 Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile Ile Thr Ala Cys Ala  
 215 220 225

atg aag tgc atg ggt ggc gaa atc cag ggc atc ctg gcc cca atg aac 835  
 Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile Leu Ala Pro Met Asn  
 230 235 240 245

gat ttc gag cgc cag aag gca cac gac gct ggt ctg gtt ctt gat cag 883  
 Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly Leu Val Leu Asp Gln  
 250 255 260

gtt ctg cac acc aac gat ctg gtg agc tcc gac aac tgc tac ttc gtg 931  
 Val Leu His Thr Asn Asp Leu Val Ser Ser Asp Asn Cys Tyr Phe Val  
 265 270 275

gca acc ggt gtg acc aac ggt gac atg ctc cgt ggc gtt tcc tac cgc 979  
 Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg Gly Val Ser Tyr Arg  
 280 285 290

gca aac ggc gca acc acc cgt tcc ctg gtt atg cgc gca aag tca ggc 1027  
 Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met Arg Ala Lys Ser Gly  
 295 300 305

acc atc cgc cac atc gag tct gtc cac cag ctg tcc aag ctg cag gaa 1075  
 Thr Ile Arg His Ile Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu  
 310 315 320 325

tac tcc gtg gtt gac tac acc acc gcg acc taagagctct tagttcgaaa 1125  
 Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr  
 330 335

aac 1128

&lt;210&gt; 166

&lt;211&gt; 335

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 166

Met Asn Leu Lys Asn Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu  
 1 5 10 15

Leu Val Arg Val Thr Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val  
 20 25 30

Gly Arg Gly Met Lys Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met

35					40					45						
Arg	Gln	Leu	Ile	Asn	Ser	Val	Thr	Met	Lys	Gly	Val	Val	Val	Ile	Gly	
50					55					60						
Glu	Gly	Glu	Lys	Asp	Glu	Ala	Pro	Met	Leu	Tyr	Asn	Gly	Glu	Glu	Val	
65					70					75					80	
Gly	Thr	Gly	Phe	Gly	Pro	Glu	Val	Asp	Ile	Ala	Val	Asp	Pro	Val	Asp	
85					90					95						
Gly	Thr	Thr	Leu	Met	Ala	Glu	Gly	Arg	Pro	Asn	Ala	Ile	Ser	Ile	Leu	
100					105					110						
Ala	Ala	Ala	Glu	Arg	Gly	Thr	Met	Tyr	Asp	Pro	Ser	Ser	Val	Phe	Tyr	
115					120					125						
Met	Lys	Lys	Ile	Ala	Val	Gly	Pro	Glu	Ala	Ala	Gly	Lys	Ile	Asp	Ile	
130					135					140						
Glu	Ala	Pro	Val	Ala	His	Asn	Ile	Asn	Ala	Val	Ala	Lys	Ser	Lys	Gly	
145					150					155					160	
Ile	Asn	Pro	Ser	Asp	Val	Thr	Val	Val	Val	Leu	Asp	Arg	Pro	Arg	His	
165					170					175						
Ile	Glu	Leu	Ile	Ala	Asp	Ile	Arg	Arg	Ala	Gly	Ala	Lys	Val	Arg	Leu	
180					185					190						
Ile	Ser	Asp	Gly	Asp	Val	Ala	Gly	Ala	Val	Ala	Ala	Ala	Gln	Asp	Ser	
195					200					205						
Asn	Ser	Val	Asp	Ile	Met	Met	Gly	Thr	Gly	Gly	Thr	Pro	Glu	Gly	Ile	
210					215					220						
Ile	Thr	Ala	Cys	Ala	Met	Lys	Cys	Met	Gly	Gly	Glu	Ile	Gln	Gly	Ile	
225					230					235					240	
Leu	Ala	Pro	Met	Asn	Asp	Phe	Glu	Arg	Gln	Lys	Ala	His	Asp	Ala	Gly	
245					250					255						
Leu	Val	Leu	Asp	Gln	Val	Leu	His	Thr	Asn	Asp	Leu	Val	Ser	Ser	Asp	
260					265					270						
Asn	Cys	Tyr	Phe	Val	Ala	Thr	Gly	Val	Thr	Asn	Gly	Asp	Met	Leu	Arg	
275					280					285						
Gly	Val	Ser	Tyr	Arg	Ala	Asn	Gly	Ala	Thr	Thr	Arg	Ser	Leu	Val	Met	
290					295					300						
Arg	Ala	Lys	Ser	Gly	Thr	Ile	Arg	His	Ile	Glu	Ser	Val	His	Gln	Leu	
305					310					315					320	
Ser	Lys	Leu	Gln	Glu	Tyr	Ser	Val	Val	Asp	Tyr	Thr	Thr	Ala	Thr		
325					330					335						

&lt;210&gt; 167

&lt;211&gt; 1035

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

<223> RXN02920

tgcattgcaga ttattctgtcc aactacgccca gccgcgcgta aagcgcgggc ctgctggtgg 60

gat gtg ttt gtg ctc atc ctg ccg ctg act gat gcc act tat cag atc 691  
Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile  
185 190 195

gtc aat gca gaa act ttg ggc aag atg aag cct tct gcc gtg gtg gtc 739  
 Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val  
 200 205 210

aat gtg ggg cgt ggc ccg ctg atc aac acc gat gat ctg gtg gat gca 787  
 Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala  
 215 220 225

ttg aac aac ggc acc att gcg ggt gct gcg ctg gac gtt acc gat cct 835  
 Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro  
 230 235 240 245

gag cca ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt 883  
 Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val  
 250 255 260

atc act cct cat act gca aac acg aat gag agg att cgt gct ttg acc 931  
 Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr  
 265 270 275

ggc gaa ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag 979  
 Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln  
 280 285 290

atg gcc acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat 1032  
 Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr  
 295 300

ccg 1035

&lt;210&gt; 168

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 168

Met Lys Phe Val Met Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val  
 1 5 10 15

Ile Glu Gly Gly Gly His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp  
 20 25 30

Phe Ile Phe Phe Asn Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu  
 35 40 45

Asn Ile Lys Phe Val Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val  
 50 55 60

Lys Arg Gly Val Val Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly  
 65 70 75 80

Leu Tyr Ala Asp Thr Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala  
 85 90 95

Gln Met His Met His Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val  
 100 105 110

Arg Pro Glu Val Glu Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr  
 115 120 125

Val Ala Ile Leu Gly Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met  
 130 135 140  
 Leu Lys Pro Phe Asn Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg  
 145 150 155 160  
 Pro Val Glu Gly Ala Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His  
 165 170 175  
 Val Trp Ala Glu Ala Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp  
 180 185 190  
 Ala Thr Tyr Gln Ile Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro  
 195 200 205  
 Ser Ala Val Val Val Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp  
 210 215 220  
 Asp Leu Val Asp Ala Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu  
 225 230 235 240  
 Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu  
 245 250 255  
 Met Asp Asn Val Val Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg  
 260 265 270  
 Ile Arg Ala Leu Thr Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe  
 275 280 285  
 Glu Ala Gly Glu Gln Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr  
 290 295 300

&lt;210&gt; 169

&lt;211&gt; 779

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (52)..(756)

&lt;223&gt; FRXA02379

&lt;400&gt; 169

tgcaggcctc catggcgggt attgatgcgc tggtaagcg tgggtgctgc a atg aga 57  
 Met Arg  
 1  
 aag cac cgt tgg gca aac gcg gct ggc ctg tac gct gac acc gtt gct 105  
 Lys His Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr Val Ala  
 5 10 15  
 gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat gcg acg 153  
 Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His Ala Thr  
 20 25 30  
 act cgt ttg gct aag tcg tgg agc gtg cgg cct gag gtg gaa aac aac 201



Thr	Arg	Leu	Ala	Lys	Ser	Trp	Ser	Val	Arg	Pro	Glu	Val	Glu	Asn	Asn		
35					40					45					50		
aag	tca	tgg	ctg	cat	gac	aat	aaa	act	gtc	gct	att	ttg	ggc	gcc	ggt	249	
Lys	Ser	Trp	Leu	His	Asp	Asn	Lys	Thr	Val	Ala	Ile	Leu	Gly	Ala	Gly		
				55					60					65			
ggc	att	ggc	gtg	cgt	ctg	ctg	gaa	atg	ctc	aag	ccg	ttc	aac	gtg	aag	297	
Gly	Ile	Gly	Val	Arg	Leu	Leu	Glu	Met	Leu	Lys	Pro	Phe	Asn	Val	Lys		
			70					75					80				
acc	att	gcg	gtt	aat	aac	tct	ggt	cgt	ccg	gtg	gaa	ggt	gca	gat	gaa	345	
Thr	Ile	Ala	Val	Asn	Asn	Ser	Gly	Arg	Pro	Val	Glu	Gly	Ala	Asp	Glu		
		85					90					95					
acc	ttc	gcc	atg	gat	aag	gct	gag	cac	gtg	tgg	gct	gag	gct	gat	gtg	393	
Thr	Phe	Ala	Met	Asp	Lys	Ala	Glu	His	Val	Trp	Ala	Glu	Ala	Asp	Val		
	100					105					110						
ttt	gtg	ctc	atc	ctg	ccg	ctg	act	gat	gcc	act	tat	cag	atc	gtc	aat	441	
Phe	Val	Leu	Ile	Leu	Pro	Leu	Thr	Asp	Ala	Thr	Tyr	Gln	Ile	Val	Asn		
115					120				125						130		
gca	gaa	act	ttg	ggc	aag	atg	aag	cct	tct	gcc	gtg	gtg	gtc	aat	gtg	489	
Ala	Glu	Thr	Leu	Gly	Lys	Met	Lys	Pro	Ser	Ala	Val	Val	Val	Asn	Val		
				135				140						145			
ggg	cgt	ggc	ccg	ctg	atc	aac	acc	gat	gat	ctg	gtg	gat	gca	ttg	aac	537	
Gly	Arg	Gly	Pro	Leu	Ile	Asn	Thr	Asp	Asp	Leu	Val	Asp	Ala	Leu	Asn		
			150					155					160				
aac	ggc	acc	att	gcg	ggt	gct	gcg	ctg	gac	gtt	acc	gat	cct	gag	cca	585	
Asn	Gly	Thr	Ile	Ala	Gly	Ala	Ala	Leu	Asp	Val	Thr	Asp	Pro	Glu	Pro		
		165					170					175					
ctt	cct	gac	agc	cac	ccg	ctg	tgg	gag	atg	gac	aat	gtg	gtt	atc	act	633	
Leu	Pro	Asp	Ser	His	Pro	Leu	Trp	Glu	Met	Asp	Asn	Val	Val	Ile	Thr		
	180					185					190						
cct	cat	act	gca	aac	acg	aat	gag	agg	att	cgt	gct	ttg	acc	ggc	gaa	681	
Pro	His	Thr	Ala	Asn	Thr	Asn	Glu	Arg	Ile	Arg	Ala	Leu	Thr	Gly	Glu		
195					200					205					210		
ctc	acc	ttg	cgc	aac	att	gag	ttg	ttt	gag	gca	ggc	gag	cag	atg	gcc	729	
Leu	Thr	Leu	Arg	Asn	Ile	Glu	Leu	Phe	Glu	Ala	Gly	Glu	Gln	Met	Ala		
				215					220					225			
acc	gag	gtc	gat	gtg	gtg	gct	ggc	tac	taggcctttt	atggtgtgat	ccg					779	
Thr	Glu	Val	Asp	Val	Val	Ala	Gly	Tyr									
			230				235										

&lt;210&gt; 170

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 170

Met	Arg	Lys	His	Arg	Trp	Ala	Asn	Ala	Ala	Gly	Leu	Tyr	Ala	Asp	Thr
1				5					10					15	

Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His  
                   20                                  25                                  30  
 Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu  
                   35                                  40                                  45  
 Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly  
                   50                                  55                                  60  
 Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn  
                   65                                  70                                  75                                  80  
 Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala  
                                   85                                  90                                  95  
 Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala  
                   100                                  105                                  110  
 Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile  
                   115                                  120                                  125  
 Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val  
                   130                                  135                                  140  
 Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala  
                   145                                  150                                  155                                  160  
 Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro  
                                   165                                  170                                  175  
 Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val  
                   180                                  185                                  190  
 Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr  
                   195                                  200                                  205  
 Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln  
                   210                                  215                                  220  
 Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr  
                   225                                  230                                  235

&lt;210&gt; 171

&lt;211&gt; 792

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(769)

&lt;223&gt; RXN02688

&lt;400&gt; 171

gtgcggaaga cagcacgccc caaaccgacc aactagctaa gctacacaag gcggacgaat 60

gggttcgcg agcaagcgaa ggaaggaaac ttaactagcc atg gcc ggc cgg att 115

Met Ala Gly Arg Ile

1

5

att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg 163

Ile	Leu	Leu	Arg	His	Gly	Gln	Thr	His	Asn	Asn	Val	Lys	His	Leu	Leu		
				10					15					20			
gac	acc	cgc	cca	cca	gga	gct	gaa	ctc	acc	gac	ctg	ggc	cgt	aaa	caa	211	
Asp	Thr	Arg	Pro	Pro	Gly	Ala	Glu	Leu	Thr	Asp	Leu	Gly	Arg	Lys	Gln		
			25					30					35				
gcc	ctt	gaa	gtt	ggc	cac	gaa	cta	gcc	acc	tac	tcc	ggg	gag	cgc	ctc	259	
Ala	Leu	Glu	Val	Gly	His	Glu	Leu	Ala	Thr	Tyr	Ser	Gly	Glu	Arg	Leu		
		40					45					50					
gcc	cat	gtg	tac	agc	tcc	atc	gtg	ttg	cgc	gcc	caa	caa	acc	gcc	gtg	307	
Ala	His	Val	Tyr	Ser	Ser	Ile	Val	Leu	Arg	Ala	Gln	Gln	Thr	Ala	Val		
	55					60					65						
ctt	gcc	acc	tct	acc	ttt	gaa	aaa	gct	cgc	gac	atg	cag	tcc	ggg	gcg	355	
Leu	Ala	Thr	Ser	Thr	Phe	Glu	Lys	Ala	Arg	Asp	Met	Gln	Ser	Gly	Ala		
70					75					80					85		
att	cca	ctc	gac	gtt	gtg	gaa	ggc	att	cag	gaa	atc	aac	gtc	ggc	gac	403	
Ile	Pro	Leu	Asp	Val	Val	Glu	Gly	Ile	Gln	Glu	Ile	Asn	Val	Gly	Asp		
				90					95					100			
ttt	gaa	atg	cgc	ggc	gat	gaa	gaa	gcc	cac	atg	aat	tac	tcc	cgc	gca	451	
Phe	Glu	Met	Arg	Gly	Asp	Glu	Glu	Ala	His	Met	Asn	Tyr	Ser	Arg	Ala		
			105					110					115				
ctc	aac	ggc	tgg	ctt	cac	ggg	gat	cct	gcc	gct	ggg	ctt	ccc	ggc	ggg	499	
Leu	Asn	Gly	Trp	Leu	His	Gly	Asp	Pro	Ala	Ala	Gly	Leu	Pro	Gly	Gly		
		120					125					130					
gag	acc	tac	aaa	gac	gtg	ctg	aac	cgc	tac	cag	ccg	act	ctt	gat	cga	547	
Glu	Thr	Tyr	Lys	Asp	Val	Leu	Asn	Arg	Tyr	Gln	Pro	Thr	Leu	Asp	Arg		
	135					140					145						
atc	atg	gac	agc	cac	gac	ctt	gac	gac	gac	cgc	gac	gtt	gcc	gtt	gtc	595	
Ile	Met	Asp	Ser	His	Asp	Leu	Asp	Asp	Asp	Arg	Asp	Val	Ala	Val	Val		
150					155					160					165		
agc	cac	ggc	gcc	gtc	atc	cgc	atc	gtg	gca	aca	cac	gca	act	ggg	gtg	643	
Ser	His	Gly	Ala	Val	Ile	Arg	Ile	Val	Ala	Thr	His	Ala	Thr	Gly	Val		
				170					175					180			
gat	ccc	aac	ttt	gcg	ttc	aac	acc	tac	ctg	ggc	aac	tgc	cgc	ttc	gtg	691	
Asp	Pro	Asn	Phe	Ala	Phe	Asn	Thr	Tyr	Leu	Gly	Asn	Cys	Arg	Phe	Val		
			185					190					195				
gtg	ctg	gag	cca	aac	ggg	aag	aaa	ttc	agc	caa	tgg	gat	gtt	gtg	cgc	739	
Val	Leu	Glu	Pro	Asn	Gly	Lys	Lys	Phe	Ser	Gln	Trp	Asp	Val	Val	Arg		
		200					205					210					
tgg	act	gac	agc	cca	ctg	cca	tgg	cag	gag	taattgagac	caaaggctcg					789	
Trp	Thr	Asp	Ser	Pro	Leu	Pro	Trp	Gln	Glu								
	215					220											
gat																	792

&lt;210&gt; 172

&lt;211&gt; 223

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 172

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Met Ala Gly Arg Ile Ile Leu Leu Arg His Gly Gln Thr His Asn Asn
 1           5           10           15

Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp
          20           25           30

Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr
          35           40           45

Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala
          50           55           60

Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp
          65           70           75           80

Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu
          85           90           95

Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met
          100          105          110

Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala
          115          120          125

Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln
          130          135          140

Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg
          145          150          155          160

Asp Val Ala Val Val Ser His Gly Ala Val Ile Arg Ile Val Ala Thr
          165          170          175

His Ala Thr Gly Val Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly
          180          185          190

Asn Cys Arg Phe Val Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln
          195          200          205

Trp Asp Val Val Arg Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
          210          215          220

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<210> 173

<211> 336

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(313)

<223> RXN03087

<400> 173

gttgccgccca gccgttccag ggcgcttgag ctggtcagcg acatcgcaat gatcaaccag 60

gaatacctgg aaaagagctg atattgatag ggtttaagtc atg aag atc tac gca 115  
Met Lys Ile Tyr Ala

```

                                1           5
cct ttt gct gga atc gtc cac tat ttt gtc gat gaa ggc gat ccc gtg 163
Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp Glu Gly Asp Pro Val
      10           15           20

gaa acc ggc atg caa ctg gga acg gta gaa acc atc aaa ctc gag gca 211
Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr Ile Lys Leu Glu Ala
      25           30           35

cca atc atg gca ccg gga cct ggc atc gta gct aag gtt tct ttt gat 259
Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala Lys Val Ser Phe Asp
      40           45           50

gat ttc tcc gac gtc acc ggc ggc gat gaa ctc ctc gaa ttg gag gca 307
Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu Leu Glu Leu Glu Ala
      55           60           65

aag aac taatgggtca aaccgcacatc att 336
Lys Asn
      70

```

<210> 174  
 <211> 71  
 <212> PRT  
 <213> Corynebacterium glutamicum

```

<400> 174
Met Lys Ile Tyr Ala Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp
  1           5           10           15

Glu Gly Asp Pro Val Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr
      20           25           30

Ile Lys Leu Glu Ala Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala
      35           40           45

Lys Val Ser Phe Asp Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu
      50           55           60

Leu Glu Leu Glu Ala Lys Asn
      65           70

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<210> 175  
 <211> 310  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(310)  
 <223> RXN03186

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<400> 175
ttcgtgcact tcggcgtgtc acaattaggt acgaccaaga atgggaccgg gaaaccggga 60

cgtataaacg aaataaaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115
      Met Ala Asp Gln Ala
      1           5

```

aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163  
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg  
                   10                                  15                                  20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211  
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn  
                   25                                  30                                  35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259  
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu  
                   40                                  45                                  50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307  
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys  
                   55                                  60                                  65

cgc 310  
 Arg  
   70

<210> 176

<211> 70

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn  
   1                                  5                                  10                                  15

Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp  
                   20                                  25                                  30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln  
                   35                                  40                                  45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu  
                   50                                  55                                  60

Arg Ala Ser Ala Lys Arg  
   65                                  70

<210> 177

<211> 302

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(279)

<223> RXN03187

<400> 177

gtt gca gtg tct gac ttc tcc act gat ctg cca aac cag atc cgt gaa 48  
 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu  
   1                                  5                                  10                                  15

tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96  
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe

	20	25	30	
tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag				144
Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu				
	35	40	45	
tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc				192
Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile				
	50	55	60	
gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat				240
Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp				
	65	70	75	80
cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct				289
Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu				
	85	90		
caagggacag ata				302

<210> 178  
 <211> 93  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 178  
 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu  
 1 5 10 15  
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe  
 20 25 30  
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu  
 35 40 45  
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile  
 50 55 60  
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp  
 65 70 75 80  
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu  
 85 90

<210> 179  
 <211> 1953  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1930)  
 <223> RXN02591

<400> 179  
 atgtgtccgt tgtctcacct aaagtttttaa ctagttctgt atctgaaagc tacgctaggg 60  
 ggcgagaact ctgtcgaatg acacaaaatc tggagaagta atg act act gct gca 115  
 Met Thr Thr Ala Ala

															1						5	
atc	agg	ggc	ctt	cag	ggc	gag	gcg	ccg	acc	aag	aat	aag	gaa	ctg	ctg	163						
Ile	Arg	Gly	Leu	Gln	Gly	Glu	Ala	Pro	Thr	Lys	Asn	Lys	Glu	Leu	Leu							
				10					15					20								
aac	tgg	atc	gca	gac	gcc	gtc	gag	ctc	ttc	cag	cct	gag	gct	glt	gtg	211						
Asn	Trp	Ile	Ala	Asp	Ala	Val	Glu	Leu	Phe	Gln	Pro	Glu	Ala	Val	Val							
				25					30					35								
ttc	gtt	gat	gga	tcc	cag	gct	gag	tgg	gat	cgc	atg	gcg	gag	gat	ctt	259						
Phe	Val	Asp	Gly	Ser	Gln	Ala	Glu	Trp	Asp	Arg	Met	Ala	Glu	Asp	Leu							
				40					45					50								
gtt	gaa	gcc	ggt	acc	ctc	atc	aag	ctc	aac	gag	gaa	aag	cgt	ccg	aac	307						
Val	Glu	Ala	Gly	Thr	Leu	Ile	Lys	Leu	Asn	Glu	Glu	Lys	Arg	Pro	Asn							
				55					60					65								
agc	tac	cta	gct	cgt	tcc	aac	cca	tct	gac	gtt	gcg	cgc	gtt	gag	tcc	355						
Ser	Tyr	Leu	Ala	Arg	Ser	Asn	Pro	Ser	Asp	Val	Ala	Arg	Val	Glu	Ser							
				70					75					80	85							
cgc	acc	ttc	atc	tgc	tcc	gag	aag	gaa	gaa	gat	gct	ggc	cca	acc	aac	403						
Arg	Thr	Phe	Ile	Cys	Ser	Glu	Lys	Glu	Glu	Asp	Ala	Gly	Pro	Thr	Asn							
				90					95					100								
aac	tgg	gct	cca	cca	cag	gca	atg	aag	gac	gaa	atg	tcc	aag	cat	tac	451						
Asn	Trp	Ala	Pro	Pro	Gln	Ala	Met	Lys	Asp	Glu	Met	Ser	Lys	His	Tyr							
				105					110					115								
gct	ggt	tcc	atg	aag	ggg	cgc	acc	atg	tac	gtc	gtg	cct	ttc	tgc	atg	499						
Ala	Gly	Ser	Met	Lys	Gly	Arg	Thr	Met	Tyr	Val	Val	Pro	Phe	Cys	Met							
				120					125					130								
ggt	cca	atc	agc	gat	ccg	gac	cct	aag	ctt	ggt	gtg	cag	ctc	act	gac	547						
Gly	Pro	Ile	Ser	Asp	Pro	Asp	Pro	Lys	Leu	Gly	Val	Gln	Leu	Thr	Asp							
				135					140					145								
tcc	gag	tac	gtt	gtc	atg	tcc	atg	cgc	atc	atg	acc	cgc	atg	ggt	att	595						
Ser	Glu	Tyr	Val	Val	Met	Ser	Met	Arg	Ile	Met	Thr	Arg	Met	Gly	Ile							
				150					155					160	165							
gaa	gcg	ctg	gac	aag	atc	ggc	gcg	aac	ggc	agc	ttc	gtc	agg	tgc	ctc	643						
Glu	Ala	Leu	Asp	Lys	Ile	Gly	Ala	Asn	Gly	Ser	Phe	Val	Arg	Cys	Leu							
				170					175					180								
cac	tcc	gtt	ggt	gct	cct	ttg	gag	cca	ggc	cag	gaa	gac	gtt	gca	tgg	691						
His	Ser	Val	Gly	Ala	Pro	Leu	Glu	Pro	Gly	Gln	Glu	Asp	Val	Ala	Trp							
				185					190					195								
cct	tgc	aac	gac	acc	aag	tac	atc	acc	cag	ttc	cca	gag	acc	aag	gaa	739						
Pro	Cys	Asn	Asp	Thr	Lys	Tyr	Ile	Thr	Gln	Phe	Pro	Glu	Thr	Lys	Glu							
				200					205					210								
att	tgg	tcc	tac	ggt	tcc	ggc	tac	ggc	gga	aac	gca	atc	ctg	gca	aag	787						
Ile	Trp	Ser	Tyr	Gly	Ser	Gly	Tyr	Gly	Gly	Asn	Ala	Ile	Leu	Ala	Lys							
				215					220					225								
aag	tgc	tac	gca	ctg	cgt	atc	gca	tct	gtc	atg	gct	cgc	gaa	gaa	gga	835						
Lys	Cys	Tyr	Ala	Leu	Arg	Ile	Ala	Ser	Val	Met	Ala	Arg	Glu	Glu	Gly							
				230					235					240	245							



tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc	883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly	
250 255 260	
aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc	931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr	
265 270 275	
aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt	979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val	
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gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac	1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr	
295 300 305	
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Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn	
310 315 320 325	
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Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr	
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Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu	
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ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac	1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn	
360 365 370	
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Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg	
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Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn	
390 395 400 405	
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Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg	
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Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly	
425 430 435	
acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca	1459
Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala	
440 445 450	
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Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro	
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Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met	
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 Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp  
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aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt 1699  
 Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val  
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ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc 1747  
 Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu  
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gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg 1795  
 Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu  
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acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag 1843  
 Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu  
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 Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln  
                   585                  590                  595

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<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

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                   20                  25                  30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg  
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Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu  
                   50                  55                  60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val  
                   65                  70                  75                  80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp  
                   85                  90                  95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu  
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Met	Ser	Lys	His	Tyr	Ala	Gly	Ser	Met	Lys	Gly	Arg	Thr	Met	Tyr	Val		
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Val	Pro	Phe	Cys	Met	Gly	Pro	Ile	Ser	Asp	Pro	Asp	Pro	Lys	Leu	Gly		
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Val	Gln	Leu	Thr	Asp	Ser	Glu	Tyr	Val	Val	Met	Ser	Met	Arg	Ile	Met		
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Thr	Arg	Met	Gly	Ile	Glu	Ala	Leu	Asp	Lys	Ile	Gly	Ala	Asn	Gly	Ser		
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Phe	Val	Arg	Cys	Leu	His	Ser	Val	Gly	Ala	Pro	Leu	Glu	Pro	Gly	Gln		
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Glu	Asp	Val	Ala	Trp	Pro	Cys	Asn	Asp	Thr	Lys	Tyr	Ile	Thr	Gln	Phe		
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Pro	Glu	Thr	Lys	Glu	Ile	Trp	Ser	Tyr	Gly	Ser	Gly	Tyr	Gly	Gly	Asn		
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Ala	Arg	Glu	Glu	Gly	Trp	Met	Ala	Glu	His	Met	Leu	Ile	Leu	Lys	Leu		
				245					250					255			
Ile	Asn	Pro	Glu	Gly	Lys	Ala	Tyr	His	Ile	Ala	Ala	Ala	Phe	Pro	Ser		
			260					265					270				
Ala	Cys	Gly	Lys	Thr	Asn	Leu	Ala	Met	Ile	Thr	Pro	Thr	Ile	Pro	Gly		
		275					280					285					
Trp	Thr	Ala	Gln	Val	Val	Gly	Asp	Asp	Ile	Ala	Trp	Leu	Lys	Leu	Arg		
	290					295					300						
Glu	Asp	Gly	Leu	Tyr	Ala	Val	Asn	Pro	Glu	Asn	Gly	Phe	Phe	Gly	Val		
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Ala	Pro	Gly	Thr	Asn	Tyr	Ala	Ser	Asn	Pro	Ile	Ala	Met	Lys	Thr	Met		
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Glu	Pro	Gly	Asn	Thr	Leu	Phe	Thr	Asn	Val	Ala	Leu	Thr	Asp	Asp	Gly		
			340					345					350				
Asp	Ile	Trp	Trp	Glu	Gly	Met	Asp	Gly	Asp	Ala	Pro	Ala	His	Leu	Ile		
		355					360					365					
Asp	Trp	Met	Gly	Asn	Asp	Trp	Thr	Pro	Glu	Ser	Asp	Glu	Asn	Ala	Ala		
	370					375					380						
His	Pro	Asn	Ser	Arg	Tyr	Cys	Val	Ala	Ile	Asp	Gln	Ser	Pro	Ala	Ala		
385					390					395					400		
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Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly	
55 60 65	
tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg	355
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val	
70 75 80 85	
tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc	403
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val	
90 95 100	
att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt	451
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly	
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Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu	
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Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys	
135 140 145	
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Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg	
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Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp	
170 175 180	
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe	
185 190 195	
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Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu	
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Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val	
215 220 225	
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Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala	
230 235 240 245	
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly	
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Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr	
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 280 285 290

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 Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe  
 295 300 305

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 Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala  
 310 315 320 325

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 Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu  
 330 335 340

gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag 1171  
 Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln  
 345 350 355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac 1219  
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cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga 1267  
 Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly  
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cac atg atc aac ttc tagaatccac ctcgttggcc ctg 1305  
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&lt;210&gt; 182

&lt;211&gt; 394

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 182

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Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys  
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Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe  
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Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala  
 85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe  
 100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe

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Ala	Lys	Ala	Tyr	Lys	Lys	Met	Gly	Val	Lys	Leu	Leu	Pro	Gly	His	Ala	
145					150					155					160	
Thr	Thr	Ala	Val	Arg	Asp	Asn	Gly	Asp	Phe	Val	Glu	Val	Asp	Tyr	Gln	
165					170					175						
Lys	Lys	Gly	Ser	Asp	Lys	Thr	Glu	Thr	Leu	Thr	Val	Asp	Arg	Val	Met	
180					185					190						
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn	
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Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr	
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Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala	
225					230					235					240	
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala	
245					250					255						
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met	
260					265					270						
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr	
275					280					285						
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val	
290					295					300						
Ala	Ser	Phe	Pro	Phe	Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu	
305					310					315					320	
Thr	Asp	Gly	Phe	Ala	Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu	
325					330					335						
Leu	Gly	Ala	His	Leu	Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Ile	Asn	Glu	
340					345					350						
Leu	Val	Leu	Ala	Gln	Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg	
355					360					365						
Ser	Val	His	Ile	His	Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala	
370					375					380						
His	Gly	Ile	Ser	Gly	His	Met	Ile	Asn	Phe							
385					390											

&lt;210&gt; 183

&lt;211&gt; 294

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

<223> RXS01261

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gat caa aaa cgc tgaagttgcc cataccttta ccc 294  
Asp Gln Lys Arg  
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<213> Corynebacterium glutamicum

Pro Ser Lys Val Ser Asp Gln Lys Arg  
50 55

<213> Corynebacterium glutamicum

<223> RXA02640

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Met Arg Ile Ser Lys



1												5				
gcc	aat	gcg	tat	gtt	gca	gcg	att	gac	caa	ggc	acc	act	tcc	act	cgg	163
Ala	Asn	Ala	Tyr	Val	Ala	Ala	Ile	Asp	Gln	Gly	Thr	Thr	Ser	Thr	Arg	
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Cys	Ile	Phe	Ile	Asp	Ala	Gln	Gly	Lys	Val	Val	Ser	Ser	Ala	Ser	Lys	
				25					30					35		
gag	cac	cgc	caa	atc	ttc	cca	caa	cag	ggc	tgg	gta	gag	cac	gat	cct	259
Glu	His	Arg	Gln	Ile	Phe	Pro	Gln	Gln	Gly	Trp	Val	Glu	His	Asp	Pro	
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gaa	gaa	att	tgg	gac	aac	att	cga	tct	gtc	gtc	agc	cag	gcg	atg	gtc	307
Glu	Glu	Ile	Trp	Asp	Asn	Ile	Arg	Ser	Val	Val	Ser	Gln	Ala	Met	Val	
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tcc	att	gac	atc	acc	cca	cac	gag	gtt	gca	tcg	ctg	gga	gtc	acc	aac	355
Ser	Ile	Asp	Ile	Thr	Pro	His	Glu	Val	Ala	Ser	Leu	Gly	Val	Thr	Asn	
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cag	cgc	gaa	acc	acc	gtg	gtg	tgg	gac	aag	cac	acc	ggc	gaa	cct	gtc	403
Gln	Arg	Glu	Thr	Thr	Val	Val	Trp	Asp	Lys	His	Thr	Gly	Glu	Pro	Val	
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tac	aac	gca	atc	gtg	tgg	caa	gac	acc	cgc	acc	tct	gac	att	tgc	cta	451
Tyr	Asn	Ala	Ile	Val	Trp	Gln	Asp	Thr	Arg	Thr	Ser	Asp	Ile	Cys	Leu	
				105					110					115		
gag	atc	gcg	ggc	gaa	gaa	ggc	cag	gaa	aag	tgg	ctt	gac	cgc	acc	ggc	499
Glu	Ile	Ala	Gly	Glu	Glu	Gly	Gln	Glu	Lys	Trp	Leu	Asp	Arg	Thr	Gly	
				120					125					130		
ctg	ctg	atc	aac	tcc	tac	cca	tcg	ggg	ccc	aaa	atc	aag	tgg	att	ctc	547
Leu	Leu	Ile	Asn	Ser	Tyr	Pro	Ser	Gly	Pro	Lys	Ile	Lys	Trp	Ile	Leu	
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gac	aac	gtt	gag	gga	gct	cgc	gaa	cgc	gcc	gaa	aag	ggc	gac	ctt	ttg	595
Asp	Asn	Val	Glu	Gly	Ala	Arg	Glu	Arg	Ala	Glu	Lys	Gly	Asp	Leu	Leu	
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ttt	ggc	acc	atg	gat	acc	tgg	gtg	ctg	tgg	aac	ctg	acc	ggc	ggt	gtc	643
Phe	Gly	Thr	Met	Asp	Thr	Trp	Val	Leu	Trp	Asn	Leu	Thr	Gly	Gly	Val	
				170					175					180		
cgc	ggc	gac	gac	ggt	gat	gat	gcc	atc	cac	gtc	acc	gat	gtc	acc	aac	691
Arg	Gly	Asp	Asp	Gly	Asp	Asp	Ala	Ile	His	Val	Thr	Asp	Val	Thr	Asn	
				185					190					195		
gca	tcc	cgc	aca	cta	ttg	atg	gat	ctc	cgc	acg	caa	cag	tgg	gat	cca	739
Ala	Ser	Arg	Thr	Leu	Leu	Met	Asp	Leu	Arg	Thr	Gln	Gln	Trp	Asp	Pro	
				200					205					210		
gaa	cta	tgc	gaa	gcc	cta	gac	att	ccg	atg	tcc	atg	ctc	cct	gag	att	787
Glu	Leu	Cys	Glu	Ala	Leu	Asp	Ile	Pro	Met	Ser	Met	Leu	Pro	Glu	Ile	
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cgt	ccc	tcc	gtc	gga	gaa	ttc	cgc	tcc	gtg	cgc	cac	cgc	gga	acc	cta	835
Arg	Pro	Ser	Val	Gly	Glu	Phe	Arg	Ser	Val	Arg	His	Arg	Gly	Thr	Leu	
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Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly	
265 270 275	
acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc	979
Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser	
280 285 290	
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Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala	
295 300 305	
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Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val	
310 315 320 325	
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Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile	
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Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg	
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375 380 385	
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Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp	
390 395 400 405	
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Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu Ser Leu Arg Val Asp	
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Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe	
425 430 435	
ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc	1459
Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val	
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Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr	
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gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac	1555
Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp	
470 475 480 485	

atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca 1603  
 Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala  
                     490                    495                    500

gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta 1650  
 Val Glu His Ser Tyr Asp Gln Ala  
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<210> 186

<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

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Thr Thr Ser Thr Arg Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val  
                     20                    25                    30

Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp  
                     35                    40                    45

Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val  
                     50                    55                    60

Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser  
   65                    70                    75                    80

Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His  
                     85                    90                    95

Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr  
                     100                    105                    110

Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp  
                     115                    120                    125

Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys  
   130                    135                    140

Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu  
  145                    150                    155                    160

Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn  
                     165                    170                    175

Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val  
                     180                    185                    190

Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr  
  195                    200                    205

Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser  
  210                    215                    220

Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg  
  225                    230                    235                    240

His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp

245										250					255				
Gln	Gln	Ala	Ala	Leu	Phe	Gly	Gln	Gly	Gly	Phe	His	Glu	Gly	Ala	Ala				
			260					265					270						
Lys	Asn	Thr	Tyr	Gly	Thr	Gly	Leu	Phe	Leu	Leu	Met	Asn	Thr	Gly	Thr				
		275					280					285							
Ser	Leu	Lys	Ile	Ser	Glu	His	Gly	Leu	Leu	Ser	Thr	Ile	Ala	Tyr	Gln				
	290					295					300								
Arg	Glu	Gly	Ser	Ala	Pro	Val	Tyr	Ala	Leu	Glu	Gly	Ser	Val	Ser	Met				
305					310					315					320				
Gly	Gly	Ser	Leu	Val	Gln	Trp	Leu	Arg	Asp	Asn	Leu	Gln	Leu	Ile	Pro				
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Asn	Ala	Pro	Ala	Ile	Glu	Asn	Leu	Ala	Arg	Glu	Val	Glu	Asp	Asn	Gly				
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Gly	Val	His	Val	Val	Pro	Ala	Phe	Thr	Gly	Leu	Phe	Ala	Pro	Arg	Trp				
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Arg	Pro	Asp	Ala	Arg	Gly	Val	Ile	Thr	Gly	Leu	Thr	Arg	Phe	Ala	Asn				
	370					375					380								
Arg	Lys	His	Ile	Ala	Arg	Ala	Val	Leu	Glu	Ala	Asn	Ala	Phe	Gln	Thr				
385					390					395					400				
Arg	Glu	Val	Val	Asp	Ala	Met	Ala	Lys	Asp	Ala	Gly	Lys	Ala	Leu	Glu				
				405					410					415					
Ser	Leu	Arg	Val	Asp	Gly	Ala	Met	Val	Glu	Asn	Asp	Leu	Leu	Met	Gln				
			420					425					430						
Met	Gln	Ala	Asp	Phe	Leu	Gly	Ile	Asp	Val	Gln	Arg	Leu	Glu	Asp	Val				
		435					440					445							
Glu	Thr	Thr	Ala	Val	Gly	Val	Ala	Phe	Ala	Ala	Gly	Leu	Gly	Ser	Gly				
	450					455					460								
Phe	Phe	Lys	Thr	Thr	Asp	Glu	Ile	Glu	Lys	Leu	Ile	Ala	Val	Lys	Lys				
465					470					475					480				
Val	Trp	Asn	Pro	Asp	Met	Ser	Glu	Glu	Glu	Arg	Glu	Arg	Arg	Tyr	Ala				
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Glu	Trp	Asn	Arg	Ala	Val	Glu	His	Ser	Tyr	Asp	Gln	Ala							
				500				505											

&lt;210&gt; 187

&lt;211&gt; 1119

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1096)

&lt;223&gt; RXN01025

&lt;400&gt; 187

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ctgagacggt taaatatcgt ttctgaaagg tgggtttcgc gtg gtt tct gta agc 115
Val Val Ser Val Ser
1 5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
10 15 20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
25 30 35

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
40 45 50

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
55 60 65

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
70 75 80 85

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
90 95 100

gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt 451
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser
105 110 115

gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg 499
Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val
120 125 130

ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca 547
Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala
135 140 145

gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag 595
Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln
150 155 160 165

gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg 643
Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val
170 175 180

gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc 691
Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala
185 190 195

tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg 739
Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser
200 205 210

ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg 787
Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu

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Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu			
230	235	240	245
gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag			883
Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu			
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cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat			931
Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn			
	265	270	275
ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt			979
Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu			
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gcc acc aag ctt ggt gtg gag atg ccg atc acc cag gct gtc tac ggt			1027
Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln Ala Val Tyr Gly			
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gtg tgc cac cga gat atg aaa gta act gac atg att gtg gct ctc atg			1075
Val Cys His Arg Asp Met Lys Val Thr Asp Met Ile Val Ala Leu Met			
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ggc agg tct aag aag gct gag tagtccttagg ttgtaagctt caa			1119
Gly Arg Ser Lys Lys Ala Glu			
	330		

&lt;210&gt; 188

&lt;211&gt; 332

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 188

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Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp	
35 40 45	
Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser	
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Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro	
65 70 75 80	
Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro	
85 90 95	
Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr	
100 105 110	
His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro	
115 120 125	

Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala  
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 Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg  
 145 150 155 160  
 Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr  
 165 170 175  
 Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn  
 180 185 190  
 Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu  
 195 200 205  
 Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg  
 210 215 220  
 Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala  
 225 230 235 240  
 Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn  
 245 250 255  
 Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala  
 260 265 270  
 Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln  
 275 280 285  
 Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr  
 290 295 300  
 Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met  
 305 310 315 320  
 Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu  
 325 330

&lt;210&gt; 189

&lt;211&gt; 1015

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1015)

&lt;223&gt; FRXA01025

&lt;400&gt; 189

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ctgaracggt taaatatcgt tttcgaaagg tgggtttcgc gtg gtt tct gta agc 115  
 Val Val Ser Val Ser  
 1 5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163  
 Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser  
 10 15 20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca	211
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala	
25 30 35	
agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att	259
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile	
40 45 50	
acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta	307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu	
55 60 65	
gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt	355
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg	
70 75 80 85	
ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg	403
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu	
90 95 100	
gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg ccg atg agt	451
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser	
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gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg	499
Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val	
120 125 130	
ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca	547
Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala	
135 140 145	
gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag	595
Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln	
150 155 160 165	
gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg	643
Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val	
170 175 180	
gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc	691
Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala	
185 190 195	
tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg	739
Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser	
200 205 210	
ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg	787
Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu	
215 220 225	
ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg	835
Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu	
230 235 240 245	
gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag	883
Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu	
250 255 260	
cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat	931



Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn  
 265 270 275

ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt 979  
 Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu  
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 Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln  
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<210> 190

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

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 20 25 30

Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp  
 35 40 45

Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser  
 50 55 60

Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro  
 65 70 75 80

Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro  
 85 90 95

Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr  
 100 105 110

His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro  
 115 120 125

Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala  
 130 135 140

Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg  
 145 150 155 160

Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr  
 165 170 175

Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn  
 180 185 190

Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu  
 195 200 205

Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg  
 210 215 220

Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala

Gln  
305

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<221> CDS
<222> (101)..(1786)
<223> RXA01851
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Met Thr Ser Ala His 1 5																
ttt gaa tcc cgc cgg att ggc cct ccg ctt cgc gat aat tat gac gtc																163
Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg Asp Asn Tyr Asp Val 10 15 20																
att gtg att ggc ggt ggt atc tca ggt gta cag att gcg cga cat gct																211
Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln Ile Ala Arg His Ala 25 30 35																
caa ggc cgc ggt tta cgc act gtg atg ttt gag gcc aga gat tat tct																259
Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu Ala Arg Asp Tyr Ser 40 45 50																
tct gga aca tca tcc aca acc tcc aag atg att cat ggt ggt ttg cgc																307
Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile His Gly Gly Leu Arg 55 60 65																
tat ttg gag cag tac gat ttc ggc gtg gtc cag gaa gcc gtg aag gaa																355
Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln Glu Ala Val Lys Glu 70 75 80 85																
cgc cgg tac cta ggt atc gcc gct ccg cat ttg gtg gct cca cgc agt																403
Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu Val Ala Pro Arg Ser 90 95 100																
ttc atg ctc acg gcg ttt gat tgg tca gag ccg aaa gcc cct atg ttg																451
Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro Lys Ala Pro Met Leu																

105							110							115							
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Gly	Ala	Gly	Val	Ala	Leu	Tyr	Glu	Thr	Met	Ala	Trp	Gln	Arg	Asn	Gln						
		120					125					130									
ggg	caa	tcg	aag	gaa	aac	cac	tcg	ccg	cgt	ttc	cgg	tgg	att	cct	aaa						547
Gly	Gln	Ser	Lys	Glu	Asn	His	Ser	Pro	Arg	Phe	Arg	Trp	Ile	Pro	Lys						
	135					140					145										
aat	gca	ctg	ctc	aag	gaa	gtc	ccg	tgg	ctt	gac	ccg	gag	ggc	ttg	aag						595
Asn	Ala	Leu	Leu	Lys	Glu	Val	Pro	Trp	Leu	Asp	Pro	Glu	Gly	Leu	Lys						
150					155					160					165						
gga	gcg	tgg	cgc	cac	gat	gat	acg	ttg	aat	ctc	cat	gca	gaa	cga	ctc						643
Gly	Ala	Trp	Arg	His	Asp	Asp	Thr	Leu	Asn	Leu	His	Ala	Glu	Arg	Leu						
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ctc	ctc	gcg	gtg	att	aaa	gct	ttt	gcg	gca	gat	ggc	gga	acg	gcg	atc						691
Leu	Leu	Ala	Val	Ile	Lys	Ala	Phe	Ala	Ala	Asp	Gly	Gly	Thr	Ala	Ile						
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aac	cac	gcc	aaa	gtc	act	cgc	att	ctc	cgg	aac	gtg	gaa	gaa	ggc	cgc						739
Asn	His	Ala	Lys	Val	Thr	Arg	Ile	Leu	Arg	Asn	Val	Glu	Glu	Gly	Arg						
		200					205				210										
gtc	aag	ggt	gta	gaa	gtg	act	gat	cag	gtc	acc	aac	acc	acg	cat	gag						787
Val	Lys	Gly	Val	Glu	Val	Thr	Asp	Gln	Val	Thr	Asn	Thr	Thr	His	Glu						
	215					220					225										
gtg	aat	gcc	cct	gtg	gtg	atc	aac	gct	gcg	ggt	ccg	tgg	gtt	gcg	cag						835
Val	Asn	Ala	Pro	Val	Val	Ile	Asn	Ala	Ala	Gly	Pro	Trp	Val	Ala	Gln						
230					235					240					245						
gcg	ttg	ggt	gat	ttg	gcg	gag	gta	acc	aag	ttg	aag	gtg	cgc	caa	tcc						883
Ala	Leu	Gly	Asp	Leu	Ala	Glu	Val	Thr	Lys	Leu	Lys	Val	Arg	Gln	Ser						
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aag	gga	gtg	cat	ttg	ctc	act	ggt	gat	ttg	ggc	agc	cag	agt	ggc	gtg						931
Lys	Gly	Val	His	Leu	Leu	Thr	Gly	Asp	Leu	Gly	Ser	Gln	Ser	Gly	Val						
			265					270				275									
ttt	gtg	cgt	ggc	aaa	aac	ggc	aag	cat	gtg	atc	gtg	aat	ccg	tgg	atg						979
Phe	Val	Arg	Gly	Lys	Asn	Gly	Lys	His	Val	Ile	Val	Asn	Pro	Trp	Met						
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ggg	cgc	acc	ctt	att	ggt	cca	acc	gac	acc	atg	att	gac	ggt	gac	gct						1027
Gly	Arg	Thr	Leu	Ile	Gly	Pro	Thr	Asp	Thr	Met	Ile	Asp	Gly	Asp	Ala						
		295				300					305										
gat	gat	gcg	gct	gca	gat	gaa	agc	gat	atc	gat	ttg	ctg	ctt	gag	acc						1075
Asp	Asp	Ala	Ala	Ala	Asp	Glu	Ser	Asp	Ile	Asp	Leu	Leu	Leu	Glu	Thr						
310					315					320					325						
atc	gat	tcg	gta	cgc	gct	aca	ccg	ctt	gat	cgc	aaa	gag	atc	atc	tcc						1123
Ile	Asp	Ser	Val	Arg	Ala	Thr	Pro	Leu	Asp	Arg	Lys	Glu	Ile	Ile	Ser						
				330					335					340							
acg	ctg	gtg	ggt	gtg	cgc	ccg	ctt	gtt	gat	gac	ggc	acc	gac	acc	tac						1171
Thr	Leu	Val	Gly	Val	Arg	Pro	Leu	Val	Asp	Asp	Gly	Thr	Asp	Thr	Tyr						
			345					350					355								

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 Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His Ala Asn Val Gly Ile  
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gat ggt ttg gtg tct gtc tct ggc ggc aag tgg acc act tcc cgc gtg 1267  
 Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp Thr Thr Ser Arg Val  
 375 380 385

atg ggg tac aag gtg att gag cat gtg gtg gag cac caa gct gcg gtg 1315  
 Met Gly Tyr Lys Val Ile Glu His Val Val Glu His Gln Ala Ala Val  
 390 395 400 405

tta cct ccg ctg cgc cac ttt gac tcc agg cag atg ccg ttg agt act 1363  
 Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln Met Pro Leu Ser Thr  
 410 415 420

tct ttt ggc gcg tat gag tcc gtg gct gat tcc ttt gag tca gcg ctt 1411  
 Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser Phe Glu Ser Ala Leu  
 425 430 435

cgc agc cac ccc gag ctg gat gtg gat gat gaa atc cgc gtg cat ctg 1459  
 Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu Ile Arg Val His Leu  
 440 445 450

gcc aga ctg tat gga act gag cat gaa aaa gtg ctg gat ctc gtc gca 1507  
 Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val Leu Asp Leu Val Ala  
 455 460 465

aag caa ccc gac ctg ggg cgc cga ctt gac cca gac aac ctt gat atc 1555  
 Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro Asp Asn Leu Asp Ile  
 470 475 480 485

gcg gcg cag gcc gtt ttt gct gtc gcc gag gag gcg gcc gtc gac ctg 1603  
 Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu Ala Ala Val Asp Leu  
 490 495 500

gcg gac gtg ctg gat cgt cgc atc gtg ctc ggc acg ctg ggt tat gtg 1651  
 Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val  
 505 510 515

caa ccg gct gcc gtg cgt gcg acg gcc gaa gca atg gcg cag gtc acc 1699  
 Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr  
 520 525 530

ggg tgg tca gct gag ctt atc gac gcc cag tgc cag tcc tac ctc gcc 1747  
 Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys Gln Ser Tyr Leu Ala  
 535 540 545

aag caa gac aaa atc caa gcc gtg tta aag ccg tac cgc taacactccg 1796  
 Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro Tyr Arg  
 550 555 560

tcatcgacac cgg 1809

&lt;210&gt; 192

&lt;211&gt; 562

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 192

Met	Thr	Ser	Ala	His	Phe	Glu	Ser	Arg	Arg	Ile	Gly	Pro	Pro	Leu	Arg	1	5	10	15
Asp	Asn	Tyr	Asp	Val	Ile	Val	Ile	Gly	Gly	Gly	Ile	Ser	Gly	Val	Gln	20	25	30	
Ile	Ala	Arg	His	Ala	Gln	Gly	Arg	Gly	Leu	Arg	Thr	Val	Met	Phe	Glu	35	40	45	
Ala	Arg	Asp	Tyr	Ser	Ser	Gly	Thr	Ser	Ser	Thr	Thr	Ser	Lys	Met	Ile	50	55	60	
His	Gly	Gly	Leu	Arg	Tyr	Leu	Glu	Gln	Tyr	Asp	Phe	Gly	Val	Val	Gln	65	70	75	80
Glu	Ala	Val	Lys	Glu	Arg	Arg	Tyr	Leu	Gly	Ile	Ala	Ala	Pro	His	Leu	85	90	95	
Val	Ala	Pro	Arg	Ser	Phe	Met	Leu	Thr	Ala	Phe	Asp	Trp	Ser	Glu	Pro	100	105	110	
Lys	Ala	Pro	Met	Leu	Gly	Ala	Gly	Val	Ala	Leu	Tyr	Glu	Thr	Met	Ala	115	120	125	
Trp	Gln	Arg	Asn	Gln	Gly	Gln	Ser	Lys	Glu	Asn	His	Ser	Pro	Arg	Phe	130	135	140	
Arg	Trp	Ile	Pro	Lys	Asn	Ala	Leu	Leu	Lys	Glu	Val	Pro	Trp	Leu	Asp	145	150	155	160
Pro	Glu	Gly	Leu	Lys	Gly	Ala	Trp	Arg	His	Asp	Asp	Thr	Leu	Asn	Leu	165	170	175	
His	Ala	Glu	Arg	Leu	Leu	Leu	Ala	Val	Ile	Lys	Ala	Phe	Ala	Ala	Asp	180	185	190	
Gly	Gly	Thr	Ala	Ile	Asn	His	Ala	Lys	Val	Thr	Arg	Ile	Leu	Arg	Asn	195	200	205	
Val	Glu	Glu	Gly	Arg	Val	Lys	Gly	Val	Glu	Val	Thr	Asp	Gln	Val	Thr	210	215	220	
Asn	Thr	Thr	His	Glu	Val	Asn	Ala	Pro	Val	Val	Ile	Asn	Ala	Ala	Gly	225	230	235	240
Pro	Trp	Val	Ala	Gln	Ala	Leu	Gly	Asp	Leu	Ala	Glu	Val	Thr	Lys	Leu	245	250	255	
Lys	Val	Arg	Gln	Ser	Lys	Gly	Val	His	Leu	Leu	Thr	Gly	Asp	Leu	Gly	260	265	270	
Ser	Gln	Ser	Gly	Val	Phe	Val	Arg	Gly	Lys	Asn	Gly	Lys	His	Val	Ile	275	280	285	
Val	Asn	Pro	Trp	Met	Gly	Arg	Thr	Leu	Ile	Gly	Pro	Thr	Asp	Thr	Met	290	295	300	
Ile	Asp	Gly	Asp	Ala	Asp	Asp	Ala	Ala	Ala	Asp	Glu	Ser	Asp	Ile	Asp	305	310	315	320

Leu Leu Leu Glu Thr Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg  
 325 330 335  
 Lys Glu Ile Ile Ser Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp  
 340 345 350  
 Gly Thr Asp Thr Tyr Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His  
 355 360 365  
 Ala Asn Val Gly Ile Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp  
 370 375 380  
 Thr Thr Ser Arg Val Met Gly Tyr Lys Val Ile Glu His Val Val Glu  
 385 390 395 400  
 His Gln Ala Ala Val Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln  
 405 410 415  
 Met Pro Leu Ser Thr Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser  
 420 425 430  
 Phe Glu Ser Ala Leu Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu  
 435 440 445  
 Ile Arg Val His Leu Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val  
 450 455 460  
 Leu Asp Leu Val Ala Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro  
 465 470 475 480  
 Asp Asn Leu Asp Ile Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu  
 485 490 495  
 Ala Ala Val Asp Leu Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly  
 500 505 510  
 Thr Leu Gly Tyr Val Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala  
 515 520 525  
 Met Ala Gln Val Thr Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys  
 530 535 540  
 Gln Ser Tyr Leu Ala Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro  
 545 550 555 560  
 Tyr Arg

&lt;210&gt; 193

&lt;211&gt; 900

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(877)

&lt;223&gt; RXA01242

&lt;400&gt; 193

cgccggcaac caaatgaggc ttttgggcgt tggacagtga gacaatgggt aagaaattcg 60

gacatatttta gtaaattggc tttttgcttt aaggagtgc	atg tac gca gag gag	115
	Met Tyr Ala Glu Glu	
	1 5	
cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat	163	
Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn		
	10 15 20	
gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga	211	
Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg		
	25 30 35	
cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac	259	
Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His		
	40 45 50	
ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg	307	
Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu		
	55 60 65	
gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag	355	
Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys		
	70 75 80 85	
gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat	403	
Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp		
	90 95 100	
gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct	451	
Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro		
	105 110 115	
agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt	499	
Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu		
	120 125 130	
aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc	547	
Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser		
	135 140 145	
gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act	595	
Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr		
	150 155 160 165	
ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg	643	
Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu		
	170 175 180	
acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg	691	
Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met		
	185 190 195	
aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac	739	
Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp		
	200 205 210	
tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc	787	
Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser		
	215 220 225	

gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835  
 Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val  
 230 235 240 245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877  
 Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu  
 250 255

tgattcttac agtcactgca agt 900

<210> 194

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

Met Tyr Ala Glu Glu Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val  
 1 5 10 15

Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr  
 20 25 30

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile  
 35 40 45

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr  
 50 55 60

Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys  
 65 70 75 80

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly  
 85 90 95

Gly Leu Phe Leu Asp Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu  
 100 105 110

Ile Ser Glu His Pro Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys  
 115 120 125

Leu Pro Ile Ala Leu Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln  
 130 135 140

Leu Leu Gly Gly Ser Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp  
 145 150 155 160

Thr Ala Leu Arg Thr Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile  
 165 170 175

Gly Thr Asn Ala Leu Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser  
 180 185 190

Gln Glu Ala Ala Met Lys Ser Ala Met Ile Thr Asn Ala His Lys Val  
 195 200 205

Val Val Leu Cys Asp Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser  
 210 215 220

Phe Gly Ala Ile Ser Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala  
 225 230 235 240



Pro Ala Ser Phe Val Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val  
                   245                                  250                                  255

Ile Ala Glu

<210> 195

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> RXA02288

<400> 195

aacaacaatc taacgccatc atgttataaa aaagcaagac ctaacataaa aatgtagaa 60

agtgtggtgat ctaacaacat ttccgtggta actttttcac atg tcc caa gtg att 115  
   Met Ser Gln Val Ile  
   1                                  5

ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc 163  
  Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val  
                                   10                                  15                                  20

acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag 211  
  Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu  
                                   25                                  30                                  35

gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac 259  
  Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp  
                                   40                                  45                                  50

aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg 307  
  Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser  
                                   55                                  60                                  65

atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt 355  
  Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val  
                                   70                                  75                                  80                                  85

aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct 403  
  Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala  
                                   90                                  95                                  100

gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag 451  
  Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys  
                                   105                                  110                                  115

ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca 499  
  Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr  
                                   120                                  125                                  130

atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att 547  
  Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile  
                                   135                                  140                                  145

gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag 595  
 Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys  
 150 155 160 165  
  
 gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt 643  
 Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val  
 170 175 180  
  
 tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat 691  
 Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His  
 185 190 195  
  
 cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt 739  
 Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly  
 200 205 210  
  
 agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt 787  
 Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly  
 215 220 225  
  
 gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat 835  
 Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp  
 230 235 240 245  
  
 cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg 883  
 Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala  
 250 255 260  
  
 cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca 931  
 Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro  
 265 270 275  
  
 acg gaa gag gat ttt taagatggct ttggttcttg gaa 969  
 Thr Glu Glu Asp Phe  
 280

&lt;210&gt; 196

&lt;211&gt; 282

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 196

Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg  
 1 5 10 15  
  
 Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu  
 20 25 30  
  
 Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu  
 35 40 45  
  
 Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg  
 50 55 60  
  
 Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His  
 65 70 75 80  
  
 Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu  
 85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu  
 100 105 110  
 Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr  
 115 120 125  
 His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser  
 130 135 140  
 Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp  
 145 150 155 160  
 Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala  
 165 170 175  
 Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val  
 180 185 190  
 Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala  
 195 200 205  
 Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys  
 210 215 220  
 Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp  
 225 230 235 240  
 His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu  
 245 250 255  
 Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu  
 260 265 270  
 Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe  
 275 280

<210> 197  
 <211> 887  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(864)  
 <223> RXN01891

<400> 197  
 ggt ggc cac tat ggt ttg cct ttc gct cgc tcc act gtc ctc ttc tac 48  
 Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr  
 1 5 10 15  
 tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc cca 96  
 Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro  
 20 25 30  
 gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg 144  
 Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala  
 35 40 45  
 atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt 192

Met	Asp	Ser	Gly	Phe	Ala	His	Gly	Trp	Gly	Asp	Ala	Thr	Asn	Tyr	Leu	
50						55					60					
tct	tgg	act	ttc	gaa	ggc	cca	atg	tgg	tcc	ctc	ggc	ggc	aac	tac	tct	240
Ser	Trp	Thr	Phe	Glu	Gly	Pro	Met	Trp	Ser	Leu	Gly	Gly	Asn	Tyr	Ser	80
65					70					75						
gaa	ggg	tgg	gag	tcc	cgt	ctg	act	acc	cca	gag	acc	atc	cgt	gca	gtt	288
Glu	Gly	Trp	Glu	Ser	Arg	Leu	Thr	Thr	Pro	Glu	Thr	Ile	Arg	Ala	Val	
				85					90					95		
gag	tgg	ctc	aag	tcc	acc	gtt	gat	gaa	ggg	ttc	gca	acc	gtc	tcc	acc	336
Glu	Trp	Leu	Lys	Ser	Thr	Val	Asp	Glu	Gly	Phe	Ala	Thr	Val	Ser	Thr	
			100				105						110			
gac	gtc	acc	aac	gag	ttc	gca	acc	ggc	ctg	atc	ggg	tca	tgc	atc	cag	384
Asp	Val	Thr	Asn	Glu	Phe	Ala	Thr	Gly	Leu	Ile	Gly	Ser	Cys	Ile	Gln	
		115					120					125				
tcc	acc	ggg	gat	ctg	tct	tcg	gtt	gcc	ggc	gct	gca	agc	ttc	gac	tgg	432
Ser	Thr	Gly	Asp	Leu	Ser	Ser	Val	Ala	Gly	Ala	Ala	Ser	Phe	Asp	Trp	
			130			135					140					
ggc	gta	gca	gca	ctt	cct	aac	cca	acc	ggc	gag	ggc	gct	tgc	cca	acc	480
Gly	Val	Ala	Ala	Leu	Pro	Asn	Pro	Thr	Gly	Glu	Gly	Ala	Cys	Pro	Thr	
145					150					155					160	
ggg	ggc	gca	ggc	ctg	gga	atc	cca	tct	ggc	atc	tct	gag	cag	cgt	cag	528
Gly	Gly	Ala	Gly	Leu	Gly	Ile	Pro	Ser	Gly	Ile	Ser	Glu	Gln	Arg	Gln	
				165					170					175		
gac	aac	gcc	ctg	aag	ttc	atc	gac	ttc	ctc	acc	aac	gcc	gcg	aac	act	576
Asp	Asn	Ala	Leu	Lys	Phe	Ile	Asp	Phe	Leu	Thr	Asn	Ala	Ala	Asn	Thr	
			180					185					190			
ggc	tac	tgg	tcc	cgc	gag	acc	ggg	tat	gtt	cca	gtt	cgt	aag	gat	gct	624
Gly	Tyr	Trp	Ser	Arg	Glu	Thr	Gly	Tyr	Val	Pro	Val	Arg	Lys	Asp	Ala	
		195					200					205				
gca	tct	gat	cca	gat	cac	gca	gca	ttc	ctc	gag	gag	aac	cct	gca	tac	672
Ala	Ser	Asp	Pro	Asp	His	Ala	Ala	Phe	Leu	Glu	Glu	Asn	Pro	Ala	Tyr	
	210					215				220						
aac	gtt	gca	gtg	gag	cag	ctt	cct	gat	acc	cgt	tcc	cag	gac	aac	ttc	720
Asn	Val	Ala	Val	Glu	Gln	Leu	Pro	Asp	Thr	Arg	Ser	Gln	Asp	Asn	Phe	
225					230					235					240	
cgc	gtg	ctg	ctg	cca	aac	ggg	gac	cgc	acc	atc	ggg	gac	gca	ctg	gag	768
Arg	Val	Leu	Leu	Pro	Asn	Gly	Asp	Arg	Thr	Ile	Gly	Asp	Ala	Leu	Glu	
				245					250					255		
aag	atc	tgc	ctg	act	ggg	gca	gac	atc	gat	gtc	acc	ctg	gct	gag	gtt	816
Lys	Ile	Cys	Leu	Thr	Gly	Ala	Asp	Ile	Asp	Val	Thr	Leu	Ala	Glu	Val	
			260					265				270				
gag	acc	aag	ctg	aac	acc	atc	tac	acc	cgc	gac	atc	gaa	cca	ctt	att	864
Glu	Thr	Lys	Leu	Asn	Thr	Ile	Tyr	Thr	Arg	Asp	Ile	Glu	Pro	Leu	Ile	
		275					280					285				
taatccgaqc acttcaqcta cac																887

&lt;210&gt; 198

&lt;211&gt; 288

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 198

Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr  
 1 5 10 15

Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro  
 20 25 30

Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala  
 35 40 45

Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu  
 50 55 60

Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser  
 65 70 75 80

Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val  
 85 90 95

Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr  
 100 105 110

Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln  
 115 120 125

Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp  
 130 135 140

Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr  
 145 150 155 160

Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln  
 165 170 175

Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr  
 180 185 190

Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala  
 195 200 205

Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr  
 210 215 220

Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe  
 225 230 235 240

Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu  
 245 250 255

Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val  
 260 265 270

Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile  
 275 280 285

<210> 199  
 <211> 842  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(819)  
 <223> FRXA01891

<400> 199  
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 Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly  
 1 5 10 15  
 cca gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa 96  
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu  
 20 25 30  
 gcg atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac 144  
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr  
 35 40 45  
 ctt tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac 192  
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr  
 50 55 60  
 tct gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca 240  
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala  
 65 70 75 80  
 gtt gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc 288  
 Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser  
 85 90 95  
 acc gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc 336  
 Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile  
 100 105 110  
 cag tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac 384  
 Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp  
 115 120 125  
 tgg ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca 432  
 Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro  
 130 135 140  
 acc ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt 480  
 Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg  
 145 150 155 160  
 cag gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac 528  
 Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn  
 165 170 175  
 act ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat 576  
 Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp

180										185					190					
gct	gca	tct	gat	cca	gat	cac	gca	gca	ttc	ctc	gag	gag	aac	cct	gca	624				
Ala	Ala	Ser	Asp	Pro	Asp	His	Ala	Ala	Phe	Leu	Glu	Glu	Asn	Pro	Ala					
		195					200						205							
tac	aac	gtt	gca	gtg	gag	cag	ctt	cct	gat	acc	cgt	tcc	cag	gac	aac	672				
Tyr	Asn	Val	Ala	Val	Glu	Gln	Leu	Pro	Asp	Thr	Arg	Ser	Gln	Asp	Asn					
	210					215					220									
ttc	cgc	gtg	ctg	ctg	cca	aac	ggc	gac	cgc	acc	atc	ggc	gac	gca	ctg	720				
Phe	Arg	Val	Leu	Leu	Pro	Asn	Gly	Asp	Arg	Thr	Ile	Gly	Asp	Ala	Leu					
225					230				235						240					
gag	aag	atc	tgc	ctg	act	ggc	gca	gac	atc	gat	gtc	acc	ctg	gct	gag	768				
Glu	Lys	Ile	Cys	Leu	Thr	Gly	Ala	Asp	Ile	Asp	Val	Thr	Leu	Ala	Glu					
				245					250					255						
gtt	gag	acc	aag	ctg	aac	acc	atc	tac	acc	cgc	gac	atc	gaa	cca	ctt	816				
Val	Glu	Thr	Lys	Leu	Asn	Thr	Ile	Tyr	Thr	Arg	Asp	Ile	Glu	Pro	Leu					
			260					265					270							
att	taatccgagc	acttcagcta	cac													842				
Ile																				

&lt;210&gt; 200

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 200

Tyr	Tyr	Asn	Lys	Asp	Leu	Trp	Ala	Lys	Ala	Gly	Leu	Glu	Asp	Arg	Gly
1				5					10					15	

Pro	Glu	Ser	Trp	Glu	Glu	Phe	Ser	Glu	Trp	Gly	Pro	Lys	Leu	Gln	Glu
			20					25					30		

Ala	Met	Asp	Ser	Gly	Phe	Ala	His	Gly	Trp	Gly	Asp	Ala	Thr	Asn	Tyr
		35					40					45			

Leu	Ser	Trp	Thr	Phe	Glu	Gly	Pro	Met	Trp	Ser	Leu	Gly	Gly	Asn	Tyr
	50					55					60				

Ser	Glu	Gly	Trp	Glu	Ser	Arg	Leu	Thr	Thr	Pro	Glu	Thr	Ile	Arg	Ala
	65				70					75					80

Val	Glu	Trp	Leu	Lys	Ser	Thr	Val	Asp	Glu	Gly	Phe	Ala	Thr	Val	Ser
				85					90					95	

Thr	Asp	Val	Thr	Asn	Glu	Phe	Ala	Thr	Gly	Leu	Ile	Gly	Ser	Cys	Ile
		100						105					110		

Gln	Ser	Thr	Gly	Asp	Leu	Ser	Ser	Val	Ala	Gly	Ala	Ala	Ser	Phe	Asp
		115					120					125			

Trp	Gly	Val	Ala	Ala	Leu	Pro	Asn	Pro	Thr	Gly	Glu	Gly	Ala	Cys	Pro
	130					135					140				

Thr	Gly	Gly	Ala	Gly	Leu	Gly	Ile	Pro	Ser	Gly	Ile	Ser	Glu	Gln	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145		150		155		160
Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn						
	165			170		175
Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp						
	180			185		190
Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala						
	195		200		205	
Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn						
	210		215		220	
Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu						
	225		230		235	240
Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu						
	245		250			255
Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu						
	260		265		270	

Ile

&lt;210&gt; 201

&lt;211&gt; 776

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(753)

&lt;223&gt; RXA02414

&lt;400&gt; 201

```

tttacc atg agt tac aac agc ccg tat aac aac acg aat ttc agc acc act 51
  Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr
        1             5             10             15

```

```

ggc gcg ttc caa cct gct ggt ggg ccg gtg aag ccg tgg aat aag ccc 99
Gly Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro
        20             25             30

```

```

gat gcc agc ctg aat cag cag ctg aaa aac aaa tcc cgt gtg cgc aca 147
Asp Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr
        35             40             45

```

```

ggt ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat 195
Gly Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His
        50             55             60

```

```

ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac 243
Leu Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn
        65             70             75

```

```

ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc 291
Phe Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr
        80             85             90             95

```



tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt 339  
 Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val  
 100 105 110

cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg 387  
 Pro Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val  
 115 120 125

ttc tgg gaa gtc acg att atc gca ggt ctc atc ggc ggt ctt ggt aca 435  
 Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr  
 130 135 140

tgg att ttc ggt gga atc ggc acc aac cac atc ggt gcg tcc ggc ctg 483  
 Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu  
 145 150 155

att tat ggc tgg ctt ggc tac ctg atc gtg cgt gga att ttc aac aag 531  
 Ile Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys  
 160 165 170 175

gat att aaa cag ttc ctg ctt ggc ata gtt ttg gcg ttc att tac tcc 579  
 Asp Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser  
 180 185 190

ggt ttg ttc tgg ggt ctg cta cct act caa atc ggt gtg tcc tgg cag 627  
 Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln  
 195 200 205

ggc cac ctt ttc ggt gca ctt ggt gga atc ggt gcg ggt gct ttt atc 675  
 Gly His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile  
 210 215 220

gcc tcg gat gac ccg gca gcg ttg aaa gcg aag aag caa cag aag aaa 723  
 Ala Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys  
 225 230 235

tta gaa aag caa caa cgc caa aga ggc tta tagttttcac ctagecgacta 773  
 Leu Glu Lys Gln Gln Arg Gln Arg Gly Leu  
 240 245

cac 776

&lt;210&gt; 202

&lt;211&gt; 249

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 202

Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr Gly  
 1 5 10 15

Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro Asp  
 20 25 30

Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr Gly  
 35 40 45

Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His Leu  
 50 55 60

Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn Phe  
65 70 75 80

Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr Ser  
85 90 95

Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val Pro  
100 105 110

Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val Phe  
115 120 125

Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr Trp  
130 135 140

Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu Ile  
145 150 155 160

Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys Asp  
165 170 175

Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser Gly  
180 185 190

Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln Gly  
195 200 205

His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile Ala  
210 215 220

Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys Leu  
225 230 235 240

Glu Lys Gln Gln Arg Gln Arg Gly Leu  
245

&lt;210&gt; 203

&lt;211&gt; 840

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(817)

&lt;223&gt; RXN01580

&lt;400&gt; 203

cggtaaacgc ctcattaaag tccaatgccca tgctcataac actaacagtt aaccgtgcgg 60

tcaactttgc tccctatcct taaaaagccc acagaaaagg atg tat aag aat atg 115  
Met Tyr Lys Asn Met  
1 5

cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc 163  
His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr  
10 15 20

atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat 211  
Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp

25										30					35					
atc	cac	gcc	acc	gct	gac	aat	cag	gtc	gtc	gtt	atc	cac	gac	cgc	acc	259				
Ile	His	Ala	Thr	Ala	Asp	Asn	Gln	Val	Val	Val	Ile	His	Asp	Arg	Thr					
40				45				50												
gca	gcg	cgt	gtt	gcc	gcg	cca	gat	tcc	ctg	cac	cgc	gac	acc	ccg	gtt	307				
Ala	Ala	Arg	Val	Ala	Ala	Pro	Asp	Ser	Leu	His	Arg	Asp	Thr	Pro	Val					
55				60				65												
gcg	cgc	tta	agc	gcc	gcg	caa	atc	aag	gag	ata	acg	ctt	atc	gac	gga	355				
Ala	Arg	Leu	Ser	Ala	Ala	Gln	Ile	Lys	Glu	Ile	Thr	Leu	Ile	Asp	Gly					
70				75				80				85								
tcc	ccc	gta	cca	acc	ctg	gag	gaa	gtt	cta	ctc	cag	acg	agc	ctg	ccg	403				
Ser	Pro	Val	Pro	Thr	Leu	Glu	Glu	Val	Leu	Leu	Gln	Thr	Ser	Leu	Pro					
90				95				100												
atc	caa	gtg	gaa	atc	aaa	tct	gcc	ggt	gca	gtt	cca	gca	gcc	gca	gca	451				
Ile	Gln	Val	Glu	Ile	Lys	Ser	Ala	Gly	Ala	Val	Pro	Ala	Ala	Ala	Ala					
105				110				115												
tta	ttg	cag	aaa	tac	cca	gag	cac	ctg	gag	cgc	ctg	ctg	ttc	atc	agt	499				
Leu	Leu	Gln	Lys	Tyr	Pro	Glu	His	Leu	Glu	Arg	Leu	Leu	Phe	Ile	Ser					
120				125				130												
ttc	atc	gat	gca	gca	ctg	gtg	gaa	atc	gtg	gat	cga	ctg	cca	gaa	gct	547				
Phe	Ile	Asp	Ala	Ala	Leu	Val	Glu	Ile	Val	Asp	Arg	Leu	Pro	Glu	Ala					
135				140				145												
cgc	gtg	gga	atc	ttg	cgc	gat	gcg	tcc	atg	gat	gat	ctg	cgc	att	ctt	595				
Arg	Val	Gly	Ile	Leu	Arg	Asp	Ala	Ser	Met	Asp	Asp	Leu	Arg	Ile	Leu					
150				155				160				165								
gat	tac	atc	ccg	cta	aaa	aat	gtg	ggc	gcg	atc	ttg	ccc	tcg	tgg	aaa	643				
Asp	Tyr	Ile	Pro	Leu	Lys	Asn	Val	Gly	Ala	Ile	Leu	Pro	Ser	Trp	Lys					
170				175				180												
gca	cta	aac	gtg	gcg	tca	att	gct	gat	cta	cat	acc	aag	gga	atc	aag	691				
Ala	Leu	Asn	Val	Ala	Ser	Ile	Ala	Asp	Leu	His	Thr	Lys	Gly	Ile	Lys					
185				190				195												
gtt	ggc	tgc	tgg	aca	att	cgg	gat	gaa	aat	gcg	ttt	ggg	atc	gca	caa	739				
Val	Gly	Cys	Trp	Thr	Ile	Arg	Asp	Glu	Asn	Ala	Phe	Gly	Ile	Ala	Gln					
200				205				210												
caa	gct	ggc	gtt	gat	tac	gcc	act	gtt	agc	gat	ccc	tct	cgt	ttc	ctc	787				
Gln	Ala	Gly	Val	Asp	Tyr	Ala	Thr	Val	Ser	Asp	Pro	Ser	Arg	Phe	Leu					
215				220				225												
gcg	ccc	tcc	cct	gct	ggg	gag	ttg	cac	tgg	taaataatct	agtgaccaga					837				
Ala	Pro	Ser	Pro	Ala	Gly	Glu	Leu	His	Trp											
230				235																
ctg															840					

&lt;210&gt; 204

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 204

Met Tyr Lys Asn Met His Ile Val Ala His Arg Gly Ala Glu Asp Leu  
 1 5 10 15

His Leu Glu Asn Thr Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp  
 20 25 30

Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val  
 35 40 45

Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His  
 50 55 60

Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile  
 65 70 75 80

Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu  
 85 90 95

Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val  
 100 105 110

Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg  
 115 120 125

Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp  
 130 135 140

Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp  
 145 150 155 160

Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile  
 165 170 175

Leu Pro Ser Trp Lys Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His  
 180 185 190

Thr Lys Gly Ile Lys Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala  
 195 200 205

Phe Gly Ile Ala Gln Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp  
 210 215 220

Pro Ser Arg Phe Leu Ala Pro Ser Pro Ala Gly Glu Leu His Trp  
 225 230 235

&lt;210&gt; 205

&lt;211&gt; 1314

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1291)

&lt;223&gt; RXA01436

&lt;400&gt; 205

gcctaaacaa accagtcaac gacctttccc gtggcgcaac agtccttgac atcgtaaca 60.

cagtagccat	cacagcaatt	caggcaggag	gacgcagcta	atg	gca	ttg	gca	ctt	115
				Met	Ala	Leu	Ala	Leu	
				1				5	
ggt ttg aac tcc ggt tca tct tcc atc aaa ttc cag ctg gtc aac ccc	163								
Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu Val Asn Pro									
	10 15 20								
gaa aac tct gcc atc gac gag cca tat gtt tct ggt ctt gtg gag cag	211								
Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu Val Glu Gln									
	25 30 35								
att ggt gag cca aac ggc cgc atc gta ctc aaa ata gag ggt gaa aaa	259								
Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Ile Glu Gly Glu Lys									
	40 45 50								
tat acc cta gag aca ccc atc gca gat cac tcc gaa ggc cta aac ctg	307								
Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly Leu Asn Leu									
	55 60 65								
gcg ttc gat ctc atg gac cag cac aac tgt ggt cct tcc caa ctg gaa	355								
Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser Gln Leu Glu									
	70 75 80 85								
atc acc gca gtt gga cac cgc gtg gtc cac ggc gga atc ttg ttc tcc	403								
Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile Leu Phe Ser									
	90 95 100								
gca ccg gaa ctt atc act gat gaa atc gtg gaa atg atc cgc gat ctc	451								
Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu Met Ile Arg Asp Leu									
	105 110 115								
att cca ctc gca cca ctg cac aac cct gca aac gtt gac ggc att gat	499								
Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn Val Asp Gly Ile Asp									
	120 125 130								
ggt gct cga aaa att ctc ccc gat gtc cca cac gta gct gtc ttt gac	547								
Val Ala Arg Lys Ile Leu Pro Asp Val Pro His Val Ala Val Phe Asp									
	135 140 145								
acc ggt ttc ttc cac tca ctt cca cca gca gct gcg ctg tat gcc atc	595								
Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala Leu Tyr Ala Ile									
	150 155 160 165								
aac aag gat gtc gca gct gaa cac gga atc agg cgc tat ggt ttc cac	643								
Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg Arg Tyr Gly Phe His									
	170 175 180								
ggc acc tcc cat gaa ttt gtg tcc aag cgc gtg gtg gaa att ctg gaa	691								
Gly Thr Ser His Glu Phe Val Ser Lys Arg Val Val Glu Ile Leu Glu									
	185 190 195								
aag ccc acc gaa gac atc aac acc atc acc ttc cac ctg ggc aac ggc	739								
Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe His Leu Gly Asn Gly									
	200 205 210								
gca tcc atg gct gct gtt caa ggt ggc cgt gcg gta gat act tcc atg	787								
Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala Val Asp Thr Ser Met									
	215 220 225								
ggt atg aca cct ctc gcg ggc ctt gtc atg ggt acc cga agc ggt gac	835								

Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly Thr Arg Ser Gly Asp  
 230 235 240 245  
 att gat cca ggt atc gtc ttc cac ctt tcc cgc acc gct ggc atg agc 883  
 Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg Thr Ala Gly Met Ser  
 250 255 260  
 atc gat gag atc gat aat ctg ctg aac aaa aag tcg ggt gta aag gga 931  
 Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys Ser Gly Val Lys Gly  
 265 270 275  
 ctt tcc ggt gtt aat gat ttc cgt gaa ctg cgg gaa atg atc gac aac 979  
 Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg Glu Met Ile Asp Asn  
 280 285 290  
 aat gat caa gat gcc tgg tcc gcg tac aac att tac ata cac caa ctc 1027  
 Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile Tyr Ile His Gln Leu  
 295 300 305  
 cgc cgc tac ctc ggt tcc tac atg gtg gca ctg gga cgg gta gac acc 1075  
 Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu Gly Arg Val Asp Thr  
 310 315 320 325  
 atc gtg ttc acc gcc ggt gtc ggt gaa aat gcc cag ttt gtc cgt gag 1123  
 Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala Gln Phe Val Arg Glu  
 330 335 340  
 gat gcc ttg gca ggt ttg gaa atg tac gga att gag atc gat cca gag 1171  
 Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile Glu Ile Asp Pro Glu  
 345 350 355  
 cgt aac gca ttg cca aac gat ggt cct cga ttg att tcc acc gat gcc 1219  
 Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu Ile Ser Thr Asp Ala  
 360 365 370  
 tcc aag gtg aag gtg ttt gtt att cca act aat gaa gag tta gct atc 1267  
 Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu Ala Ile  
 375 380 385  
 gct agg tac gcg gtg aag ttc gct tagctctcct ggtaggatac cac 1314  
 Ala Arg Tyr Ala Val Lys Phe Ala  
 390 395

&lt;210&gt; 206

&lt;211&gt; 397

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 206

Met Ala Leu Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe  
 1 5 10 15  
 Gln Leu Val Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser  
 20 25 30  
 Gly Leu Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys  
 35 40 45  
 Ile Glu Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser  
 50 55 60

Glu	Gly	Leu	Asn	Leu	Ala	Phe	Asp	Leu	Met	Asp	Gln	His	Asn	Cys	Gly	65	70	75	80
Pro	Ser	Gln	Leu	Glu	Ile	Thr	Ala	Val	Gly	His	Arg	Val	Val	His	Gly	85	90	95	
Gly	Ile	Leu	Phe	Ser	Ala	Pro	Glu	Leu	Ile	Thr	Asp	Glu	Ile	Val	Glu	100	105	110	
Met	Ile	Arg	Asp	Leu	Ile	Pro	Leu	Ala	Pro	Leu	His	Asn	Pro	Ala	Asn	115	120	125	
Val	Asp	Gly	Ile	Asp	Val	Ala	Arg	Lys	Ile	Leu	Pro	Asp	Val	Pro	His	130	135	140	
Val	Ala	Val	Phe	Asp	Thr	Gly	Phe	Phe	His	Ser	Leu	Pro	Pro	Ala	Ala	145	150	155	160
Ala	Leu	Tyr	Ala	Ile	Asn	Lys	Asp	Val	Ala	Ala	Glu	His	Gly	Ile	Arg	165	170	175	
Arg	Tyr	Gly	Phe	His	Gly	Thr	Ser	His	Glu	Phe	Val	Ser	Lys	Arg	Val	180	185	190	
Val	Glu	Ile	Leu	Glu	Lys	Pro	Thr	Glu	Asp	Ile	Asn	Thr	Ile	Thr	Phe	195	200	205	
His	Leu	Gly	Asn	Gly	Ala	Ser	Met	Ala	Ala	Val	Gln	Gly	Gly	Arg	Ala	210	215	220	
Val	Asp	Thr	Ser	Met	Gly	Met	Thr	Pro	Leu	Ala	Gly	Leu	Val	Met	Gly	225	230	235	240
Thr	Arg	Ser	Gly	Asp	Ile	Asp	Pro	Gly	Ile	Val	Phe	His	Leu	Ser	Arg	245	250	255	
Thr	Ala	Gly	Met	Ser	Ile	Asp	Glu	Ile	Asp	Asn	Leu	Leu	Asn	Lys	Lys	260	265	270	
Ser	Gly	Val	Lys	Gly	Leu	Ser	Gly	Val	Asn	Asp	Phe	Arg	Glu	Leu	Arg	275	280	285	
Glu	Met	Ile	Asp	Asn	Asn	Asp	Gln	Asp	Ala	Trp	Ser	Ala	Tyr	Asn	Ile	290	295	300	
Tyr	Ile	His	Gln	Leu	Arg	Arg	Tyr	Leu	Gly	Ser	Tyr	Met	Val	Ala	Leu	305	310	315	320
Gly	Arg	Val	Asp	Thr	Ile	Val	Phe	Thr	Ala	Gly	Val	Gly	Glu	Asn	Ala	325	330	335	
Gln	Phe	Val	Arg	Glu	Asp	Ala	Leu	Ala	Gly	Leu	Glu	Met	Tyr	Gly	Ile	340	345	350	
Glu	Ile	Asp	Pro	Glu	Arg	Asn	Ala	Leu	Pro	Asn	Asp	Gly	Pro	Arg	Leu	355	360	365	
Ile	Ser	Thr	Asp	Ala	Ser	Lys	Val	Lys	Val	Phe	Val	Ile	Pro	Thr	Asn	370	375	380	

Glu Glu Leu Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala  
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<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(904)

<223> RXA00686

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ttcatcggag tgccagggga acttagagga gcattaaata atg gcg gga gga aat 115  
 Met Ala Gly Gly Asn  
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cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga 163  
 Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly  
 10 15 20

gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag 211  
 Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu  
 25 30 35

ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta 259  
 Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu  
 40 45 50

acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg 307  
 Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu  
 55 60 65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc 355  
 Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg  
 70 75 80 85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag 403  
 Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu  
 90 95 100

act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac 451  
 Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp  
 105 110 115

cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt 499  
 Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly  
 120 125 130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt 547  
 Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe  
 135 140 145

gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc 595  
 Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala  
 150 155 160 165



tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg 643  
 Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu  
 170 175 180

aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga 691  
 Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg  
 185 190 195

atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg 739  
 Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu  
 200 205 210

gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt 787  
 Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu  
 215 220 225

gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa 835  
 Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys  
 230 235 240 245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat 883  
 Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn  
 250 255 260

gca gaa cga aaa ggc gat acc taaacccgcc ctccatctgc ata 927  
 Ala Glu Arg Lys Gly Asp Thr  
 265

&lt;210&gt; 208

&lt;211&gt; 268

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 208

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Ile Ala Val Leu Gly Ala Phe Glu His Thr Met Arg Pro Leu Gly Val  
 20 25 30

Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg  
 35 40 45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp  
 50 55 60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr  
 65 70 75 80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr  
 85 90 95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu  
 100 105 110

Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser  
 115 120 125

Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys  
 130 135 140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys  
145 150 155 160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val  
165 170 175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr  
180 185 190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp  
195 200 205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala  
210 215 220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser  
225 230 235 240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu  
245 250 255

Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr  
260 265

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<223> RXA00246

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gcaatttgcc aagtaatcca agcgagaagg agtgagtttt atg acc act gct gca 115  
Met Thr Thr Ala Ala  
1 5

ccc caa gaa ttt acc gct gct gtt gtt gaa aaa ttc ggt cat gac gtg 163  
Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys Phe Gly His Asp Val  
10 15 20

acc gtg aag gat att gac ctt cca aag cca ggg cca cac cag gca ttg 211  
Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly Pro His Gln Ala Leu  
25 30 35

gtg aag gta ctc acc tcc ggc atc tgc cac acc gac ctc cac gcc ttg 259  
Val Lys Val Leu Thr Ser Gly Ile Cys His Thr Asp Leu His Ala Leu  
40 45 50

gag ggc gat tgg cca gta aag ccg gaa cca cca ttc gta cca gga cac 307  
Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro Phe Val Pro Gly His  
55 60 65

gaa ggt gta ggt gaa gtt gtt gag ctc gga cca ggt gaa cac gat gtg 355  
Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro Gly Glu His Asp Val

70				75				80				85				
aag	gtc	ggc	gat	att	gtc	ggc	aat	gcg	tgg	ctc	tgg	tca	gcg	tgt	ggc	403
Lys	Val	Gly	Asp	Ile	Val	Gly	Asn	Ala	Trp	Leu	Trp	Ser	Ala	Cys	Gly	
				90					95					100		
acc	tgc	gaa	tac	tgc	atc	acc	ggc	agg	gaa	act	cag	tgc	aac	gaa	gct	451
Thr	Cys	Glu	Tyr	Cys	Ile	Thr	Gly	Arg	Glu	Thr	Gln	Cys	Asn	Glu	Ala	
			105					110					115			
gag	tat	ggg	ggc	tac	acc	caa	aat	gga	tcc	ttc	ggc	cag	tac	atg	ctg	499
Glu	Tyr	Gly	Gly	Tyr	Thr	Gln	Asn	Gly	Ser	Phe	Gly	Gln	Tyr	Met	Leu	
		120					125					130				
gtg	gat	acc	cgt	tac	gcc	gct	cgc	atc	cca	gac	ggc	gtg	gac	tac	ctc	547
Val	Asp	Thr	Arg	Tyr	Ala	Ala	Arg	Ile	Pro	Asp	Gly	Val	Asp	Tyr	Leu	
	135					140					145					
gaa	gca	gca	cca	att	ctg	tgt	gca	ggc	gtg	act	gtc	tac	aag	gca	ctc	595
Glu	Ala	Ala	Pro	Ile	Leu	Cys	Ala	Gly	Val	Thr	Val	Tyr	Lys	Ala	Leu	
150					155					160					165	
aaa	gtc	tct	gaa	acc	cgc	ccg	ggc	caa	ttc	atg	gtg	atc	tcc	ggg	gtc	643
Lys	Val	Ser	Glu	Thr	Arg	Pro	Gly	Gln	Phe	Met	Val	Ile	Ser	Gly	Val	
				170					175					180		
ggc	gga	ctt	ggc	cac	atc	gca	gtc	caa	tac	gca	gcg	gcg	atg	ggc	atg	691
Gly	Gly	Leu	Gly	His	Ile	Ala	Val	Gln	Tyr	Ala	Ala	Ala	Met	Gly	Met	
		185						190					195			
cgt	gtc	att	gcg	gta	gat	att	gcc	gat	gac	aag	ctg	gaa	ctt	gcc	cgt	739
Arg	Val	Ile	Ala	Val	Asp	Ile	Ala	Asp	Asp	Lys	Leu	Glu	Leu	Ala	Arg	
		200					205					210				
aag	cac	ggg	gcg	gaa	ttt	acc	gtg	aat	gcg	cgt	aat	gaa	gat	tca	ggc	787
Lys	His	Gly	Ala	Glu	Phe	Thr	Val	Asn	Ala	Arg	Asn	Glu	Asp	Ser	Gly	
	215					220					225					
gaa	gct	gta	cag	aag	tac	acc	aac	ggg	ggc	gca	cac	ggc	gtg	ctt	gtg	835
Glu	Ala	Val	Gln	Lys	Tyr	Thr	Asn	Gly	Gly	Ala	His	Gly	Val	Leu	Val	
230					235					240					245	
act	gca	gtt	cac	gag	gca	gca	ttc	ggc	cag	gca	ctg	gat	atg	gct	cga	883
Thr	Ala	Val	His	Glu	Ala	Ala	Phe	Gly	Gln	Ala	Leu	Asp	Met	Ala	Arg	
				250					255					260		
cgt	gca	gga	aca	att	gtg	ttc	aac	ggg	ctg	cca	ccg	gga	gag	ttc	cca	931
Arg	Ala	Gly	Thr	Ile	Val	Phe	Asn	Gly	Leu	Pro	Pro	Gly	Glu	Phe	Pro	
			265					270					275			
gca	tcc	gtg	ttc	aac	atc	gta	ttc	aag	ggc	ctg	acc	atc	cgt	gga	tcc	979
Ala	Ser	Val	Phe	Asn	Ile	Val	Phe	Lys	Gly	Leu	Thr	Ile	Arg	Gly	Ser	
		280					285					290				
ctc	gtg	gga	acc	cgc	caa	gac	ttg	gcc	gaa	gcg	ctc	gat	ttc	ttt	gca	1027
Leu	Val	Gly	Thr	Arg	Gln	Asp	Leu	Ala	Glu	Ala	Leu	Asp	Phe	Phe	Ala	
		295				300					305					
cgc	gga	cta	atc	aag	cca	acc	gtg	agt	gag	tgc	tcc	ctc	gat	gag	gtc	1075
Arg	Gly	Leu	Ile	Lys	Pro	Thr	Val	Ser	Glu	Cys	Ser	Leu	Asp	Glu	Val	
310					315					320					325	

aat ggt gtg ctt gac cgc atg cga aac ggc aag atc gat ggt cgt gtg 1123  
 Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys Ile Asp Gly Arg Val  
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gcg att cgt ttc taacggattg tggtgaaact gct 1158  
 Ala Ile Arg Phe  
                   345

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<213> Corynebacterium glutamicum

<400> 210

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Phe Gly His Asp Val Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly  
                   20                                  25                                  30

Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr  
                   35                                  40                                  45

Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro  
   50                                  55                                  60

Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro  
   65                                  70                                  75                                  80

Gly Glu His Asp Val Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu  
                   85                                  90                                  95

Trp Ser Ala Cys Gly Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr  
                   100                                  105                                  110

Gln Cys Asn Glu Ala Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe  
                   115                                  120                                  125

Gly Gln Tyr Met Leu Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp  
   130                                  135                                  140

Gly Val Asp Tyr Leu Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr  
   145                                  150                                  155                                  160

Val Tyr Lys Ala Leu Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met  
                   165                                  170                                  175

Val Ile Ser Gly Val Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala  
                   180                                  185                                  190

Ala Ala Met Gly Met Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys  
                   195                                  200                                  205

Leu Glu Leu Ala Arg Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg  
   210                                  215                                  220

Asn Glu Asp Ser Gly Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala  
   225                                  230                                  235                                  240

His Gly Val Leu Val Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala  
 245 250 255  
 Leu Asp Met Ala Arg Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro  
 260 265 270  
 Pro Gly Glu Phe Pro Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu  
 275 280 285  
 Thr Ile Arg Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala  
 290 295 300  
 Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys  
 305 310 315 320  
 Ser Leu Asp Glu Val Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys  
 325 330 335  
 Ile Asp Gly Arg Val Ala Ile Arg Phe  
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 Val Ser Ile Ser Val 5  
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 aaa gca cta caa aag tcc ggc cca gaa gca cct ttc gag gtc aag atc 163  
 Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro Phe Glu Val Lys Ile 20  
 10 15  
 att gaa cgc cgt gac cca cgc gca gat gat gtg gtt att gat atc aaa 211  
 Ile Glu Arg Arg Asp Pro Arg Ala Asp Asp Val Val Ile Asp Ile Lys 35  
 25 30  
 gct gcg ggc atc tgc cac agc gat atc cac acc atc cgc aac gaa tgg 259  
 Ala Ala Gly Ile Cys His Ser Asp Ile His Thr Ile Arg Asn Glu Trp 50  
 40 45  
 ggc gag gcg cac ttc ccg ctc acc gtc ggc cac gaa atc gca ggc gtt 307  
 Gly Glu Ala His Phe Pro Leu Thr Val Gly His Glu Ile Ala Gly Val 65  
 55 60  
 gtc tct gcg gtt gga tcc gat gta acc aaa tgg aaa gtc ggc gac cgc 355  
 Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp Lys Val Gly Asp Arg 85  
 70 75 80  
 gtg ggc gtc ggc tgc ctc gtt aac tcc tgc ggc gaa tgc gaa cag tgc 403  
 Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly Glu Cys Glu Gln Cys

90										95					100					
gtc	gca	gga	ttt	gaa	aac	aac	tgc	ctt	cgc	gga	aac	gtc	gga	acc	tac	451				
Val	Ala	Gly	Phe	Glu	Asn	Asn	Cys	Leu	Arg	Gly	Asn	Val	Gly	Thr	Tyr					
105				110				115												
aac	tct	aac	gac	gtc	gac	ggc	acc	atc	acc	caa	ggc	ggc	tac	gct	gaa	499				
Asn	Ser	Asn	Asp	Val	Asp	Gly	Thr	Ile	Thr	Gln	Gly	Gly	Tyr	Ala	Glu					
120				125				130												
aag	gta	gtg	gtc	aac	gaa	cgt	ttc	ctg	tgc	agc	atc	cca	gag	gaa	ctt	547				
Lys	Val	Val	Val	Asn	Glu	Arg	Phe	Leu	Cys	Ser	Ile	Pro	Glu	Glu	Leu					
135				140				145												
aac	ttc	gat	gtc	gca	gca	cca	ctg	ctg	tgc	gca	ggc	atc	acc	acc	tac	595				
Asn	Phe	Asp	Val	Ala	Ala	Pro	Leu	Leu	Cys	Ala	Gly	Ile	Thr	Thr	Tyr					
150				155				160				165								
tcc	cca	atc	gct	cgc	tgg	aac	gtt	aaa	gaa	ggc	gac	aaa	gta	gca	gtc	643				
Ser	Pro	Ile	Ala	Arg	Trp	Asn	Val	Lys	Glu	Gly	Asp	Lys	Val	Ala	Val					
170				175				180												
atg	ggc	ctc	ggc	ggg	act	cgg	aca	cat	ggg	tgt	cca	gat	cgc	tgc	agc	691				
Met	Gly	Leu	Gly	Gly	Thr	Arg	Thr	His	Gly	Cys	Pro	Asp	Arg	Cys	Ser					
185				190				195												
caa	ggg	tgc	tgaggttacc	gttctgtccc	gtt											723				
Gln	Gly	Cys																		
200																				

&lt;210&gt; 212

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 212

Val	Ser	Ile	Ser	Val	Lys	Ala	Leu	Gln	Lys	Ser	Gly	Pro	Glu	Ala	Pro
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Phe	Glu	Val	Lys	Ile	Ile	Glu	Arg	Arg	Asp	Pro	Arg	Ala	Asp	Asp	Val
		20					25					30			

Val	Ile	Asp	Ile	Lys	Ala	Ala	Gly	Ile	Cys	His	Ser	Asp	Ile	His	Thr
		35					40					45			

Ile	Arg	Asn	Glu	Trp	Gly	Glu	Ala	His	Phe	Pro	Leu	Thr	Val	Gly	His
	50					55					60				

Glu	Ile	Ala	Gly	Val	Val	Ser	Ala	Val	Gly	Ser	Asp	Val	Thr	Lys	Trp
65				70						75					80

Lys	Val	Gly	Asp	Arg	Val	Gly	Val	Gly	Cys	Leu	Val	Asn	Ser	Cys	Gly
			85						90					95	

Glu	Cys	Glu	Gln	Cys	Val	Ala	Gly	Phe	Glu	Asn	Asn	Cys	Leu	Arg	Gly
			100					105					110		

Asn	Val	Gly	Thr	Tyr	Asn	Ser	Asn	Asp	Val	Asp	Gly	Thr	Ile	Thr	Gln
		115					120					125			

Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser  
 130 135 140

Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala  
 145 150 155 160

Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly  
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Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys  
 180 185 190

Pro Asp Arg Cys Ser Gln Gly Cys  
 195 200

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 Met Gly Val Gln Ile  
 1 5

gct gca gcc aag ggt gct gag gtt acc gtt ctg tcc cgt tcc ctg cgc 163  
 Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg  
 10 15 20

aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act 211  
 Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr  
 25 30 35

tct gat gag gat ttc ttc acc gaa cac gcc ggt gaa ttc gac ttc atc 259  
 Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile  
 40 45 50

ctc aac acc att agc gca tcc atc cca gtc gac aag tac ctg agc ctt 307  
 Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu  
 55 60 65

ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag 355  
 Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys  
 70 75 80 85

cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc 403  
 Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr  
 90 95 100

gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc 451  
 Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe  
 105 110 115

tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac 499  
 Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn  
           120                          125                          130

gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc 547  
 Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe  
           135                          140                          145

cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt 592  
 Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val  
           150                          155                          160

taggtttact gaagttcaga ctt 615

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<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu  
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Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala  
           20                          25                          30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly  
           35                          40                          45

Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp  
           50                          55                          60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly  
           65                          70                          75                          80

Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly  
                           85                          90                          95

Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln  
           100                          105                          110

Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu  
           115                          120                          125

Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala  
           130                          135                          140

Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu  
           145                          150                          155                          160

Val Glu Ala Val

<210> 215

<211> 1140

<212> DNA

<213> Corynebacterium glutamicum

<220>



&lt;221&gt; CDS

&lt;222&gt; (101)..(1117)

&lt;223&gt; RXA01758

&lt;400&gt; 215

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cccccttatt cagagtgatg gtctaccgga gaagtaccca gaccaatagc atcgaccaac 60

gatagcgcgc tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115
                               Met Pro Lys Tyr Ile
                               1           5

gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
                10                15                20

caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
                25                30                35

agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
                40                45                50

cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc 307
His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile
                55                60                65

gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt 355
Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val
                70                75                80                85

gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt 403
Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg
                90                95                100

gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct 451
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser
                105                110                115

tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt 499
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu
                120                125                130

gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc 547
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly
                135                140                145

tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat 595
Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp
                150                155                160                165

ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta 643
Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu
                170                175                180

gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc 691
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala
                185                190                195

cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac 739
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His

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200	205	210	
tac atc gat agc aat gat	ctg cac cct ggc cag gcg	tta ttt gaa ctt	787
Tyr Ile Asp Ser Asn Asp	Leu His Pro Gly Gln Ala	Leu Phe Glu Leu	
215	220	225	
ggc ggg gct gac ttg atc	ttg tct act gcg tcc acc acg gag cct ctt		835
Gly Gly Ala Asp Leu Ile	Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu		
230	235	240	245
tcg gag ttg tct acc ggt ctt	tct att ggc ggg cag cta acc att atc		883
Ser Glu Leu Ser Thr Gly	Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile		
250	255	260	
gga gtt gat ggg gga gat	atc acc gtt tcg gca gcc caa ttg atg atg		931
Gly Val Asp Gly Gly Asp	Ile Thr Val Ser Ala Ala Gln Leu Met Met		
265	270	275	
aac cgt cag atc atc aca	ggt cac ctc act gga agt gcg aat gac acg		979
Asn Arg Gln Ile Ile Thr	Gly His Leu Thr Gly Ser Ala Asn Asp Thr		
280	285	290	
gaa cag act atg aaa ttt	gct cat ctc cat ggc gtg aaa ccg ctt att		1027
Glu Gln Thr Met Lys Phe	Ala His Leu His Gly Val Lys Pro Leu Ile		
295	300	305	
gaa cgg atg cct ctc gat	caa gcc aac gag gct att gca cgt att tca		1075
Glu Arg Met Pro Leu Asp	Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser		
310	315	320	325
gct ggt aaa cca cgt ttc	cgt att gtc ttg gag ccg aat tca		1117
Ala Gly Lys Pro Arg Phe	Arg Ile Val Leu Glu Pro Asn Ser		
330	335		
taatgccaac agcaagccca att			1140

&lt;210&gt; 216

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 216

Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu
1 5 10 15

Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg
20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
35 40 45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
50 55 60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
65 70 75 80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
85 90 95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys  
 100 105 110  
 Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val  
 115 120 125  
 Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu  
 130 135 140  
 Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg  
 145 150 155 160  
 Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly  
 165 170 175  
 Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg  
 180 185 190  
 Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln  
 195 200 205  
 Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln  
 210 215 220  
 Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser  
 225 230 235 240  
 Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly  
 245 250 255  
 Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala  
 260 265 270  
 Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly  
 275 280 285  
 Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly  
 290 295 300  
 Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala  
 305 310 315 320  
 Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu  
 325 330 335

Pro Asn Ser

<210> 217

<211> 1641

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1618)

<223> RXA02539

<400> 217

ggctgctaag cgtgcgaatg tgcgcgttgt cacaatcgtt gaccaagtgt cacctgacgc 60

acaggtagtg	ctcaggtgga	ggtggcccaa	aggagaccca	atg	act	gtc	tac	gca	115
				Met	Thr	Val	Tyr	Ala	
				1				5	
aat cca gga acc gaa ggc tcg atc gtt aac tat gaa aag cgc tac gag	163								
Asn Pro Gly Thr	Glu Gly Ser Ile Val Asn Tyr Glu Lys Arg Tyr Glu								
10	15	20							
aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt	211								
Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val Glu Gly Gln Tyr Leu									
25	30	35							
gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt	259								
Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg									
40	45	50							
ggc acc gca gcg gac gtg gag ctt gca ctg gat gct gca cat gca gcc	307								
Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp Ala Ala His Ala Ala									
55	60	65							
gct gat gcg tgg ggc aag act tct gtc gct gaa cgt gct ctg atc ctg	355								
Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg Ala Leu Ile Leu									
70	75	80	85						
cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt	403								
His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val									
90	95	100							
gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt gct gca	451								
Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu Ala Ala									
105	110	115							
gat atc cca ctg gca atc gac cac ttc cgc tac ttt gct ggc gcg atc	499								
Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile									
120	125	130							
cgt gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct	547								
Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala									
135	140	145							
tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg	595								
Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp									
150	155	160	165						
aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct	643								
Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala									
170	175	180							
gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc	691								
Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser									
185	190	195							
att ttg tat ctg att aac atc atc ggc gat ctc atc cca gag ggc gtc	739								
Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val									
200	205	210							
ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc	787								
Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser									
215	220	225							

ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val 230 235 240 245	835
ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr 250 255 260	883
ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu 265 270 275	931
tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met 280 285 290	979
ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu 295 300 305	1027
gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg 310 315 320 325	1075
gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met 330 335 340	1123
ggt gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys Ile Ser Ser Tyr Leu 345 350 355	1171
aag atc ggc cca gaa gaa ggc gct caa acc ctc act ggt ggc aag gtc Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val 360 365 370	1219
aac aag gtt gat ggc atg gag aac ggt tac tac att gag cca acc gtt Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr Ile Glu Pro Thr Val 375 380 385	1267
ttc cgc ggc acc aac gac atg agg atc ttc cgc gag gaa atc ttc gga Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg Glu Glu Ile Phe Gly 390 395 400 405	1315
cca gtc ctt tct gtt gct acc ttc agc gac ttc gat gag gcc atc cgt Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe Asp Glu Ala Ile Arg 410 415 420	1363
att gca aac gac acc aac tac ggc ctc ggc gct ggt gtc tgg agc cgt Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg 425 430 435	1411
gac caa aac acc att tat cgt gca ggt cgc gca atc cag gct ggt cga Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala Ile Gln Ala Gly Arg 440 445 450	1459
gtt tgg gtc aac cag tac cac aac tac cca gcg cac tcc gct ttc ggt Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala His Ser Ala Phe Gly 455 460 465	1507
gga tac aag gag tcc ggc atc ggc cgt gag aac cac ctc atg atg ctg	1555

Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn His Leu Met Met Leu  
 470 475 480 485

aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac 1603  
 Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn  
 490 495 500

cca acc gga ctg ttc tgatctaagc gttaagtcct aga 1641  
 Pro Thr Gly Leu Phe  
 505

<210> 218

<211> 506

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Thr Val Tyr Ala Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr  
 1 5 10 15

Glu Lys Arg Tyr Glu Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val  
 20 25 30

Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe  
 35 40 45

Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp  
 50 55 60

Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu  
 65 70 75 80

Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu  
 85 90 95

Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg  
 100 105 110

Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr  
 115 120 125

Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp  
 130 135 140

His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly  
 145 150 155 160

Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu  
 165 170 175

Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu  
 180 185 190

Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu  
 195 200 205

Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala  
 210 215 220

Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr

225		230		235		240
Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys						
	245			250		255
Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe						
	260			265		270
Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val						
	275			280		285
Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys						
	290			295		300
Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu						
	305			310		315
Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp						
	325			330		335
Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys						
	340			345		350
Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu						
	355			360		365
Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr						
	370			375		380
Ile Glu Pro Thr Val Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg						
	385			390		395
Glu Glu Ile Phe Gly Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe						
	405			410		415
Asp Glu Ala Ile Arg Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala						
	420			425		430
Gly Val Trp Ser Arg Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala						
	435			440		445
Ile Gln Ala Gly Arg Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala						
	450			455		460
His Ser Ala Phe Gly Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn						
	465			470		475
His Leu Met Met Leu Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val						
	485			490		495
Ser Tyr Asp Pro Asn Pro Thr Gly Leu Phe						
	500			505		

&lt;210&gt; 219

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(430)

&lt;223&gt; RXN03061

&lt;400&gt; 219

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ctgccaccac tggtcattgc agaggacact ctccgtgatg gtcttcaggt gttagtcgca 60
gccctagagc gcgaaaccgc gcaccagaag gtgggctaaa gtg tct ttg acc ttc 115
                                   Val Ser Leu Thr Phe
                                   1 5
cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac 163
Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn
               10 15 20
cac gat tcc acc cag tgg atg tcc gcg ctc tct gat gca gtt gca gct 211
His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser Asp Ala Val Ala Ala
               25 30 35
ggt cct tca tgg gct gcg aaa act ccc cgc gaa aga tcc gtg gta ctc 259
Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu Arg Ser Val Val Leu
               40 45 50
acc gca atc ttc gaa gca ctg acc gaa cgc gcc caa gaa ctt gca gag 307
Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala Gln Glu Leu Ala Glu
               55 60 65
atc atc cac ctg gaa gct gga aaa tcc gat gca gaa gct ctt ggt gaa 355
Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala Glu Ala Leu Gly Glu
               70 75 80 85
gtc gct tat ggt gca gaa tac ttc cgt tgg ttt gcg gaa gaa gca gtg 403
Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe Ala Glu Glu Ala Val
               90 95 100
cgc ctg ccc ggc cgc tac gga cag tca 430
Arg Leu Pro Gly Arg Tyr Gly Gln Ser
               105 110

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&lt;210&gt; 220

&lt;211&gt; 110

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 220

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Val Ser Leu Thr Phe Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile
 1 5 10 15
Thr Glu Leu Glu Asn His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser
 20 25 30
Asp Ala Val Ala Ala Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu
 35 40 45
Arg Ser Val Val Leu Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala
 50 55 60
Gln Glu Leu Ala Glu Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala
 65 70 75 80
Glu Ala Leu Gly Glu Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe

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      85                      90                      95
Ala Glu Glu Ala Val Arg Leu Pro Gly Arg Tyr Gly Gln Ser
      100                      105                      110

<210> 221
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXN03150

<400> 221
tttaacagag tgcgtttcaa tgcctgtagt gttccggcaa ttttgaatgt cgttacggtt 60
accaaggt gaattcctga gctcaccttg tacaagatca gtg gaa gcc cag ttc 115
                               Val Glu Ala Gln Phe
                               1                      5

acc tct ccc ctg ctc aac aat ggg caa acc tgt ttc ctt ggt acc cga 163
Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys Phe Leu Gly Thr Arg
      10                      15                      20

atc ctt gct cca aaa tca cgt tac gcg gaa gta gtc gat gca ttc acc 211
Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val Val Asp Ala Phe Thr
      25                      30                      35

gct ttc gct ggc agc ctg cag gtt gga gtc acg tcc tcc cct gac act 259
Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr Ser Ser Pro Asp Thr
      40                      45                      50

cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc 307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser
      55                      60                      65

tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc 355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly
      70                      75                      80                      85

agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg 403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val
      90                      95                      100

ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc 451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe
      105                      110                      115

gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc 499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile
      120                      125                      130

caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg 547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Gly Thr Val Trp Thr
      135                      140                      145

agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga 595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly

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150          155          160          165
acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga 643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly
          170          175          180

ggg gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt 691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu
          185          190          195

gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata 744
Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
          200          205

tat 747

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<210> 222
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

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<400> 222
Val Glu Ala Gln Phe Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys
  1              5              10              15

Phe Leu Gly Thr Arg Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val
          20          25          30

Val Asp Ala Phe Thr Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr
          35          40          45

Ser Ser Pro Asp Thr Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg
  50              55              60

Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg
  65              70              75              80

Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe
          85          90          95

Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala
          100          105          110

Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp
          115          120          125

Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly
          130          135          140

Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg
          145          150          155          160

Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro
          165          170          175

Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu
          180          185          190

Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
          195          200          205

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<210> 223  
 <211> 881  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(858)  
 <223> RXN01340

<400> 223  
 aaa gtg ggg gag atc atc gcc tcc gtc ttt gat acc ttt aat atc ccg 48  
 Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro  
 1 5 10 15  
 cag ggc ttg gtc tca atc atc acc acc act cga gat gca gag cta tcg 96  
 Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser  
 20 25 30  
 gca gaa ctc atg gct gat cct cgc ttg gct aaa gtc acc ttc act gga 144  
 Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly  
 35 40 45  
 tca acc aac gtg gga cgc atc ctg gtc cgc caa tcc gcg gac cga ctg 192  
 Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu  
 50 55 60  
 ctg cgc acc tcc atg gaa ctc ggc gga aat gca gct ttt gtt atc gac 240  
 Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp  
 65 70 75 80  
 gaa gcc gca gac ctc gac gaa gcc gta tcc ggt gcc atc gcc gca aaa 288  
 Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys  
 85 90 95  
 ctc cgc aac gcc ggc caa gta tgc atc gca gct aac cgt ttc ttg gtt 336  
 Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val  
 100 105 110  
 cat gaa tcc cgc gct gcc gaa ttc acc tca aag ctg gcg aca gcc atg 384  
 His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met  
 115 120 125  
 cag aac act ccc att ggg ccg gtg att tct gcc cgc caa cgc gac cgg 432  
 Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg  
 130 135 140  
 atc gca gca cta gtg gat gaa gcc atc acc gac ggc gcc cgc ctc atc 480  
 Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile  
 145 150 155 160  
 atc ggt ggg gag gtc ccc gac ggc tcc ggc ttc ttc tat cca gcc acc 528  
 Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr  
 165 170 175  
 atc ttg gcc gat gtc cct gca cag tca cgg att gtg cat gag gaa atc 576

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Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
      180                      185                      190

ttc gga cct gtg gcc acc att gcc act ttc acc gac ttg gcc gaa ggc 624
Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
      195                      200                      205

gtt gca caa gca aat tcc acc gaa ttc ggc ctc gca gcc tac gga ttc 672
Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
      210                      215                      220

agc aac aat gtg aaa gca aca cag tac atg gcg gaa cac ttg gaa gcc 720
Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
      225                      230                      235                      240

gga atg gtc gga atc aac aga ggc gcc atc tct gac cca gca gca cct 768
Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
      245                      250                      255

ttt ggc ggc atc gga caa tcc ggc ttc ggc aga gaa ggc gga acc gaa 816
Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
      260                      265                      270

gga atc gaa gaa tat ctc tcc gtg cgt tac ctc gct ttg ccg 858
Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
      275                      280                      285

tgacacatga gctgtccggt gaa 881

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&lt;210&gt; 224

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 224

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Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
  1                      5                      10                      15

Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
      20                      25                      30

Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
      35                      40                      45

Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
      50                      55                      60

Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
      65                      70                      75                      80

Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
      85                      90                      95

Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
      100                      105                      110

His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
      115                      120                      125

Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg

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130	135	140
Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile 145 150 155 160		
Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr 165 170 175		
Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile 180 185 190		
Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly 195 200 205		
Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe 210 215 220		
Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala 225 230 235 240		
Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro 245 250 255		
Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu 260 265 270		
Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro 275 280 285		

&lt;210&gt; 225

&lt;211&gt; 1686

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1663)

&lt;223&gt; RXN01498

&lt;400&gt; 225

cagtggacaa ctacttggcg ggtcttaaat cagctgtgaa ggattctgca taagctgggc 60

accacacgag catcagaacg cgaaacgaag gtaaaagccc atg atc aaa cgt ctt	115
Met Ile Lys Arg Leu	
1 5	

cct tta ggt ccg ctg cct aaa gaa ctt cat cag act ctg ctt gat ctg	163
Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln Thr Leu Leu Asp Leu	
10 15 20	

acc gca aat gcc caa gat gcg gcg aaa gtg gag gtt ata gcg cca ttt	211
Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu Val Ile Ala Pro Phe	
25 30 35	

act ggc gag acc ctc gga ttt ggt ttt gat ggt gat gag caa gac gtc	259
Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly Asp Glu Gln Asp Val	
40 45 50	

gag cat gct ttt gca ctt tca agg gca gcc cag aaa aag tgg gtg cac	307
Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln Lys Lys Trp Val His	

55	60	65	
acc acg gca gtg gaa cgg aag aag atc ttc ctg aag gtt cat gat ctg			355
Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu Lys Val His Asp Leu			
70	75	80	85
gta ttg aaa aac cgt gag ctg ctc atg gac atc gtg cag ttg gaa aca			403
Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile Val Gln Leu Glu Thr			
	90	95	100
ggc aaa aat cga gca tcg gct gcc gat gag gtg ttg gac gtt gcg atc			451
Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val Leu Asp Val Ala Ile			
	105	110	115
acc acc cgc ttc tac gca aac aat gca gga aag ttt tta aat gac aag			499
Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys Phe Leu Asn Asp Lys			
	120	125	130
aaa cgc ccc ggc gcg ctt ccg atc atc acg aaa aac aca caa cag tat			547
Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys Asn Thr Gln Gln Tyr			
	135	140	145
gtg ccc aag gga gtg gtc ggg cag atc acg ccg tgg aat tac cct tta			595
Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro Trp Asn Tyr Pro Leu			
150	155	160	165
act ttg gga gta tct gat gct gtt ccg gcg ctg ctg gca gga aac gca			643
Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu Leu Ala Gly Asn Ala			
	170	175	180
gtg gtg gct aaa cct gac ctc gcg aca cct ttc tcc tgc ttg atc atg			691
Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe Ser Cys Leu Ile Met			
	185	190	195
gtg cac ctg ctc att gaa gcc ggt ctg ccg cgt gat ttg atg cag gtt			739
Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg Asp Leu Met Gln Val			
	200	205	210
gtc acc ggc cct ggc gat att gtt ggc ggt gcg att gca gct cag tgt			787
Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala Ile Ala Ala Gln Cys			
	215	220	225
gat ttc ctc atg ttc act gga tcc acg gcc acg ggc cgg atc ttg ggt			835
Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr Gly Arg Ile Leu Gly			
230	235	240	245
cgg aca atg ggt gag cgt ttg gtg ggt ttc tct gcg gaa tta ggc gga			883
Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser Ala Glu Leu Gly Gly			
	250	255	260
aag aac cct ctt att gtg gcc aag gat gca gat ctg gac aag gtg gaa			931
Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp Leu Asp Lys Val Glu			
	265	270	275
gct gag ctt ccg cag gcg tgt ttt tcc aac tcg ggg caa ttg tgt gtc			979
Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser Gly Gln Leu Cys Val			
	280	285	290
tcc act gaa cgt att tat gtc gag gaa gac gtg tac gag gag gtg att			1027
Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val Tyr Glu Glu Val Ile			
	295	300	305

gca cgg ttt agc aag gcg gcg aaa gcc atg tcc att ggt gcc gga ttt	1075
Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser Ile Gly Ala Gly Phe	
310 315 320 325	
gag tgg aaa tat gag atg ggt tcg ttg atc aat cac gcg cag ctg gat	1123
Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn His Ala Gln Leu Asp	
330 335 340	
cgg gtg agc acc ttt gtt gat cag gct aaa gct gcg ggc gcc acg gtg	1171
Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala Ala Gly Ala Thr Val	
345 350 355	
ctg tgc ggt ggc aag tca cgc cct gat att ggt ccc ttc ttc tat gag	1219
Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly Pro Phe Phe Tyr Glu	
360 365 370	
ccc acg gta ttg gcg gat gtc cca gag ggc acc cca ctg ctc acg gag	1267
Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr Pro Leu Leu Thr Glu	
375 380 385	
gaa gtc ttc ggg ccg gtg gtg ttc atc gaa aag gta gcc aca ctg gaa	1315
Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys Val Ala Thr Leu Glu	
390 395 400 405	
gaa gcc gtc gat aag gca aat ggc acg ccc tac ggc ctg aat gcg tcc	1363
Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr Gly Leu Asn Ala Ser	
410 415 420	
gtc ttt ggg tcg tcg gaa acc ggc aat ctt gtt gca ggc cag ctg gaa	1411
Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val Ala Gly Gln Leu Glu	
425 430 435	
gct ggc ggt atc ggt att aat gat ggc tac gcc gcg acg tgg gcg agc	1459
Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala Ala Thr Trp Ala Ser	
440 445 450	
gtg tcc acg cct ctg ggt ggc atg aag cag tcg ggg ctg ggg cac cgc	1507
Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser Gly Leu Gly His Arg	
455 460 465	
cat ggt gcg gag gga att aca aaa tat gcg gag atc cga aac atc gcg	1555
His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu Ile Arg Asn Ile Ala	
470 475 480 485	
gag cag cgc tgg atg tct atg cgt ggg ccg gcc aaa atg ccg cga aag	1603
Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala Lys Met Pro Arg Lys	
490 495 500	
gtg tac tca gac acc gtg gcc aca gcg cta aag ctg ggc aaa atc ttt	1651
Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys Leu Gly Lys Ile Phe	
505 510 515	
aaa gtt ttg ccg tagcaaaaag ccggaccctt gct	1686
Lys Val Leu Pro	
520	

&lt;210&gt; 226

&lt;211&gt; 521

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 226

Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln  
 1 5 10 15  
 Thr Leu Leu Asp Leu Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu  
 20 25 30  
 Val Ile Ala Pro Phe Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly  
 35 40 45  
 Asp Glu Gln Asp Val Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln  
 50 55 60  
 Lys Lys Trp Val His Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu  
 65 70 75 80  
 Lys Val His Asp Leu Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile  
 85 90 95  
 Val Gln Leu Glu Thr Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val  
 100 105 110  
 Leu Asp Val Ala Ile Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys  
 115 120 125  
 Phe Leu Asn Asp Lys Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys  
 130 135 140  
 Asn Thr Gln Gln Tyr Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro  
 145 150 155 160  
 Trp Asn Tyr Pro Leu Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu  
 165 170 175  
 Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe  
 180 185 190  
 Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg  
 195 200 205  
 Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala  
 210 215 220  
 Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr  
 225 230 235 240  
 Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser  
 245 250 255  
 Ala Glu Leu Gly Gly Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp  
 260 265 270  
 Leu Asp Lys Val Glu Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser  
 275 280 285  
 Gly Gln Leu Cys Val Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val  
 290 295 300  
 Tyr Glu Glu Val Ile Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser



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<210> 227
<211> 1575
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1552)
<223> RXN02674
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<400> 227
atcgacctct agggcagcag tgattgattt cataaaaatc acaagtttgt aactaaaggt 60

acagttgggtg aagtatccac aatcaacttt aggagacctt  gtg act gca aca ttt      115
                                         Val Thr Ala Thr Phe
                                         1                      5

gct gga atc gac gcc acc aaa cac ctc atc gga ggt cag tgg gtg gag      163
Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly Gly Gln Trp Val Glu

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				10				15				20				
gga	aac	tcg	gat	cga	att	tcc	acc	aat	atc	aat	cct	tac	gac	gat	tcc	211
Gly	Asn	Ser	Asp	Arg	Ile	Ser	Thr	Asn	Ile	Asn	Pro	Tyr	Asp	Asp	Ser	
25				30				35								
gta	atc	gcc	gaa	agc	aaa	caa	gct	tcc	att	gct	gat	gtt	gat	gcc	gcg	259
Val	Ile	Ala	Glu	Ser	Lys	Gln	Ala	Ser	Ile	Ala	Asp	Val	Asp	Ala	Ala	
40				45				50								
tat	gaa	gcc	gcg	aag	aag	gcc	cag	gct	gag	tgg	gca	gct	acg	ccc	gct	307
Tyr	Glu	Ala	Ala	Lys	Lys	Ala	Gln	Ala	Glu	Trp	Ala	Ala	Thr	Pro	Ala	
55				60				65								
gcg	gaa	cga	tct	gcc	atc	atc	tac	cgt	gcg	gct	gaa	ctt	ctt	gaa	gag	355
Ala	Glu	Arg	Ser	Ala	Ile	Ile	Tyr	Arg	Ala	Ala	Glu	Leu	Leu	Glu	Glu	
70				75				80				85				
cac	cgg	gag	gaa	atc	gtg	gaa	tgg	ctg	atc	aag	gaa	tcc	ggc	tcg	acg	403
His	Arg	Glu	Glu	Ile	Val	Glu	Trp	Leu	Ile	Lys	Glu	Ser	Gly	Ser	Thr	
90				95				100								
cgt	tcc	aag	gct	aat	ttg	gaa	atc	act	ttg	gca	gga	aac	atc	act	aaa	451
Arg	Ser	Lys	Ala	Asn	Leu	Glu	Ile	Thr	Leu	Ala	Gly	Asn	Ile	Thr	Lys	
105				110				115								
gaa	tcg	gct	tca	ttc	cct	ggt	cgt	gtg	cat	ggt	cga	att	tct	cct	tcg	499
Glu	Ser	Ala	Ser	Phe	Pro	Gly	Arg	Val	His	Gly	Arg	Ile	Ser	Pro	Ser	
120				125				130								
aat	act	ccg	ggc	aaa	gaa	aac	cgt	gtg	tac	cgc	gta	gcc	aag	ggc	gtt	547
Asn	Thr	Pro	Gly	Lys	Glu	Asn	Arg	Val	Tyr	Arg	Val	Ala	Lys	Gly	Val	
135				140				145								
gtc	gga	gtg	att	agt	cca	tgg	aat	ttc	cca	ctg	aac	ctc	tcg	atc	cgc	595
Val	Gly	Val	Ile	Ser	Pro	Trp	Asn	Phe	Pro	Leu	Asn	Leu	Ser	Ile	Arg	
150				155				160				165				
tcg	gtt	gct	cgc	gca	cta	gcc	gtg	ggc	aac	gcc	gta	gtg	att	aag	cct	643
Ser	Val	Ala	Pro	Ala	Leu	Ala	Val	Gly	Asn	Ala	Val	Val	Ile	Lys	Pro	
170				175				180								
gcg	agt	gat	acc	cca	gtt	act	ggt	ggt	gta	att	cct	gca	cga	atc	ttt	691
Ala	Ser	Asp	Thr	Pro	Val	Thr	Gly	Gly	Val	Ile	Pro	Ala	Arg	Ile	Phe	
185				190				195								
gag	gag	gcc	gga	gtt	cct	gca	ggc	gtg	atc	agc	acg	gtt	gcg	ggc	gca	739
Glu	Glu	Ala	Gly	Val	Pro	Ala	Gly	Val	Ile	Ser	Thr	Val	Ala	Gly	Ala	
200				205				210								
gga	tct	gaa	atc	ggt	gat	cac	ttt	gtc	acc	cac	gcc	gtg	cca	aag	ctg	787
Gly	Ser	Glu	Ile	Gly	Asp	His	Phe	Val	Thr	His	Ala	Val	Pro	Lys	Leu	
215				220				225								
att	tct	ttc	acc	ggt	tca	acc	cca	gtc	ggt	cgt	cgt	gtc	ggt	gag	ctg	835
Ile	Ser	Phe	Thr	Gly	Ser	Thr	Pro	Val	Gly	Arg	Arg	Val	Gly	Glu	Leu	
230				235				240				245				
gca	att	aat	ggt	gga	cca	atg	aaa	act	gtt	gca	cta	gag	ctc	ggt	ggc	883
Ala	Ile	Asn	Gly	Gly	Pro	Met	Lys	Thr	Val	Ala	Leu	Glu	Leu	Gly	Gly	
250				255				260								

aac gcg ccg ttc gtt gtg ctt gcc gac gcc gac atc gac gcc gct gcc	931
Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp Ile Asp Ala Ala Ala	
265 270 275	
cag gct gcc gca gtt ggc gct ttc cta cac cag gga cag att tgt atg	979
Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln Gly Gln Ile Cys Met	
280 285 290	
tca atc aac cga gtc att gtt gat gct gca gtt cat gat gaa ttc cta	1027
Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val His Asp Glu Phe Leu	
295 300 305	
gag aag ttc gtt gaa gca gtg aag aac att cca acc ggc gat cca agc	1075
Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro Thr Gly Asp Pro Ser	
310 315 320 325	
gca gaa gga acc ctt gtt gga cct gtc att aat gac agt cag ctc agt	1123
Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn Asp Ser Gln Leu Ser	
330 335 340	
ggt ttg aag gaa aag atc gag ttg gcc aaa aag gaa ggc gca acc gtc	1171
Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys Glu Gly Ala Thr Val	
345 350 355	
cag gtt gaa ggg cca att gaa ggc cga ctg gtt cat ccg cat gtg ttc	1219
Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val His Pro His Val Phe	
360 365 370	
tct gat gtc acc tct gac atg gaa atc gct cgt gag gaa atc ttc gga	1267
Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg Glu Glu Ile Phe Gly	
375 380 385	
cct ctc atc agc gtg ctg aag gcc gat gat gag gca cac gca gca gag	1315
Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu Ala His Ala Ala Glu	
390 395 400 405	
ctg gcc aat gct tcc gac ttt ggt ttg agc gcg gca gtg tgg tcg aag	1363
Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala Ala Val Trp Ser Lys	
410 415 420	
gat att gat cgt gca gcc cag ttt gct ctg cag att gat tcc ggc atg	1411
Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln Ile Asp Ser Gly Met	
425 430 435	
gtt cac atc aat gac ctc acc gtc aac gat gaa cca cac gtg atg ttc	1459
Val His Ile Asn Asp Leu Thr Val Asn Asp Glu Pro His Val Met Phe	
440 445 450	
ggt ggt tca aag aac tct ggc ctc ggc cgc ttc aac ggc gat tgg gcg	1507
Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe Asn Gly Asp Trp Ala	
455 460 465	
atc gag gag ttc acc aca gat cga tgg atc ggc atc aag cgc agc	1552
Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly Ile Lys Arg Ser	
470 475 480	
taattgtttt tcgacgtaac ccc	1575

&lt;211&gt; 484

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 228

Val Thr Ala Thr Phe Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly  
 1 5 10 15

Gly Gln Trp Val Glu Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn  
 20 25 30

Pro Tyr Asp Asp Ser Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala  
 35 40 45

Asp Val Asp Ala Ala Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp  
 50 55 60

Ala Ala Thr Pro Ala Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala  
 65 70 75 80

Glu Leu Leu Glu Glu His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys  
 85 90 95

Glu Ser Gly Ser Thr Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala  
 100 105 110

Gly Asn Ile Thr Lys Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly  
 115 120 125

Arg Ile Ser Pro Ser Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg  
 130 135 140

Val Ala Lys Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu  
 145 150 155 160

Asn Leu Ser Ile Arg Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala  
 165 170 175

Val Val Ile Lys Pro Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile  
 180 185 190

Pro Ala Arg Ile Phe Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser  
 195 200 205

Thr Val Ala Gly Ala Gly Ser Glu Ile Gly Asp His Phe Val Thr His  
 210 215 220

Ala Val Pro Lys Leu Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg  
 225 230 235 240

Arg Val Gly Glu Leu Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala  
 245 250 255

Leu Glu Leu Gly Gly Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp  
 260 265 270

Ile Asp Ala Ala Ala Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln  
 275 280 285

Gly Gln Ile Cys Met Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val  
 290 295 300

His Asp Glu Phe Leu Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro  
 305 310 315 320  
 Thr Gly Asp Pro Ser Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn  
 325 330 335  
 Asp Ser Gln Leu Ser Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys  
 340 345 350  
 Glu Gly Ala Thr Val Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val  
 355 360 365  
 His Pro His Val Phe Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg  
 370 375 380  
 Glu Glu Ile Phe Gly Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu  
 385 390 395 400  
 Ala His Ala Ala Glu Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala  
 405 410 415  
 Ala Val Trp Ser Lys Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln  
 420 425 430  
 Ile Asp Ser Gly Met Val His Ile Asn Asp Leu Thr Val Asn Asp Glu  
 435 440 445  
 Pro His Val Met Phe Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe  
 450 455 460  
 Asn Gly Asp Trp Ala Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly  
 465 470 475 480  
 Ile Lys Arg Ser

<210> 229  
 <211> 2034  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2011)  
 <223> RXN00868

<400> 229  
 cgatgaccca gcgcacgcct gggttcgaga tacatggacc gggcaagcat ttgatgatcg 60  
 cttgccatat gagaacgcaa acaaggaggg ataaaatttc atg gct gaa acg aag 115  
 Met Ala Glu Thr Lys  
 1 5  
 aga atg aca gtt agc cag gca ctg gtt gaa ttc ctt ggt cac cag tgg 163  
 Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe Leu Gly His Gln Trp  
 10 15 20  
 act gtc gac ggc gat atc cgc gag cgc acc att cca ggc atg ttc gga 211  
 Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile Pro Gly Met Phe Gly

25				30				35								
att Ile	ttc Phe	gga Gly 40	cac His	gga Gly	aac Asn	gtt Val	gct Ala 45	ggc Gly	att Ile	ggc Gly	cag Gln	gca Ala 50	ctc Leu	aag Lys	cag Gln	259
tac Tyr	aac Asn 55	gtt Val	gaa Glu	caa Gln	cct Pro	gag Glu 60	ctc Leu	atg Met	ccg Pro	tac Tyr	tac Tyr 65	cag Gln	gct Ala	cgt Arg	aat Asn	307
gag Glu 70	cag Gln	gcg Ala	atg Met	gtg Val	cac His 75	cag Gln	tct Ser	gtt Val	gga Gly	tat Tyr 80	gca Ala	cgc Arg	atg Met	cac His	cgc Arg 85	355
cgt Arg	cgt Arg	ggc Gly	aca Thr	tac Tyr 90	gca Ala	tct Ser	gcc Ala	gca Ala	tct Ser 95	gtt Val	gga Gly	ccc Pro	ggc Gly	gcg Ala 100	acc Thr	403
aac Asn	ctg Leu	tta Leu	acc Thr 105	ggt Gly	gcg Ala	gct Ala	ctt Leu	gct Ala 110	acc Thr	acc Thr	aac Asn	cggt Arg	ttg Leu 115	cca Pro	gcg Ala	451
ttg Leu	ctg Leu	ctg Leu 120	cct Pro	agt Ser	gat Asp	act Thr	ttt Phe 125	gcc Ala	acc Thr	cgct Arg	gtg Val	gcg Ala 130	gat Asp	cca Pro	gtg Val	499
ttg Leu	cag Gln 135	cag Gln	ttg Leu	gag Glu	cag Gln	cca Pro 140	tgg Trp	gat Asp	atc Ile	ggg Gly	ctg Leu 145	acg Thr	gtt Val	aat Asn	gat Asp	547
gct Ala 150	ttc Phe	cgct Arg	cct Pro	gtg Val	tct Ser 155	aag Lys	ttc Phe	ttt Phe	gat Asp 160	cggt Arg	gtg Val	cag Gln	cgct Arg	ccg Pro	gag Glu 165	595
cag Gln	ttg Leu	ttc Phe	tct Ser	att Ile 170	gcg Ala	ttg Leu	gct Ala	gcg Ala	atg Met 175	cggt Arg	gtg Val	ttg Leu	act Thr	gat Asp 180	ccc Pro	643
gca Ala	gaa Glu	acc Thr	ggt Gly 185	gcg Ala	gtc Val	acc Thr	att Ile	gcg Ala 190	ctt Leu	cca Pro	gaa Glu	gat Asp	gtg Val 195	cag Gln	gct Ala	691
gaa Glu	atg Met	ctc Leu 200	gat Asp	gtg Val	ccg Pro	gtg Val	gag Glu 205	ttc Phe	ttg Leu	cag Gln	gat Asp	cggt Arg 210	gag Glu	tgg Trp	cac His	739
att Ile	agg Arg 215	cgct Arg	cca Pro	cggt Arg	cca Pro	gag Glu 220	cggt Arg	gct Ala	gcg Ala	ttg Leu	gct Ala 225	cggt Arg	gcg Ala	att Ile	gaa Glu	787
gtc Val 230	atc Ile	aaa Lys	aac Asn	gct Ala	aag Lys 235	aat Asn	ccg Pro	atg Met	atc Ile	att Ile 240	gct Ala	gggt Gly	ggc Gly	gga Gly	gtg Val 245	835
ttg Leu	tac Tyr	tcc Ser	gat Asp	gcg Ala 250	gaa Glu	acg Thr	cag Gln	ctg Leu	cag Gln 255	gca Ala	ctt Leu	gtg Val	gag Glu	cag Gln 260	act Thr	883
ggc Gly	att Ile	cca Pro	gtg Val 265	ggt Gly	acc Thr	tcc Ser	caa Gln	gct Ala 270	gggt Gly	gggt Gly	ggc Gly	gtg Val	ttg Leu 275	gcg Ala	tgg Trp	931

gat cat gca caa aac tta ggt ggt gtg ggt gcc acc gga acg ttg gct Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala Thr Gly Thr Leu Ala 280 285 290	979
gcc aac cgc att gcg ggt gat gct gat gtg atc atc ggt atc ggt act Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile Ile Gly Ile Gly Thr 295 300 305	1027
cgt tac agc gat ttc acc acc gca tct cgc act gcg ttc caa aac cct Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr Ala Phe Gln Asn Pro 310 315 320 325	1075
gat gtc acc ttc atc aac atc aat gtt gct tcc ttc gat gct tac aag Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser Phe Asp Ala Tyr Lys 330 335 340	1123
cat ggc act cag ttg cct gtg att gca gat gca cgc gag gca att gtg His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala Arg Glu Ala Ile Val 345 350 355	1171
gag ctt gct gaa gcc ctg cag gga ttc acc gtg gca gag gat tac gcg Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val Ala Glu Asp Tyr Ala 360 365 370	1219
cag cgc atc gcg aag gaa aag gct gcg tgg gac gca gaa gta gat aag Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp Ala Glu Val Asp Lys 375 380 385	1267
tct ttt gcc ccc tcc ggt ctt gcg ctg cct gga cag ccg gag atc atc Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly Gln Pro Glu Ile Ile 390 395 400 405	1315
ggc gcg gtg cag gcg tcg aca agc gaa aaa gac gtc att gtg cag gcc Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp Val Ile Val Gln Ala 410 415 420	1363
gct gga tcc ttg cct ggt gac ctg cac aag ctg tgg cgt gtg cgc gat Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu Trp Arg Val Arg Asp 425 430 435	1411
gcg ctg ggc tac cac gtg gaa tat gcg ttc tcg tgc atg ggc tat gaa Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser Cys Met Gly Tyr Glu 440 445 450	1459
atc gcg ggc ggt atc ggc gcg aag cgt gga ctt gat gcc gca ggc gat Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu Asp Ala Ala Gly Asp 455 460 465	1507
gac cgc gac gtg gtg atc atg gtt ggt gat ggg tcc tac ctc atg ctc Asp Arg Asp Val Val Ile Met Val Gly Asp Gly Ser Tyr Leu Met Leu 470 475 480 485	1555
aac act gag ctg gtc acg gcc gtg gca gaa ggt atc aag gtg att gtg Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly Ile Lys Val Ile Val 490 495 500	1603
gtg ctc atc caa aac cac ggt tat gcc tcc atc ggc cac ctg tct gaa Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile Gly His Leu Ser Glu 505 510 515	1651

act gtc ggt tgc cag cgt ttt ggt act tgg tac cgc gaa tat gac gct 1699  
 Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr Arg Glu Tyr Asp Ala  
 520 525 530

gag gcg aaa aac ttc cag ggc gag cag att ctg cct gtt gac ctg gcg 1747  
 Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu Pro Val Asp Leu Ala  
 535 540 545

atg aat gca cgc agc tac ggc atg gat gtc att gaa gtg gaa cca agc 1795  
 Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile Glu Val Glu Pro Ser  
 550 555 560 565

gcg aat gcg atc gag gat ctc aaa gca gcg atg gca acc gcg aag gct 1843  
 Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met Ala Thr Ala Lys Ala  
 570 575 580

tcg gag aaa tcc acc ttc atc cac atc aac agc gat ccg ttg atc tac 1891  
 Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser Asp Pro Leu Ile Tyr  
 585 590 595

gca cca gac ggt gct ggt tgg tgg gac gtg ccg gtg tcg gag acg tcc 1939  
 Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro Val Ser Glu Thr Ser  
 600 605 610

act ctg gat agc acc aac gcg gct cgt gaa gat tac ctg aaa aac caa 1987  
 Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp Tyr Leu Lys Asn Gln  
 615 620 625

gcc ctc cag cgt ccg ctg ctc ggc taaaccagtt ggctaaacca aaa 2034  
 Ala Leu Gln Arg Pro Leu Leu Gly  
 630 635

&lt;210&gt; 230

&lt;211&gt; 637

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 230

Met Ala Glu Thr Lys Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe  
 1 5 10 15

Leu Gly His Gln Trp Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile  
 20 25 30

Pro Gly Met Phe Gly Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly  
 35 40 45

Gln Ala Leu Lys Gln Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr  
 50 55 60

Tyr Gln Ala Arg Asn Glu Gln Ala Met Val His Gln Ser Val Gly Tyr  
 65 70 75 80

Ala Arg Met His Arg Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val  
 85 90 95

Gly Pro Gly Ala Thr Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr  
 100 105 110

Asn Arg Leu Pro Ala Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg



115					120					125					
Val	Ala	Asp	Pro	Val	Leu	Gln	Gln	Leu	Glu	Gln	Pro	Trp	Asp	Ile	Gly
130					135					140					
Leu	Thr	Val	Asn	Asp	Ala	Phe	Arg	Pro	Val	Ser	Lys	Phe	Phe	Asp	Arg
145					150					155					160
Val	Gln	Arg	Pro	Glu	Gln	Leu	Phe	Ser	Ile	Ala	Leu	Ala	Ala	Met	Arg
				165					170					175	
Val	Leu	Thr	Asp	Pro	Ala	Glu	Thr	Gly	Ala	Val	Thr	Ile	Ala	Leu	Pro
			180					185						190	
Glu	Asp	Val	Gln	Ala	Glu	Met	Leu	Asp	Val	Pro	Val	Glu	Phe	Leu	Gln
		195					200					205			
Asp	Arg	Glu	Trp	His	Ile	Arg	Arg	Pro	Arg	Pro	Glu	Arg	Ala	Ala	Leu
		210				215					220				
Ala	Arg	Ala	Ile	Glu	Val	Ile	Lys	Asn	Ala	Lys	Asn	Pro	Met	Ile	Ile
225					230					235					240
Ala	Gly	Gly	Gly	Val	Leu	Tyr	Ser	Asp	Ala	Glu	Thr	Gln	Leu	Gln	Ala
				245					250					255	
Leu	Val	Glu	Gln	Thr	Gly	Ile	Pro	Val	Gly	Thr	Ser	Gln	Ala	Gly	Gly
			260					265					270		
Gly	Val	Leu	Ala	Trp	Asp	His	Ala	Gln	Asn	Leu	Gly	Gly	Val	Gly	Ala
		275					280					285			
Thr	Gly	Thr	Leu	Ala	Ala	Asn	Arg	Ile	Ala	Gly	Asp	Ala	Asp	Val	Ile
	290					295					300				
Ile	Gly	Ile	Gly	Thr	Arg	Tyr	Ser	Asp	Phe	Thr	Thr	Ala	Ser	Arg	Thr
305					310					315					320
Ala	Phe	Gln	Asn	Pro	Asp	Val	Thr	Phe	Ile	Asn	Ile	Asn	Val	Ala	Ser
				325					330					335	
Phe	Asp	Ala	Tyr	Lys	His	Gly	Thr	Gln	Leu	Pro	Val	Ile	Ala	Asp	Ala
			340					345					350		
Arg	Glu	Ala	Ile	Val	Glu	Leu	Ala	Glu	Ala	Leu	Gln	Gly	Phe	Thr	Val
		355					360					365			
Ala	Glu	Asp	Tyr	Ala	Gln	Arg	Ile	Ala	Lys	Glu	Lys	Ala	Ala	Trp	Asp
		370				375					380				
Ala	Glu	Val	Asp	Lys	Ser	Phe	Ala	Pro	Ser	Gly	Leu	Ala	Leu	Pro	Gly
385					390					395					400
Gln	Pro	Glu	Ile	Ile	Gly	Ala	Val	Gln	Ala	Ser	Thr	Ser	Glu	Lys	Asp
				405					410					415	
Val	Ile	Val	Gln	Ala	Ala	Gly	Ser	Leu	Pro	Gly	Asp	Leu	His	Lys	Leu
			420					425					430		
Trp	Arg	Val	Arg	Asp	Ala	Leu	Gly	Tyr	His	Val	Glu	Tyr	Ala	Phe	Ser
		435					440					445			

Cys Met Gly Tyr Glu Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu  
 450 455 460  
 Asp Ala Ala Gly Asp Asp Arg Asp Val Val Ile Met Val Gly Asp Gly  
 465 470 475 480  
 Ser Tyr Leu Met Leu Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly  
 485 490 495  
 Ile Lys Val Ile Val Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile  
 500 505 510  
 Gly His Leu Ser Glu Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr  
 515 520 525  
 Arg Glu Tyr Asp Ala Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu  
 530 535 540  
 Pro Val Asp Leu Ala Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile  
 545 550 555 560  
 Glu Val Glu Pro Ser Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met  
 565 570 575  
 Ala Thr Ala Lys Ala Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser  
 580 585 590  
 Asp Pro Leu Ile Tyr Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro  
 595 600 605  
 Val Ser Glu Thr Ser Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp  
 610 615 620  
 Tyr Leu Lys Asn Gln Ala Leu Gln Arg Pro Leu Leu Gly  
 625 630 635

&lt;210&gt; 231

&lt;211&gt; 1142

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1119)

&lt;223&gt; RXN01143

&lt;400&gt; 231

atc cca gtt gtc acc acc ttg atg gct ttg ggt act ttc cca gag tct 48  
 Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser  
 1 5 10 15

cac gag ctg cac atg ggt atg cca ggc atg cat ggc act gtg tcc gct 96  
 His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala  
 20 25 30

gtt ggt gca ctg cag cgc agc gac ctg ctg att gct atc ggc tcc cgc 144  
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg  
 35 40 45

ttt gat gac cgc gtc acc ggt gac gtt gac acc ttc gcg cct gac gcc	192
Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala	
50 55 60	
aag atc att cac gcc gac att gat cct gcc gaa atc ggc aag atc aag	240
Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys	
65 70 75 80	
cag gtt gag gtt cca atc gtg ggc gat gcc cgc gaa gtt ctt gct cgt	288
Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg	
85 90 95	
ctg ctg gaa acc acc aag gca agc aag gca gag acc gag gac atc tcc	336
Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser	
100 105 110	
gag tgg gtt gac tac ctc aag ggc ctc aag gca cgt ttc ccg cgt ggc	384
Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly	
115 120 125	
tac gac gag cag cca ggc gat ctg ctg gca cca cag ttt gtc att gaa	432
Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu	
130 135 140	
acc ctg tcc aag gaa gtt ggc ccc gac gca att tac tgc gcc ggc gtt	480
Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val	
145 150 155 160	
ggc cag cac caa atg tgg gca gct cag ttc gtt gac ttt gaa aag cca	528
Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro	
165 170 175	
cgc acc tgg ctc aac tcc ggt gga ctg ggc acc atg ggc tac gca gtt	576
Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val	
180 185 190	
cct gcg gcc ctt gga gca aag gct ggc gca cct gac aag gaa gtc tgg	624
Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp	
195 200 205	
gct atc gac ggc gac ggc tgt ttc cag atg acc aac cag gaa ctc acc	672
Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr	
210 215 220	
acc gcc gca gtt gaa ggt ttc ccc att aag atc gca cta atc aac aac	720
Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn	
225 230 235 240	
gga aaa cct ggg gca tgg gtt cgc caa tgg cag acc cta ttc tat gaa	768
Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu	
245 250 255	
gga cgg tac tca aat act aaa ctt cgt aac cag ggc gag tac atg ccc	816
Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro	
260 265 270	
gac ttt gtt acc ctt tct gag gga ctt ggc tgt gtt gcc atc cgc gtc	864
Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val	
275 280 285	
acc aaa gcg gag gaa gta ctg cca gcc atc caa aag gct cga gag atc	912

Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile  
 290 295 300  
 aac gac cgc cca gta gtc atc gac ttc atc gtc ggt gaa gac gca cag 960  
 Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln  
 305 310 315 320  
 gta tgg cca atg gtg tct gct gga tca tcc aac tcc gat atc cag tac 1008  
 Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr  
 325 330 335  
 gca ctc gga ttg cgc cca ttc ttt gat ggt gat gaa tct gca gca gaa 1056  
 Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu  
 340 345 350  
 gat cct gcc gac att cac gaa gcc gtc agc gac att gat gcc gcc gtt 1104  
 Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val  
 355 360 365  
 gaa tcg acc gag gca taaggagaga cccaagatgg cta 1142  
 Glu Ser Thr Glu Ala  
 370

&lt;210&gt; 232

&lt;211&gt; 373

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 232

Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser  
 1 5 10 15  
 His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala  
 20 25 30  
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg  
 35 40 45  
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala  
 50 55 60  
 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys  
 65 70 75 80  
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg  
 85 90 95  
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser  
 100 105 110  
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly  
 115 120 125  
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu  
 130 135 140  
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val  
 145 150 155 160  
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro

165										170					175				
Arg	Thr	Trp	Leu	Asn	Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Tyr	Ala	Val				
			180					185					190						
Pro	Ala	Ala	Leu	Gly	Ala	Lys	Ala	Gly	Ala	Pro	Asp	Lys	Glu	Val	Trp				
			195				200					205							
Ala	Ile	Asp	Gly	Asp	Gly	Cys	Phe	Gln	Met	Thr	Asn	Gln	Glu	Leu	Thr				
			210			215					220								
Thr	Ala	Ala	Val	Glu	Gly	Phe	Pro	Ile	Lys	Ile	Ala	Leu	Ile	Asn	Asn				
					230					235					240				
Gly	Lys	Pro	Gly	Ala	Trp	Val	Arg	Gln	Trp	Gln	Thr	Leu	Phe	Tyr	Glu				
				245					250					255					
Gly	Arg	Tyr	Ser	Asn	Thr	Lys	Leu	Arg	Asn	Gln	Gly	Glu	Tyr	Met	Pro				
			260					265					270						
Asp	Phe	Val	Thr	Leu	Ser	Glu	Gly	Leu	Gly	Cys	Val	Ala	Ile	Arg	Val				
			275				280					285							
Thr	Lys	Ala	Glu	Glu	Val	Leu	Pro	Ala	Ile	Gln	Lys	Ala	Arg	Glu	Ile				
			290			295					300								
Asn	Asp	Arg	Pro	Val	Val	Ile	Asp	Phe	Ile	Val	Gly	Glu	Asp	Ala	Gln				
					310					315					320				
Val	Trp	Pro	Met	Val	Ser	Ala	Gly	Ser	Ser	Asn	Ser	Asp	Ile	Gln	Tyr				
				325					330					335					
Ala	Leu	Gly	Leu	Arg	Pro	Phe	Phe	Asp	Gly	Asp	Glu	Ser	Ala	Ala	Glu				
			340					345					350						
Asp	Pro	Ala	Asp	Ile	His	Glu	Ala	Val	Ser	Asp	Ile	Asp	Ala	Ala	Val				
			355				360					365							
Glu	Ser	Thr	Glu	Ala															
			370																

&lt;210&gt; 233

&lt;211&gt; 793

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(793)

&lt;223&gt; RXN01146

&lt;400&gt; 233

tatttagtaa aggagccaga aagtcgtgaa tgtggcagct tctcaacagc ccaactcccg 60

cacggttgca	agccgtgggc	gatccgccgc	ccctgagcgg	atg	aca	ggt	gca	aag	115
				Met	Thr	Gly	Ala	Lys	
				1				5	

gca	att	gtt	cga	tcg	ctc	gag	gag	ctt	aac	gcc	gac	atc	gtg	ttc	ggt	163
Ala	Ile	Val	Arg	Ser	Leu	Glu	Glu	Leu	Asn	Ala	Asp	Ile	Val	Phe	Gly	

10										15					20					
att	cct	ggt	ggt	gcg	gtg	cta	ccg	gtg	tat	gac	ccg	ctc	tat	tcc	tcc	211				
Ile	Pro	Gly	Gly	Ala	Val	Leu	Pro	Val	Tyr	Asp	Pro	Leu	Tyr	Ser	Ser					
25				30				35												
aca	aag	gtg	cgc	cac	gtc	ttg	gtg	cgc	cac	gag	cag	ggc	gca	ggc	cac	259				
Thr	Lys	Val	Arg	His	Val	Leu	Val	Arg	His	Glu	Gln	Gly	Ala	Gly	His					
40				45				50												
gca	gca	acc	ggc	tac	gcg	cag	gtt	act	gga	cgc	gtt	ggc	gtc	tgc	att	307				
Ala	Ala	Thr	Gly	Tyr	Ala	Gln	Val	Thr	Gly	Arg	Val	Gly	Val	Cys	Ile					
55				60				65												
gca	acc	tct	ggc	cca	gga	gca	acc	aac	ttg	gtt	acc	cca	atc	gct	gat	355				
Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	Thr	Pro	Ile	Ala	Asp					
70				75				80				85								
gca	aac	ttg	gac	tcc	gtt	ccc	atg	gtt	gcc	atc	acc	ggc	cag	gtc	gga	403				
Ala	Asn	Leu	Asp	Ser	Val	Pro	Met	Val	Ala	Ile	Thr	Gly	Gln	Val	Gly					
90				95				100												
agt	ggc	ctg	ctg	ggt	acc	gac	gct	ttc	cag	gaa	gcc	gat	atc	cgc	ggc	451				
Ser	Gly	Leu	Leu	Gly	Thr	Asp	Ala	Phe	Gln	Glu	Ala	Asp	Ile	Arg	Gly					
105				110				115												
atc	acc	atg	cca	gtg	acc	aag	cac	aac	ttc	atg	gtc	acc	aac	cct	aac	499				
Ile	Thr	Met	Pro	Val	Thr	Lys	His	Asn	Phe	Met	Val	Thr	Asn	Pro	Asn					
120				125				130												
gac	att	cca	cag	gca	ttg	gct	gag	gca	ttc	cac	ctc	gcg	att	act	ggt	547				
Asp	Ile	Pro	Gln	Ala	Leu	Ala	Glu	Ala	Phe	His	Leu	Ala	Ile	Thr	Gly					
135				140				145												
cgc	cct	ggc	cct	gtt	ctg	gtg	gat	att	cct	aag	gat	gtc	cag	aac	gct	595				
Arg	Pro	Gly	Pro	Val	Leu	Val	Asp	Ile	Pro	Lys	Asp	Val	Gln	Asn	Ala					
150				155				160				165								
gaa	ttg	gat	ttc	gtc	tgg	cca	cca	aag	atc	gac	ctg	cca	ggc	tac	cgc	643				
Glu	Leu	Asp	Phe	Val	Trp	Pro	Pro	Lys	Ile	Asp	Leu	Pro	Gly	Tyr	Arg					
170				175				180												
cca	gtt	tca	aca	cca	cat	gct	cgc	cag	atc	gag	cag	gca	gtc	aag	ctg	691				
Pro	Val	Ser	Thr	Pro	His	Ala	Arg	Gln	Ile	Glu	Gln	Ala	Val	Lys	Leu					
185				190				195												
atc	ggt	gag	gcc	aag	aag	ccc	gtc	ctt	tac	gtt	ggt	ggt	ggc	gta	atc	739				
Ile	Gly	Glu	Ala	Lys	Lys	Pro	Val	Leu	Tyr	Val	Gly	Gly	Gly	Val	Ile					
200				205				210												
aag	gct	gac	gca	cac	gaa	gag	ctt	cgt	gcg	ttc	gct	gag	tac	acc	ggc	787				
Lys	Ala	Asp	Ala	His	Glu	Glu	Leu	Arg	Ala	Phe	Ala	Glu	Tyr	Thr	Gly					
215				220				225												
atc	cca															793				
Ile	Pro																			
230																				

&lt;210&gt; 234

&lt;211&gt; 231

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 234

Met Thr Gly Ala Lys Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala  
 1 5 10 15

Asp Ile Val Phe Gly Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp  
 20 25 30

Pro Leu Tyr Ser Ser Thr Lys Val Arg His Val Leu Val Arg His Glu  
 35 40 45

Gln Gly Ala Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg  
 50 55 60

Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val  
 65 70 75 80

Thr Pro Ile Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile  
 85 90 95

Thr Gly Gln Val Gly Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu  
 100 105 110

Ala Asp Ile Arg Gly Ile Thr Met Pro Val Thr Lys His Asn Phe Met  
 115 120 125

Val Thr Asn Pro Asn Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His  
 130 135 140

Leu Ala Ile Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys  
 145 150 155 160

Asp Val Gln Asn Ala Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp  
 165 170 175

Leu Pro Gly Tyr Arg Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu  
 180 185 190

Gln Ala Val Lys Leu Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val  
 195 200 205

Gly Gly Gly Val Ile Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe  
 210 215 220

Ala Glu Tyr Thr Gly Ile Pro  
 225 230

&lt;210&gt; 235

&lt;211&gt; 639

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(616)

&lt;223&gt; RXN01144

&lt;400&gt; 235

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ggtgatgaat ctgcagcaga agatcctgcc gacattcacg aagccgtcag cgacattgat 60
gccgccgttg aatcgaccga ggcataagga gagacccaag atg gct aat tct gac 115
                                         Met Ala Asn Ser Asp
                                         1 5

gtc acc cgc cac atc ctg tcc gta ctc gtt cag gac gta gac gga atc 163
Val Thr Arg His Ile Leu Ser Val Leu Val Gln Asp Val Asp Gly Ile
                        10 15 20

att tcc cgc gta tca ggt atg ttc acc cga cgc gca ttc aac ctc gtg 211
Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg Ala Phe Asn Leu Val
                        25 30 35

ttc ctc gtg tct gca aag acc gaa aca cac ggc atc aac cgc atc acg 259
Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly Ile Asn Arg Ile Thr
                        40 45 50

gtt gtt gtc gac gcc gac gag ctc aac att gag cag atc acc aag cag 307
Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu Gln Ile Thr Lys Gln
                        55 60 65

ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg cga ctt gat gaa gag 355
Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val Arg Leu Asp Glu Glu
                        70 75 80 85

acc act atc gcc cgc gca atc atg ctg gtt aag gtc tct gcg gac agc 403
Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys Val Ser Ala Asp Ser
                        90 95 100

acc aac cgt ccg cag atc gtc gac gcc gcg aac atc ttc cgc gcc cga 451
Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn Ile Phe Arg Ala Arg
                        105 110 115

gtc gtc gac gtg gct cca gac tct gtg gtt att gaa tcc aca ggc acc 499
Val Val Asp Val Ala Pro Asp Ser Val Val Ile Glu Ser Thr Gly Thr
                        120 125 130

cca ggc aag ctc cgc gca ctg ctt gac gtg atg gaa cca ttc gga atc 547
Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met Glu Pro Phe Gly Ile
                        135 140 145

cgc gaa ctg atc caa tcc gga cag att gca ctc aac cgc ggt ccg aag 595
Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu Asn Arg Gly Pro Lys
                        150 155 160 165

acc atg gct ccg gcc aag atc taaacagcaa ttaatctgat tgc 639
Thr Met Ala Pro Ala Lys Ile
                        170

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&lt;210&gt; 236

&lt;211&gt; 172

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 236

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Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
 1 5 10 15

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Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg

```



20					25					30					
Ala	Phe	Asn	Leu	Val	Phe	Leu	Val	Ser	Ala	Lys	Thr	Glu	Thr	His	Gly
		35					40					45			
Ile	Asn	Arg	Ile	Thr	Val	Val	Val	Asp	Ala	Asp	Glu	Leu	Asn	Ile	Glu
	50					55					60				
Gln	Ile	Thr	Lys	Gln	Leu	Asn	Lys	Leu	Ile	Pro	Val	Leu	Lys	Val	Val
	65					70					75				80
Arg	Leu	Asp	Glu	Glu	Thr	Thr	Ile	Ala	Arg	Ala	Ile	Met	Leu	Val	Lys
				85					90					95	
Val	Ser	Ala	Asp	Ser	Thr	Asn	Arg	Pro	Gln	Ile	Val	Asp	Ala	Ala	Asn
			100					105					110		
Ile	Phe	Arg	Ala	Arg	Val	Val	Asp	Val	Ala	Pro	Asp	Ser	Val	Val	Ile
		115					120					125			
Glu	Ser	Thr	Gly	Thr	Pro	Gly	Lys	Leu	Arg	Ala	Leu	Leu	Asp	Val	Met
		130				135					140				
Glu	Pro	Phe	Gly	Ile	Arg	Glu	Leu	Ile	Gln	Ser	Gly	Gln	Ile	Ala	Leu
	145					150					155				160
Asn	Arg	Gly	Pro	Lys	Thr	Met	Ala	Pro	Ala	Lys	Ile				
			165						170						

&lt;210&gt; 237

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(874)

&lt;223&gt; RXA02474

&lt;400&gt; 237

tgctggtcta ttgtggcgac cgagggcctt tgaaggttcg acaaactgta taaggccttg 60

aatcttgaga	atttattttg	aggaagcaag	aggaagtgtc	atg	agc	aaa	gtt	gca	115
				Met	Ser	Lys	Val	Ala	
				1				5	

atg	gtt	acc	ggt	ggt	gca	caa	ggc	atc	ggt	cgt	gga	att	tca	gag	aag	163
Met	Val	Thr	Gly	Gly	Ala	Gln	Gly	Ile	Gly	Arg	Gly	Ile	Ser	Glu	Lys	
			10					15						20		

ctg	gca	gca	gat	ggt	ttc	gat	att	gcc	gta	gcc	gac	ctg	cca	caa	cag	211
Leu	Ala	Ala	Asp	Gly	Phe	Asp	Ile	Ala	Val	Ala	Asp	Leu	Pro	Gln	Gln	
			25					30						35		

gaa	gaa	caa	gct	gca	gag	acc	atc	aag	ttg	att	gaa	gct	gca	ggt	caa	259
Glu	Glu	Gln	Ala	Ala	Glu	Thr	Ile	Lys	Leu	Ile	Glu	Ala	Ala	Gly	Gln	
		40					45					50				

aag	gct	gta	ttc	gtt	gga	tta	gat	gtc	acc	gat	aag	gct	aat	ttc	gac	307
Lys	Ala	Val	Phe	Val	Gly	Leu	Asp	Val	Thr	Asp	Lys	Ala	Asn	Phe	Asp	

55	60	65	
agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta			355
Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu			
70	75	80	85
gta aac aac gcc ggc atc gca caa att aag cca ctt ctg gaa gtc acc			403
Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr			
	90	95	100
gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt			451
Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe			
	105	110	115
ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa			499
Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys			
	120	125	130
ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca			547
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro			
	135	140	145
atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc			595
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr			
	150	155	160
cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc			643
Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala			
	170	175	180
tac gca cct ggc atc gtg ggc acc gga atg tgg gag caa atc gat gcc			691
Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp Glu Gln Ile Asp Ala			
	185	190	195
gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag			739
Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu			
	200	205	210
tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta			787
Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val			
	215	220	225
gcc ggt ctg gtt tcg ttc ctg gct tct gaa aac tcc aac tac atc acc			835
Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr			
	230	235	240
gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac tagggggtgc			884
Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn			
	250	255	
tttcccgcac tca			897

&lt;210&gt; 238

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 238

Met	Ser	Lys	Val	Ala	Met	Val	Thr	Gly	Gly	Ala	Gln	Gly	Ile	Gly	Arg
1				5				10					15		

Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala  
                   20                  25                  30  
 Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile  
                   35                  40                  45  
 Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp  
                   50                  55                  60  
 Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly  
                   65                  70                  75                  80  
 Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro  
                   85                  90                  95  
 Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn  
                   100                  105                  110  
 Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp  
                   115                  120                  125  
 Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala  
                   130                  135                  140  
 Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala  
                   145                  150                  155                  160  
 Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly  
                   165                  170                  175  
 His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp  
                   180                  185                  190  
 Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly  
                   195                  200                  205  
 Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser  
                   210                  215                  220  
 Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn  
                   225                  230                  235                  240  
 Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu  
                   245                  250                  255

Tyr Asn

<210> 239

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXA02453

<400> 239

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tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc 115  
Met Lys Ser Ile Phe  
1 5  
att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163  
Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe  
10 15 20  
ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211  
Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr  
25 30 35  
tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc 259  
Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser  
40 45 50  
gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307  
Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly  
55 60 65  
acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355  
Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro  
70 75 80 85  
ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403  
Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn  
90 95 100  
gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg 451  
Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala  
105 110 115  
cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg 499  
Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val  
120 125 130  
tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc 547  
Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val  
135 140 145  
gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att 595  
Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile  
150 155 160 165  
cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac 643  
Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn  
170 175 180  
ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg 691  
Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro  
185 190 195  
gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct ccg 739  
Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg  
200 205 210  
tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg 787  
Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala  
215 220 225

ctg tat ctc atg aaa tct ctg tcg cct gat cgg gta gcg atg tgt ttt 835  
 Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe  
 230 235 240 245

gcg cga cta atc gcc gga taaatgaatt gattatttta ggc 876  
 Ala Arg Leu Ile Ala Gly  
 250

<210> 240

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala  
 1 5 10 15

Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp  
 20 25 30

Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu  
 35 40 45

Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala  
 50 55 60

Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val  
 65 70 75 80

Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys  
 85 90 95

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala  
 100 105 110

His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser  
 115 120 125

Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala  
 130 135 140

Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp  
 145 150 155 160

Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys  
 165 170 175

Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly  
 180 185 190

Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val  
 195 200 205

His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser  
 210 215 220

Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg  
 225 230 235 240

<400> 241																
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gatagcgcgc	tcagaagttc	tttagtgaaa	gcagaaccaa	atg	ccc	aaa	tac	att	115							
				Met	Pro	Lys	Tyr	Ile	5							
				1												
gcc	atg	cag	gta	tcc	gaa	tcc	ggt	gca	ccg	tta	gcc	gcg	aat	ctc	gtg	163
Ala	Met	Gln	Val	Ser	Glu	Ser	Gly	Ala	Pro	Leu	Ala	Ala	Asn	Leu	Val	
				10					15					20		
caa	cct	gct	ccg	ttg	aaa	tcg	agg	gaa	gtc	cgc	gtg	gaa	atc	gct	gct	211
Gln	Pro	Ala	Pro	Leu	Lys	Ser	Arg	Glu	Val	Arg	Val	Glu	Ile	Ala	Ala	
				25				30					35			
agt	ggt	gtg	tgc	cat	gca	gat	att	ggc	acg	gca	gca	gca	tcg	ggg	aag	259
Ser	Gly	Val	Cys	His	Ala	Asp	Ile	Gly	Thr	Ala	Ala	Ala	Ser	Gly	Lys	
		40					45					50				
cac	act	gtt	ttt	cct	gtt	acc	cct	ggt	cat	gag	att	gca	gga	acc	atc	307
His	Thr	Val	Phe	Pro	Val	Thr	Pro	Gly	His	Glu	Ile	Ala	Gly	Thr	Ile	
		55					60				65					
gcg	gaa	att	ggt	gaa	aac	gta	tct	cgg	tgg	acg	gtt	ggt	gat	cgc	gtt	355
Ala	Glu	Ile	Gly	Glu	Asn	Val	Ser	Arg	Trp	Thr	Val	Gly	Asp	Arg	Val	
	70				75				80						85	
gca	atc	ggt	tgg	ttt	ggt	ggc	aat	tgc	ggt	gac	tgc	gct	ttt	tgt	cgt	403
Ala	Ile	Gly	Trp	Phe	Gly	Gly	Asn	Cys	Gly	Asp	Cys	Ala	Phe	Cys	Arg	
				90				95						100		
gca	ggt	gat	cct	gtg	cat	tgc	aga	gag	cgg	aag	att	cct	ggc	gtt	tct	451
Ala	Gly	Asp	Pro	Val	His	Cys	Arg	Glu	Arg	Lys	Ile	Pro	Gly	Val	Ser	
			105					110					115			
tat	gcg	ggt	ggt	tgg	gca	cag	aat	att	gtt	gtt	cca	gcg	gag	gct	ctt	499
Tyr	Ala	Gly	Gly	Trp	Ala	Gln	Asn	Ile	Val	Val	Pro	Ala	Glu	Ala	Leu	
		120					125					130				
gct	gcg	att	cca	gat	ggc	atg	gac	ttt	tac	gag	ccc	gcc	ccg	atg	ggc	547
Ala	Ala	Ile	Pro	Asp	Gly	Met	Asp	Phe	Tyr	Glu	Pro	Ala	Pro	Met	Gly	
		135				140					145					
tgc	gca	ggt	gtg	aca	aca	ttc	aat	gcg	ttg	cga	aac	ctg	aag	ctg	gat	595
Cys	Ala	Gly	Val	Thr	Thr	Phe	Asn	Ala	Leu	Arg	Asn	Leu	Lys	Leu	Asp	
	150				155				160						165	

ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta 643  
 Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu  
 170 175 180

gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc 691  
 Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala  
 185 190 195

cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac 739  
 Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His  
 200 205 210

tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt 787  
 Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu  
 215 220 225

ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt 835  
 Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu  
 230 235 240 245

tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc 883  
 Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile  
 250 255 260

gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg 931  
 Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met  
 265 270 275

aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg 979  
 Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr  
 280 285 290

gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att 1027  
 Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile  
 295 300 305

gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca 1075  
 Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser  
 310 315 320 325

gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca 1117  
 Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser  
 330 335

taatgccaac agcaagccca att 1140

&lt;210&gt; 242

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 242

Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu  
 1 5 10 15

Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg  
 20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala  
 35 40 45

$\langle 210 \rangle$	243
$\langle 211 \rangle$	1665



&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1642)

&lt;223&gt; RXA02737

&lt;400&gt; 243

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agcacgctgc atcagtaacg ggcacatgaa atcgaattag ttcgatctta tgtggccggt 60
acacatcttt cattaaagaa aggatcgtga cactaccatc gtg agc aca aac acg 115
                               Val Ser Thr Asn Thr
                               1 5
acc ccc tcc agc tgg aca aac cca ctg cgc gac ccg cag gat aaa cga 163
Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp Pro Gln Asp Lys Arg
                               10 15 20
ctc ccc cgc atc gct ggc cct tcc ggc atg gtg atc ttc ggt gtc act 211
Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val Ile Phe Gly Val Thr
                               25 30 35
ggc gac ttg gct cga aag aag ctg ctc ccc gcc att tat gat cta gca 259
Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala Ile Tyr Asp Leu Ala
                               40 45 50
aac cgc gga ttg ctg ccc cca gga ttc tcg ttg gta ggt tac ggc cgc 307
Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg
                               55 60 65
cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca 355
Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala
                               70 75 80 85
agt gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc 403
Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu
                               90 95 100
gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gat gca gct 451
Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Asp Ala Ala
                               105 110 115
ttc gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc 499
Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile Asp Lys Thr Arg Gly
                               120 125 130
acc gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc 547
Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile Pro Pro Asp Ser Phe
                               135 140 145
aca gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc 595
Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr
                               150 155 160 165
gaa gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac 643
Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn
                               170 175 180
ctc gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca 691
Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro

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185				190				195				
gaa tct tct gtg ttc cgc atc gac cac tat ttg ggc aag gaa aca gtt	739											
Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val												
200	205				210							
caa aac atc ctg gct ctg cgt ttt gct aac cag ctg ttt gag cca ctg	787											
Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln Leu Phe Glu Pro Leu												
215	220				225							
tgg aac tcc aac tac gtt gac cac gtc cag atc acc atg gct gaa gat	835											
Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile Thr Met Ala Glu Asp												
230	235				240				245			
att ggc ttg ggt gga cgt gct ggt tac tac gac ggc atc ggc gca gcc	883											
Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp Gly Ile Gly Ala Ala												
250	255				260							
cgc gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc	931											
Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala												
265	270				275							
atg gaa gaa cca att tct ttc gtg cca gcg cag ctg cag gca gaa aag	979											
Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys												
280	285				290							
atc aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc	1027											
Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr												
295	300				305							
tcc gct cgt ggt cag tac gct gcc ggt tgg cag ggc tct gag tta gtc	1075											
Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln Gly Ser Glu Leu Val												
310	315				320				325			
aag gga ctt cgc gaa gaa gat ggc ttc aac cct gag tcc acc act gag	1123											
Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro Glu Ser Thr Thr Glu												
330	335				340							
act ttt gcg gct tgt acc tta gag atc acg tct cgt cgc tgg gct ggt	1171											
Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly												
345	350				355							
gtg ccg ttc tac ctg cgc acc ggt aag cgt ctt ggt cgc cgt gtt act	1219											
Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Arg Val Thr												
360	365				370							
gag att gcc gtg gtg ttt aaa gac gca cca cac cag cct ttc gac ggc	1267											
Glu Ile Ala Val Val Phe Lys Asp Ala Pro His Gln Pro Phe Asp Gly												
375	380				385							
gac atg act gta tcc ctt ggc caa aac gcc atc gtg att cgc gtg cag	1315											
Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile Val Ile Arg Val Gln												
390	395				400				405			
cct gat gaa ggt gtg ctc atc cgc ttc ggt tcc aag gtt cca ggt tct	1363											
Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser Lys Val Pro Gly Ser												
410	415				420							
gcc atg gaa gtc cgt gac gtc aac atg gac ttc tcc tac tca gaa tcc	1411											
Ala Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser												
425	430				435							

ttc act gaa gaa tca cct gaa gca tac gag cgc ctc att ttg gat gcg 1459  
 Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala  
 440 445 450  
 ctg tta gat gaa tcc agc ctc ttc cct acc aac gag gaa gtg gaa ctg 1507  
 Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn Glu Glu Val Glu Leu  
 455 460 465  
 agc tgg aag att ctg gat cca att ctt gaa gca tgg gat gcc gat gga 1555  
 Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala Trp Asp Ala Asp Gly  
 470 475 480 485  
 gaa cca gag gat tac cca gcg ggt acg tgg ggt cca aag agc gct gat 1603  
 Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp  
 490 495 500  
 gaa atg ctt tcc cgc aac ggt cac acc tgg cgc agg cca taatttaggg 1652  
 Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg Arg Pro  
 505 510  
 gcaaaaaatg atc 1665

&lt;210&gt; 244

&lt;211&gt; 514

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 244

Val Ser Thr Asn Thr Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp  
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 Pro Gln Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val  
 20 25 30  
 Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala  
 35 40 45  
 Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu  
 50 55 60  
 Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr  
 65 70 75 80  
 Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn  
 85 90 95  
 Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe  
 100 105 110  
 Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile  
 115 120 125  
 Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile  
 130 135 140  
 Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly  
 145 150 155 160  
 Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys

165										170					175				
Pro	Phe	Gly	His	Asn	Leu	Glu	Ser	Ala	His	Glu	Leu	Asn	Gln	Leu	Val				
			180					185					190						
Asn	Ala	Val	Phe	Pro	Glu	Ser	Ser	Val	Phe	Arg	Ile	Asp	His	Tyr	Leu				
		195					200					205							
Gly	Lys	Glu	Thr	Val	Gln	Asn	Ile	Leu	Ala	Leu	Arg	Phe	Ala	Asn	Gln				
	210					215					220								
Leu	Phe	Glu	Pro	Leu	Trp	Asn	Ser	Asn	Tyr	Val	Asp	His	Val	Gln	Ile				
225					230					235					240				
Thr	Met	Ala	Glu	Asp	Ile	Gly	Leu	Gly	Gly	Arg	Ala	Gly	Tyr	Tyr	Asp				
				245					250					255					
Gly	Ile	Gly	Ala	Ala	Arg	Asp	Val	Ile	Gln	Asn	His	Leu	Ile	Gln	Leu				
			260					265					270						
Leu	Ala	Leu	Val	Ala	Met	Glu	Glu	Pro	Ile	Ser	Phe	Val	Pro	Ala	Gln				
		275					280					285							
Leu	Gln	Ala	Glu	Lys	Ile	Lys	Val	Leu	Ser	Ala	Thr	Lys	Pro	Cys	Tyr				
	290					295					300								
Pro	Leu	Asp	Lys	Thr	Ser	Ala	Arg	Gly	Gln	Tyr	Ala	Ala	Gly	Trp	Gln				
305					310					315					320				
Gly	Ser	Glu	Leu	Val	Lys	Gly	Leu	Arg	Glu	Glu	Asp	Gly	Phe	Asn	Pro				
				325					330					335					
Glu	Ser	Thr	Thr	Glu	Thr	Phe	Ala	Ala	Cys	Thr	Leu	Glu	Ile	Thr	Ser				
			340					345					350						
Arg	Arg	Trp	Ala	Gly	Val	Pro	Phe	Tyr	Leu	Arg	Thr	Gly	Lys	Arg	Leu				
		355					360					365							
Gly	Arg	Arg	Val	Thr	Glu	Ile	Ala	Val	Val	Phe	Lys	Asp	Ala	Pro	His				
	370					375					380								
Gln	Pro	Phe	Asp	Gly	Asp	Met	Thr	Val	Ser	Leu	Gly	Gln	Asn	Ala	Ile				
385					390					395					400				
Val	Ile	Arg	Val	Gln	Pro	Asp	Glu	Gly	Val	Leu	Ile	Arg	Phe	Gly	Ser				
				405				410						415					
Lys	Val	Pro	Gly	Ser	Ala	Met	Glu	Val	Arg	Asp	Val	Asn	Met	Asp	Phe				
			420					425					430						
Ser	Tyr	Ser	Glu	Ser	Phe	Thr	Glu	Glu	Ser	Pro	Glu	Ala	Tyr	Glu	Arg				
		435					440					445							
Leu	Ile	Leu	Asp	Ala	Leu	Leu	Asp	Glu	Ser	Ser	Leu	Phe	Pro	Thr	Asn				
	450					455					460								
Glu	Glu	Val	Glu	Leu	Ser	Trp	Lys	Ile	Leu	Asp	Pro	Ile	Leu	Glu	Ala				
465					470					475					480				
Trp	Asp	Ala	Asp	Gly	Glu	Pro	Glu	Asp	Tyr	Pro	Ala	Gly	Thr	Trp	Gly				
				485					490					495					

Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg  
                   500                                  505                                  510

Arg Pro

<210> 245

<211> 1203

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1180)

<223> RXA02738

<400> 245

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cacagttcaa gaacaattct ttttaaggaaa atttagtttc atg tct cac att gat 115
                                         Met Ser His Ile Asp
                                         1                  5

gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac ctc tcc cgc 163
Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp Leu Ser Arg
                        10                  15                  20

gag cgc att act tcc ggc aat ctc agc cag gtt att gag gaa aag tct 211
Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu Glu Lys Ser
                        25                  30                  35

gta gtc ggt gtc acc acc aac cca gct att ttc gca gca gca atg tcc 259
Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala Ala Met Ser
                        40                  45                  50

aag ggc gat tcc tac gac gct cag atc gca gag ctc aag gcc gct ggc 307
Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys Ala Ala Gly
                        55                  60                  65

gca tct gtt gac cag gct gtt tac gcc atg agc atc gac gac gtt cgc 355
Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp Asp Val Arg
                        70                  75                  80                  85

aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc aac ggc tac 403
Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser Asn Gly Tyr
                        90                  95                  100

gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct gct gac cgc 451
Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser Ala Asp Arg
                        105                  110                  115

gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag gtt gat cgt 499
Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys Val Asp Arg
                        120                  125                  130

cca aac gtc atg atc aag atc cct gca acc cca ggt tct ttg cca gca 547
Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser Leu Pro Ala
                        135                  140                  145

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atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc acc ttg atc 595  
 Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val Thr Leu Ile  
 150 155 160 165

ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg ttc atc gag ggc 643  
 Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Phe Ile Glu Gly  
 170 175 180

atc aag cag gct gct gca aac ggc cac gac gtc tcc aag atc cac tct 691  
 Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val Ser Lys Ile His Ser  
 185 190 195

gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt gag atc gac aag cgc 739  
 Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile Asp Lys Arg  
 200 205 210

ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc ggc aag gca 787  
 Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg Gly Lys Ala  
 215 220 225

ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag gag ctt ttc 835  
 Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys Glu Leu Phe  
 230 235 240 245

gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc cca ctg tgg 883  
 Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg Pro Leu Trp  
 250 255 260

gca tcc acc ggc gtg aag aac cct gcg tac gct gca act ctt tac gtt 931  
 Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala Ala Thr Leu Tyr Val  
 265 270 275

tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca gaa ggc acc 979  
 Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro Glu Gly Thr  
 280 285 290

atc gac gcg gtt ctg gag cag ggc aac ctg cac ggt gac acc ctg tcc 1027  
 Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His Gly Asp Thr Leu Ser  
 295 300 305

aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt gag gct ctg 1075  
 Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser Gln Leu Glu Ala Leu  
 310 315 320 325

ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc gag ggt gtg 1123  
 Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr Glu Gly Val  
 330 335 340

gac aag ttc gtt gct tct tgg agc gaa ctg ctt gag tcc atg gaa gct 1171  
 Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser Met Glu Ala  
 345 350 355

cgc ctg aag tagaatcagc acgctgcatc agt 1203  
 Arg Leu Lys  
 360

&lt;210&gt; 246

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 246

Met Ser His Ile Asp Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu  
 1 5 10 15  
 Asp Asp Leu Ser Arg Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val  
 20 25 30  
 Ile Glu Glu Lys Ser Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe  
 35 40 45  
 Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu  
 50 55 60  
 Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser  
 65 70 75 80  
 Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu  
 85 90 95  
 Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg  
 100 105 110  
 Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp  
 115 120 125  
 Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro  
 130 135 140  
 Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val  
 145 150 155 160  
 Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala  
 165 170 175  
 Ala Phe Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val  
 180 185 190  
 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val  
 195 200 205  
 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala  
 210 215 220  
 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val  
 225 230 235 240  
 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr  
 245 250 255  
 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala  
 260 265 270  
 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr  
 275 280 285  
 Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His  
 290 295 300  
 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser  
 305 310 315 320

Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu  
                                   325                                  330                                  335

Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu  
                                   340                                  345                                  350

Glu Ser Met Glu Ala Arg Leu Lys  
                                   355                                  360

<210> 247

<211> 2223

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2200)

<223> RXA02739

<400> 247

cctttgccaa atttgaacca attaacctaa gtcgtagatc tgatcatcgg atctaacgaa 60

aacgaaccaa aactttggtc ccggtttaac ccaggaagga ttg acc acc ttg acg 115  
   Leu Thr Thr Leu Thr  
   1  5

ctg tca cct gaa ctt cag gcg ctc act gta cgc aat tac ccc tct gat 163  
   Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg Asn Tyr Pro Ser Asp  
   10  15  20

tgg tcc gat gtg gac acc aag gct gta gac act gtt cgt gtc ctc gct 211  
   Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr Val Arg Val Leu Ala  
   25  30  35

gca gac gct gta gaa aac tgt ggc tcc ggc cac cca ggc acc gca atg 259  
   Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His Pro Gly Thr Ala Met  
   40  45  50

agc ctg gct ccc ctt gca tac acc ttg tac cag cgg gtt atg aac gta 307  
   Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln Arg Val Met Asn Val  
   55  60  65

gat cca cag gac acc aac tgg gca ggc cgt gac cgc ttc gtt ctt tct 355  
   Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp Arg Phe Val Leu Ser  
   70  75  80  85

tgt ggc cac tcc tct ttg acc cag tac atc cag ctt tac ttg ggt gga 403  
   Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln Leu Tyr Leu Gly Gly  
   90  95  100

ttc ggc ctt gag atg gat gac ctg aag gct ctg cgc acc tgg gat tcc 451  
   Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu Arg Thr Trp Asp Ser  
   105  110  115

ttg acc cca gga cac cct gag tac cgc cac acc aag ggc gtt gag atc 499  
   Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr Lys Gly Val Glu Ile  
   120  125  130

acc act ggc cct ctt ggc cag ggt ctt gca tct gca gtt ggt atg gcc 547



Thr	Thr	Gly	Pro	Leu	Gly	Gln	Gly	Leu	Ala	Ser	Ala	Val	Gly	Met	Ala		
135						140					145						
atg	gct	gct	cgt	cgt	gag	cgt	ggc	cta	ttc	gac	cca	acc	gct	gct	gag	595	
Met	Ala	Ala	Arg	Arg	Glu	Arg	Gly	Leu	Phe	Asp	Pro	Thr	Ala	Ala	Glu		
150					155					160					165		
ggc	gaa	tcc	cca	ttc	gac	cac	cac	atc	tac	gtc	att	gct	tct	gat	ggc	643	
Gly	Glu	Ser	Pro	Phe	Asp	His	His	Ile	Tyr	Val	Ile	Ala	Ser	Asp	Gly		
				170					175					180			
gac	ctg	cag	gaa	ggc	gtc	acc	tct	gag	gca	tcc	tcc	atc	gct	ggc	acc	691	
Asp	Leu	Gln	Glu	Gly	Val	Thr	Ser	Glu	Ala	Ser	Ser	Ile	Ala	Gly	Thr		
			185					190					195				
cag	cag	ctg	ggc	aac	ctc	atc	gtg	ttc	tgg	gat	gac	aac	cgc	atc	tcc	739	
Gln	Gln	Leu	Gly	Asn	Leu	Ile	Val	Phe	Trp	Asp	Asp	Asn	Arg	Ile	Ser		
		200					205					210					
atc	gaa	gac	aac	act	gag	atc	gct	ttc	aac	gag	gac	gtt	gtt	gct	cgt	787	
Ile	Glu	Asp	Asn	Thr	Glu	Ile	Ala	Phe	Asn	Glu	Asp	Val	Val	Ala	Arg		
	215					220				225							
tac	aag	gct	tac	ggc	tgg	cag	acc	att	gag	gtt	gag	gct	ggc	gag	gac	835	
Tyr	Lys	Ala	Tyr	Gly	Trp	Gln	Thr	Ile	Glu	Val	Glu	Ala	Gly	Glu	Asp		
230				235					240					245			
gtt	gca	gca	atc	gaa	gct	gca	gtg	gct	gag	gct	aag	aag	gac	acc	aag	883	
Val	Ala	Ala	Ile	Glu	Ala	Ala	Val	Ala	Glu	Ala	Lys	Lys	Asp	Thr	Lys		
				250					255					260			
cga	cct	acc	ttc	atc	cgc	gtt	cgc	acc	atc	atc	ggc	ttc	cca	gct	cca	931	
Arg	Pro	Thr	Phe	Ile	Arg	Val	Arg	Thr	Ile	Ile	Gly	Phe	Pro	Ala	Pro		
			265					270					275				
act	atg	atg	aac	acc	ggc	gct	gtg	cac	ggc	gct	gct	ctt	ggc	gca	gct	979	
Thr	Met	Met	Asn	Thr	Gly	Ala	Val	His	Gly	Ala	Ala	Leu	Gly	Ala	Ala		
		280					285					290					
gag	gtt	gca	gca	acc	aag	act	gag	ctt	gga	ttc	gat	cct	gag	gct	cac	1027	
Glu	Val	Ala	Ala	Thr	Lys	Thr	Glu	Leu	Gly	Phe	Asp	Pro	Glu	Ala	His		
	295					300					305						
ttc	gcg	atc	gac	gat	gag	gtt	atc	gct	cac	acc	cgc	tcc	ctc	gca	gag	1075	
Phe	Ala	Ile	Asp	Asp	Glu	Val	Ile	Ala	His	Thr	Arg	Ser	Leu	Ala	Glu		
310					315					320					325		
cgc	gct	gca	cag	aag	aag	gct	gca	tgg	cag	gtc	aag	ttc	gat	gag	tgg	1123	
Arg	Ala	Ala	Gln	Lys	Lys	Ala	Ala	Trp	Gln	Val	Lys	Phe	Asp	Glu	Trp		
				330					335					340			
gca	gct	gcc	aac	cct	gag	aac	aag	gct	ctg	ttc	gat	cgc	ctg	aac	tcc	1171	
Ala	Ala	Ala	Asn	Pro	Glu	Asn	Lys	Ala	Leu	Phe	Asp	Arg	Leu	Asn	Ser		
			345					350					355				
cgt	gag	ctt	cca	gcg	ggc	tac	gct	gac	gag	ctc	cca	aca	tgg	gat	gca	1219	
Arg	Glu	Leu	Pro	Ala	Gly	Tyr	Ala	Asp	Glu	Leu	Pro	Thr	Trp	Asp	Ala		
		360				365						370					
gat	gag	aag	ggc	gtc	gca	act	cgt	aag	gct	tcc	gag	gct	gca	ctt	cag	1267	
Asp	Glu	Lys	Gly	Val	Ala	Thr	Arg	Lys	Ala	Ser	Glu	Ala	Ala	Leu	Gln		

375	380	385	
gca ctg ggc aag acc ctt cct gag ctg tgg ggc ggt tcc gct gac ctc Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly Gly Ser Ala Asp Leu 390 395 400 405			1315
gca ggt tcc aac aac acc gtg atc aag ggc tcc cct tcc ttc ggc cct Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser Pro Ser Phe Gly Pro 410 415 420			1363
gag tcc atc tcc acc gag acc tgg tct gct gag cct tac ggc cgt aac Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu Pro Tyr Gly Arg Asn 425 430 435			1411
ctg cac ttc ggt atc cgt gag cac gct atg gga tcc atc ctc aac ggc Leu His Phe Gly Ile Arg Glu His Ala Met Gly Ser Ile Leu Asn Gly 440 445 450			1459
att tcc ctc cac ggt ggc acc cgc cca tac ggc gga acc ttc ctc atc Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly Gly Thr Phe Leu Ile 455 460 465			1507
ttc tcc gac tac atg cgt cct gca gtt cgt ctt gca gct ctc atg gag Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu Ala Ala Leu Met Glu 470 475 480 485			1555
acc gac gct tac tac gtc tgg acc cac gac tcc atc ggt ctg ggc gaa Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser Ile Gly Leu Gly Glu 490 495 500			1603
gat ggc cca acc cac cag cct gtt gaa acc ttg gct gca ctg cgc gcc Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu Ala Ala Leu Arg Ala 505 510 515			1651
atc cca ggt ctg tcc gtc ctg cgt cct gca gat gcg aac gag acc gcc Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp Ala Asn Glu Thr Ala 520 525 530			1699
cag gct tgg gct gca gca ctt gag tac aag gaa ggc cct aag ggt ctt Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu Gly Pro Lys Gly Leu 535 540 545			1747
gca ctg acc cgc cag aac gtt cct gtt ctg gaa ggc acc aag gag aag Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu Gly Thr Lys Glu Lys 550 555 560 565			1795
gct gct gaa ggc gtt cgc cgc ggt ggc tac gtc ctg gtt gag ggt tcc Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val Leu Val Glu Gly Ser 570 575 580			1843
aag gaa acc cca gat gtg atc ctc atg ggc tcc ggc tcc gag gtt cag Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser Gly Ser Glu Val Gln 585 590 595			1891
ctt gca gtt aac gct gcg aag gct ctg gaa gct gag ggc gtt gca gct Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala Glu Gly Val Ala Ala 600 605 610			1939
cgc gtt gtt tcc gtt cct tgc atg gat tgg ttc cag gag cag gac gca Arg Val Val Ser Val Pro Cys Met Asp Trp Phe Gln Glu Gln Asp Ala 615 620 625			1987

gag tac atc gag tcc gtt ctg cct gca gct gtg acc gct cgt gtg tct 2035  
 Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val Thr Ala Arg Val Ser  
 630 635 640 645

gtt gaa gct ggc atc gca atg cct tgg tac cgc ttc ttg ggc acc cag 2083  
 Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg Phe Leu Gly Thr Gln  
 650 655 660

ggc cgt gct gtc tcc ctt gag cac ttc ggt gct tct gcg gat tac cag 2131  
 Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala Ser Ala Asp Tyr Gln  
 665 670 675

acc ctg ttt gag aag ttc ggc atc acc acc gat gca gtc gtg gca gcg 2179  
 Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp Ala Val Val Ala Ala  
 680 685 690

gcc aag gac tcc att aac ggt taattgccct gctgttttta gct 2223  
 Ala Lys Asp Ser Ile Asn Gly  
 695 700

<210> 248

<211> 700

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 248

Leu Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg  
 1 5 10 15

Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr  
 20 25 30

Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His  
 35 40 45

Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln  
 50 55 60

Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp  
 65 70 75 80

Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln  
 85 90 95

Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu  
 100 105 110

Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr  
 115 120 125

Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser  
 130 135 140

Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp  
 145 150 155 160

Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val  
 165 170 175

Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser  
 180 185 190  
 Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp  
 195 200 205  
 Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu  
 210 215 220  
 Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val  
 225 230 235 240  
 Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala  
 245 250 255  
 Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile  
 260 265 270  
 Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala  
 275 280 285  
 Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe  
 290 295 300  
 Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr  
 305 310 315 320  
 Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val  
 325 330 335  
 Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe  
 340 345 350  
 Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu  
 355 360 365  
 Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser  
 370 375 380  
 Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly  
 385 390 395 400  
 Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser  
 405 410 415  
 Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu  
 420 425 430  
 Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly  
 435 440 445  
 Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly  
 450 455 460  
 Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu  
 465 470 475 480  
 Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser  
 485 490 495  
 Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu

500										505					510				
Ala	Ala	Leu	Arg	Ala	Ile	Pro	Gly	Leu	Ser	Val	Leu	Arg	Pro	Ala	Asp				
		515					520					525							
Ala	Asn	Glu	Thr	Ala	Gln	Ala	Trp	Ala	Ala	Ala	Leu	Glu	Tyr	Lys	Glu				
	530					535					540								
Gly	Pro	Lys	Gly	Leu	Ala	Leu	Thr	Arg	Gln	Asn	Val	Pro	Val	Leu	Glu				
545					550					555					560				
Gly	Thr	Lys	Glu	Lys	Ala	Ala	Glu	Gly	Val	Arg	Arg	Gly	Gly	Tyr	Val				
				565					570					575					
Leu	Val	Glu	Gly	Ser	Lys	Glu	Thr	Pro	Asp	Val	Ile	Leu	Met	Gly	Ser				
			580					585					590						
Gly	Ser	Glu	Val	Gln	Leu	Ala	Val	Asn	Ala	Ala	Lys	Ala	Leu	Glu	Ala				
		595					600					605							
Glu	Gly	Val	Ala	Ala	Arg	Val	Val	Ser	Val	Pro	Cys	Met	Asp	Trp	Phe				
	610					615					620								
Gln	Glu	Gln	Asp	Ala	Glu	Tyr	Ile	Glu	Ser	Val	Leu	Pro	Ala	Ala	Val				
625					630					635					640				
Thr	Ala	Arg	Val	Ser	Val	Glu	Ala	Gly	Ile	Ala	Met	Pro	Trp	Tyr	Arg				
				645					650					655					
Phe	Leu	Gly	Thr	Gln	Gly	Arg	Ala	Val	Ser	Leu	Glu	His	Phe	Gly	Ala				
			660					665					670						
Ser	Ala	Asp	Tyr	Gln	Thr	Leu	Phe	Glu	Lys	Phe	Gly	Ile	Thr	Thr	Asp				
		675					680					685							
Ala	Val	Val	Ala	Ala	Ala	Lys	Asp	Ser	Ile	Asn	Gly								
	690					695					700								

&lt;210&gt; 249

&lt;211&gt; 793

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (48)..(770)

&lt;223&gt; RXA00965

&lt;400&gt; 249

agattg	cggg	cctc	ggttc	attg	aaaaca	agac	ggtgtt	tgaataa	atg	aca	act	56				
									Met	Thr	Thr					
									1							
ttc	cac	gat	ctt	ccg	ctg	gag	gag	cgg	ctg	aca	ctg	gcc	agg	ttg	ggc	104
Phe	His	Asp	Leu	Pro	Leu	Glu	Glu	Arg	Leu	Thr	Leu	Ala	Arg	Leu	Gly	
	5					10					15					
aca	tcc	cac	tac	tcc	cgt	cag	ctc	tcc	ctc	gtg	gac	aac	gct	gag	ttc	152
Thr	Ser	His	Tyr	Ser	Arg	Gln	Leu	Ser	Leu	Val	Asp	Asn	Ala	Glu	Phe	
	20				25					30				35		

ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc 200  
 Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala  
                     40                    45                    50

cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca 248  
 His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala  
                     55                    60                    65

aat act ggt gag gaa acc cca atg tac gtg tgc cca gaa gcg cgc aac 296  
 Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn  
                     70                    75                    80

gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac 344  
 Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn  
                     85                    90                    95

ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg 392  
 Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr  
 100                    105                    110                    115

tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act 440  
 Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr  
                     120                    125                    130

gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc 488  
 Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile  
                     135                    140                    145

cac gca gtt gac ctc ggt gca gtg gca acc ttt ggc gac atc cca gag 536  
 His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp Ile Pro Glu  
                     150                    155                    160

gtc atc ctg cgc acc tta gct gca gaa atc aca caa aag tgg aca agc 584  
 Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys Trp Thr Ser  
                     165                    170                    175

caa gga gcc ggc gag gga ctt gtg ctt ctc gac gag ccc tcc agc act 632  
 Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro Ser Ser Thr  
 180                    185                    190                    195

cgc tac ccc gcc gcc cca ggg cag gac gag gta gta gtg tcc ggt agc 680  
 Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val Ser Gly Ser  
                     200                    205                    210

ctt gca ggc att gtt cgc tac gcc gct ggc cgc ggt tcc gat gga gtc 728  
 Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser Asp Gly Val  
                     215                    220                    225

act tct tcc act gga gag gtt cca gag cca ccg cgc tgg ctg 770  
 Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp Leu  
                     230                    235                    240

tagtttccac acattcttaa atg 793

&lt;210&gt; 250

&lt;211&gt; 241

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 250

Met Thr Thr Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala  
 1 5 10 15

Arg Leu Gly Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn  
 20 25 30

Ala Glu Phe Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His  
 35 40 45

Leu Ile Ala His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met  
 50 55 60

His Trp Ala Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu  
 65 70 75 80

Ala Arg Asn Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala  
 85 90 95

Leu Arg Asn Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp  
 100 105 110

Arg Glu Thr Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln  
 115 120 125

Gly Arg Thr Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu  
 130 135 140

Val Trp Ile His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp  
 145 150 155 160

Ile Pro Glu Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys  
 165 170 175

Trp Thr Ser Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro  
 180 185 190

Ser Ser Thr Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val  
 195 200 205

Ser Gly Ser Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser  
 210 215 220

Asp Gly Val Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp  
 225 230 235 240

Leu

&lt;210&gt; 251

&lt;211&gt; 1575

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1552)

&lt;223&gt; RXN00999

&lt;400&gt; 251

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ttgctgacac	cgggctatgc	cggtcaagtac	gatcaataac	atg Met 1	act Thr	aat Asn	gga Gly	gat Asp 5	115							
aat Asn	ctc Leu	gca Ala	cag Gln	atc Ile 10	ggc Gly	gtt Val	gta Val	ggc Gly	cta Leu 15	gca Ala	gta Val	atg Met	ggc Gly	tca Ser 20	aac Asn	163
ctc Leu	gcc Ala	cgc Arg	aac Asn 25	ttc Phe	gcc Ala	cgc Arg	aac Asn	ggc Gly 30	aac Asn	act Thr	gtc Val	gct Ala	gtc Val 35	tac Tyr	aac Asn	211
cgc Arg	agc Ser	act Thr 40	gac Asp	aaa Lys	acc Thr	gac Asp	aag Lys 45	ctc Leu	atc Ile	gcc Ala	gat Asp	cac His 50	ggc Gly	tcc Ser	gaa Glu	259
ggc Gly	aac Asn 55	ttc Phe	atc Ile	cct Pro	tct Ser	gca Ala 60	acc Thr	gtc Val	gaa Glu	gag Glu	ttc Phe 65	gta Val	gca Ala	tcc Ser	ctg Leu	307
gaa Glu 70	aag Lys	cca Pro	cgc Arg	cgc Arg	gcc Ala 75	atc Ile	atc Ile	atg Met	gtt Val	cag Gln 80	gct Ala	ggt Gly	aac Asn	gcc Ala	acc Thr 85	355
gac Asp	gca Ala	gtc Val	atc Ile 90	aac Asn	cag Gln	ctg Leu	gca Ala	gat Asp	gcc Ala 95	atg Met	gac Asp	gaa Glu	ggc Gly	gac Asp 100	atc Ile	403
atc Ile	atc Ile	gac Asp 105	ggc Gly	ggc Gly	aac Asn	gcc Ala	ctc Leu	tac Tyr 110	acc Thr	gac Asp	acc Thr	att Ile	cgt Arg 115	cgc Arg	gag Glu	451
aag Lys	gaa Glu	atc Ile 120	tcc Ser	gca Ala	cgc Arg	ggt Gly	ctc Leu 125	cac His	ttc Phe	gtc Val	ggt Gly	gct Ala 130	ggt Gly	atc Ile	tcc Ser	499
ggc Gly	ggc Gly 135	gaa Glu	gaa Glu	ggc Gly	gca Ala	ctc Leu 140	aac Asn	ggc Gly	cca Pro	tcc Ser	atc Ile 145	atg Met	cct Pro	ggt Gly	ggc Gly	547
cca Pro 150	gca Ala	aag Lys	tcc Ser	tac Tyr	gag Glu 155	tcc Ser	ctc Leu	gga Gly	cca Pro	ctg Leu 160	ctt Leu	gag Glu	tcc Ser	atc Ile	gct Ala 165	595
gcc Ala	aac Asn	gtt Val	gac Asp 170	ggc Gly	acc Thr	cca Pro	tgt Cys	gtc Val	acc Thr 175	cac His	atc Ile	ggc Gly	cca Pro	gac Asp 180	ggc Gly	643
gcc Ala	ggc Gly	cac His	ttc Phe 185	gtc Val	aag Lys	atg Met	gtc Val	cac His 190	aac Asn	ggc Gly	atc Ile	gag Glu	tac Tyr 195	gcc Ala	gac Asp	691
atg Met	cag Gln	gtc Val 200	atc Ile	ggc Gly	gag Glu	gca Ala	tac Tyr 205	cac His	ctt Leu	ctc Leu	cgc Arg	tac Tyr 210	gca Ala	gca Ala	ggc Gly	739
atg Met	cag Gln 215	ccagct ProAla	gaa Glu	atc Ile	gct Ala 220	gag Glu	gtt Val	ttc Phe	aag Lys	gaa Glu 225	tgg Trp	aac Asn	gca Ala	ggc Gly	787	



gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln 230 235 240 245	835
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala 250 255 260	883
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp 265 270 275	931
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala 280 285 290	979
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro 295 300 305	1027
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln 310 315 320 325	1075
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala 330 335 340	1123
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn 345 350 355	1171
tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys 360 365 370	1219
atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala 375 380 385	1267
aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu 390 395 400 405	1315
ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr 410 415 420	1363
cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr 425 430 435	1411
gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln 440 445 450	1459
cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly 455 460 465	1507

tcc ttc cac acc gag tgg tcc ggc gac cgc tcc gag gtt gaa gct 1552  
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser Glu Val Glu Ala  
 470 475 480

taaaggctct ccttttaaca caa 1575

<210> 252

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala  
 1 5 10 15

Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr  
 20 25 30

Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala  
 35 40 45

Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu  
 50 55 60

Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln  
 65 70 75 80

Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met  
 85 90 95

Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp  
 100 105 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val  
 115 120 125

Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser  
 130 135 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu  
 145 150 155 160

Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His  
 165 170 175

Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly  
 180 185 190

Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu  
 195 200 205

Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys  
 210 215 220

Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala  
 225 230 235 240

Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp  
 245 250 255

Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val  
 260 265 270  
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala  
 275 280 285  
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala  
 290 295 300  
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly  
 305 310 315 320  
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala  
 325 330 335  
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly  
 340 345 350  
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile  
 355 360 365  
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val  
 370 375 380  
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro  
 385 390 395 400  
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val  
 405 410 415  
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser  
 420 425 430  
 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala  
 435 440 445  
 Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg  
 450 455 460  
 Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser  
 465 470 475 480  
 Glu Val Glu Ala

<210> 253  
 <211> 1537  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1537)  
 <223> FRXA00999

<400> 253  
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ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115  
 Met Thr Asn Gly Asp

																1	5
aat	ctc	gca	cag	atc	ggc	gtt	gta	ggc	cta	gca	gta	atg	ggc	tca	aac	163	
Asn	Leu	Ala	Gln	Ile	Gly	Val	Val	Gly	Leu	Ala	Val	Met	Gly	Ser	Asn		
				10					15					20			
ctc	gcc	cgc	aac	ttc	gcc	cgc	aac	ggc	aac	act	gtc	gct	gtc	tac	aac	211	
Leu	Ala	Arg	Asn	Phe	Ala	Arg	Asn	Gly	Asn	Thr	Val	Ala	Val	Tyr	Asn		
				25					30					35			
cgc	agc	act	gac	aaa	acc	gac	aag	ctc	atc	gcc	gat	cac	ggc	tcc	gaa	259	
Arg	Ser	Thr	Asp	Lys	Thr	Asp	Lys	Leu	Ile	Ala	Asp	His	Gly	Ser	Glu		
				40					45					50			
ggc	aac	ttc	atc	cct	tct	gca	acc	gtc	gaa	gag	ttc	gta	gca	tcc	ctg	307	
Gly	Asn	Phe	Ile	Pro	Ser	Ala	Thr	Val	Glu	Glu	Phe	Val	Ala	Ser	Leu		
				55					60					65			
gaa	aag	cca	cgc	cgc	gcc	atc	atc	atg	gtt	cag	gct	ggg	aac	gcc	acc	355	
Glu	Lys	Pro	Arg	Arg	Ala	Ile	Ile	Met	Val	Gln	Ala	Gly	Asn	Ala	Thr		
				70					75					80			
gac	gca	gtc	atc	aac	cag	ctg	gca	gat	gcc	atg	gac	gaa	ggc	gac	atc	403	
Asp	Ala	Val	Ile	Asn	Gln	Leu	Ala	Asp	Ala	Met	Asp	Glu	Gly	Asp	Ile		
				90					95					100			
atc	atc	gac	ggc	ggc	aac	gcc	ctc	tac	acc	gac	acc	att	cgt	cgc	gag	451	
Ile	Ile	Asp	Gly	Gly	Asn	Ala	Leu	Tyr	Thr	Asp	Thr	Ile	Arg	Arg	Glu		
				105					110					115			
aag	gaa	atc	tcc	gca	cgc	ggg	ctc	cac	ttc	gtc	ggg	gct	ggg	atc	tcc	499	
Lys	Glu	Ile	Ser	Ala	Arg	Gly	Leu	His	Phe	Val	Gly	Ala	Gly	Ile	Ser		
				120					125					130			
ggc	ggc	gaa	gaa	ggc	gca	ctc	aac	ggc	cca	tcc	atc	atg	cct	ggg	ggc	547	
Gly	Gly	Glu	Glu	Gly	Ala	Leu	Asn	Gly	Pro	Ser	Ile	Met	Pro	Gly	Gly		
				135					140					145			
cca	gca	aag	tcc	tac	gag	tcc	ctc	gga	cca	ctg	ctt	gag	tcc	atc	gct	595	
Pro	Ala	Lys	Ser	Tyr	Glu	Ser	Leu	Gly	Pro	Leu	Leu	Glu	Ser	Ile	Ala		
				150					155					160			
gcc	aac	gtt	gac	ggc	acc	cca	tgt	gtc	acc	cac	atc	ggc	cca	gac	ggc	643	
Ala	Asn	Val	Asp	Gly	Thr	Pro	Cys	Val	Thr	His	Ile	Gly	Pro	Asp	Gly		
				170					175					180			
gcc	ggc	cac	ttc	gtc	aag	atg	gtc	cac	aac	ggc	atc	gag	tac	gcc	gac	691	
Ala	Gly	His	Phe	Val	Lys	Met	Val	His	Asn	Gly	Ile	Glu	Tyr	Ala	Asp		
				185					190					195			
atg	cag	gtc	atc	ggc	gag	gca	tac	cac	ctt	ctc	cgc	tac	gca	gca	ggc	739	
Met	Gln	Val	Ile	Gly	Glu	Ala	Tyr	His	Leu	Leu	Arg	Tyr	Ala	Ala	Gly		
				200					205					210			
atg	cag	cca	gct	gaa	atc	gct	gag	gtt	ttc	aag	gaa	tgg	aac	gca	ggc	787	
Met	Gln	Pro	Ala	Glu	Ile	Ala	Glu	Val	Phe	Lys	Glu	Trp	Asn	Ala	Gly		
				215					220					225			
gac	ctg	gat	tcc	tac	ctc	atc	gaa	atc	acc	gca	gag	gtt	ctc	tcc	cag	835	
Asp	Leu	Asp	Ser	Tyr	Leu	Ile	Glu	Ile	Thr	Ala	Glu	Val	Leu	Ser	Gln		
				230					235					240			
														245			

gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct	883
Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala	
250 255 260	
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat	931
Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp	
265 270 275	
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca	979
Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala	
280 285 290	
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct	1027
Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro	
295 300 305	
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag	1075
Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln	
310 315 320 325	
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct	1123
Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala	
330 335 340	
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac	1171
Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn	
345 350 355	
tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc	1219
Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys	
360 365 370	
atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca	1267
Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala	
375 380 385	
aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag	1315
Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu	
390 395 400 405	
ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc	1363
Leu Gly Asp Leu Ile Asp Ser Trp Arg Val Ile Val Thr Ala Thr	
410 415 420	
cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac	1411
Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr	
425 430 435	
gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag	1459
Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln	
440 445 450	
cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc	1507
Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly	
455 460 465	
tcc ttc cac acc gag tgg tcc ggc gac cgc	1537
Ser Phe His Thr Glu Trp Ser Gly Asp Arg	
470 475	

&lt;210&gt; 254

&lt;211&gt; 479

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 254

Met Thr Asn Gly Asp Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala  
 1 5 10 15

Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr  
 20 25 30

Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala  
 35 40 45

Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu  
 50 55 60

Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln  
 65 70 75 80

Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met  
 85 90 95

Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp  
 100 105 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val  
 115 120 125

Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser  
 130 135 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu  
 145 150 155 160

Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His  
 165 170 175

Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly  
 180 185 190

Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu  
 195 200 205

Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys  
 210 215 220

Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala  
 225 230 235 240

Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp  
 245 250 255

Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val  
 260 265 270

Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala  
 275 280 285

Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala  
 290 295 300  
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly  
 305 310 315 320  
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala  
 325 330 335  
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly  
 340 345 350  
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile  
 355 360 365  
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val  
 370 375 380  
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro  
 385 390 395 400  
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val  
 405 410 415  
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser  
 420 425 430  
 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala  
 435 440 445  
 Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg  
 450 455 460  
 Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg  
 465 470 475

&lt;210&gt; 255

&lt;211&gt; 1326

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1303)

&lt;223&gt; RXN02596

&lt;400&gt; 255

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 gaaatttcgg caacgccgaa tgtaagtttag tgtcgaatgc atg acg gaa tcg aaa 115  
 Met Thr Glu Ser Lys  
 1 5  
 aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163  
 Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val  
 10 15 20  
 gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211  
 Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu  
 25 30 35

cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag	259
Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu	
40 45 50	
acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc	307
Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser	
55 60 65	
aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc	355
Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly	
70 75 80 85	
tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc	403
Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe	
90 95 100	
ccg atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc	451
Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser	
105 110 115	
cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat	499
Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp	
120 125 130	
tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt	547
Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly	
135 140 145	
cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg	595
Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp	
150 155 160 165	
cag act gat cca aag aac ctc cca gcc ggc aac atc acc cgc ctg cca	643
Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn Ile Thr Arg Leu Pro	
170 175 180	
gtt cgc tac aac ttc aac aac cgc tat ttc aac gac acc tac gaa ggc	691
Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn Asp Thr Tyr Glu Gly	
185 190 195	
ctt ccc aca gac ggc tac gcg gca tgg ttg gaa aag atg gca gag cat	739
Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu Lys Met Ala Glu His	
200 205 210	
gag ctt atc gac gtc cgc ctc gac acc gac tgg ttc gac gtt cgc gat	787
Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp Phe Asp Val Arg Asp	
215 220 225	
gac ctc cgc gca agc aac ccc gac gca cct gtg gtc tac acc ggc cca	835
Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val Val Tyr Thr Gly Pro	
230 235 240 245	
ctc gac ctc tac ttc aac tac gca gag ggc aag ctg gga tgg cgc acc	883
Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys Leu Gly Trp Arg Thr	
250 255 260	
ctc gac ttt gaa acc gaa gta gta gaa acc ggt gac ttc caa gga acc	931
Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly Asp Phe Gln Gly Thr	
265 270 275	



cca gtg atg aac tac aac gat gcg gac gta cct ttc acc cgc atc cac 979  
 Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro Phe Thr Arg Ile His  
 280 285 290

gag ttc cgt cac ttc cac cca gag cgt gat gac agt tac ccc aag gat 1027  
 Glu Phe Arg His Phe His Pro Glu Arg Asp Asp Ser Tyr Pro Lys Asp  
 295 300 305

aag acc gtc atc atg cgc gag ttc tcc cgt ttc gca gat aac gag gat 1075  
 Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe Ala Asp Asn Glu Asp  
 310 315 320 325

gag cct tat tac cca atc aac act cca gac gac cga gac atg ctg aag 1123  
 Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp Arg Asp Met Leu Lys  
 330 335 340

cag tac cgc ctt ctg gct gct gaa gag gct gct aat aat aag gtg ctg 1171  
 Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala Asn Asn Lys Val Leu  
 345 350 355

ttc ggc ggt cga ctg ggc acg tac cag tac ctc gac atg cac atg gct 1219  
 Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu Asp Met His Met Ala  
 360 365 370

atc ggt tct gcg ctg agc atg ttt gac aac aag ctg gtg ccg ttc ttt 1267  
 Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys Leu Val Pro Phe Phe  
 375 380 385

gaa gaa ggc aca ccg cta gag cag gaa cgc gga cac taaaaggaag 1313  
 Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly His  
 390 395 400

ggcatctccc aca 1326

<210> 256  
 <211> 401  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 256  
 Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu  
 1 5 10 15

Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys  
 20 25 30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser  
 35 40 45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His  
 50 55 60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe  
 65 70 75 80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly  
 85 90 95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe  
 100 105 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln  
 115 120 125  
 Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala  
 130 135 140  
 Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr  
 145 150 155 160  
 Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn  
 165 170 175  
 Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn  
 180 185 190  
 Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu  
 195 200 205  
 Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp  
 210 215 220  
 Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val  
 225 230 235 240  
 Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys  
 245 250 255  
 Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly  
 260 265 270  
 Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro  
 275 280 285  
 Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg Asp Asp  
 290 295 300  
 Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe  
 305 310 315 320  
 Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp  
 325 330 335  
 Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala  
 340 345 350  
 Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu  
 355 360 365  
 Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys  
 370 375 380  
 Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly  
 385 390 395 400

His

&lt;210&gt; 257

&lt;211&gt; 512

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(489)

&lt;223&gt; FRXA02596

&lt;400&gt; 257

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cct gtg gtc tac acc ggc cca ctc gac ctc tac ttc aac tac gca gag      48
Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu
   1                               5                               10                               15

ggc aag ctg gga tgg cgc acc ctc gac ttt gaa acc gaa gta gta gaa      96
Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu
                               20                               25                               30

acc ggt gac ttc caa gga acc cca gtg atg aac tac aac gat gcg gac     144
Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp
                               35                               40                               45

gta cct ttc acc cgc atc cac gag ttc cgt cac ttc cac cca gag cgt     192
Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg
                               50                               55                               60

gat gac agt tac ccc aag gat aag acc gtc atc atg cgc gag ttc tcc     240
Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser
   65                               70                               75                               80

cgt ttc gca gat aac gag gat gag cct tat tac cca atc aac act cca     288
Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro
                               85                               90                               95

gac gac cga gac atg ctg aag cag tac cgc ctt ctg gct gct gaa gag     336
Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu
                               100                              105                              110

gct gct aat aat aag gtg ctg ttc ggc ggt cga ctg ggc acg tac cag     384
Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln
                               115                              120                              125

tac ctc gac atg cac atg gct atc ggt tct gcg ctg agc atg ttt gac     432
Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp
                               130                              135                              140

aac aag ctg gtg ccg ttc ttt gaa gaa ggc aca ccg cta gag cag gaa     480
Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu
   145                               150                               155                               160

cgc gga cac taaaaggaag ggcattctccc aca                               512
Arg Gly His

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&lt;210&gt; 258

&lt;211&gt; 163

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 258

Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu

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<210> 259
<211> 598
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(598)
<223> FRXA02642
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<400> 259
aaggtatctg ggtgtggata tgccctgcta actggagaaa cttggcccga tcgggtgtct 60

gaaatttcgg caacgccgaa tgtaagtttag tgtcgaatgc atg acg gaa tcg aaa 115
Met Thr Glu Ser Lys
1 5

aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
10 15 20

gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
25 30 35

cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259
Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
40 45 50
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acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307  
 Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser  
     55                    60                    65

aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355  
 Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly  
     70                    75                    80                    85

tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403  
 Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe  
                     90                    95                    100

ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451  
 Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser  
                     105                    110                    115

cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499  
 Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp  
                     120                    125                    130

tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547  
 Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly  
                     135                    140                    145

cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595  
 Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp  
     150                    155                    160                    165

cag 598  
 Gln

&lt;210&gt; 260

&lt;211&gt; 166

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 260

Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu  
     1                    5                    10                    15

Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys  
                     20                    25                    30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser  
                     35                    40                    45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His  
                     50                    55                    60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe  
     65                    70                    75                    80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly  
                     85                    90                    95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe  
                     100                    105                    110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln  
 115 120 125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala  
 130 135 140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr  
 145 150 155 160

Thr Ala Lys Gln Trp Gln  
 165

<210> 261  
 <211> 668  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(645)  
 <223> RXA02572

<400> 261  
 gcg gtc gct gag att tgc gag ccg acc ggc gcc gat gcg gtt gcg ctt 48  
 Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu  
 1 5 10 15

gtg gat gcc atc ggt cac gac gat cgt atc ggc cga aag ttc tta ggc 96  
 Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly  
 20 25 30

gcg ggc ctg gga ttc ggt ggc ggt tgt ttg cct aaa gac atc cgc gct 144  
 Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala  
 35 40 45

ttc atg gca cgc gcg ggc gaa ttg ggt gct gac cag gca tta acg ttc 192  
 Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe  
 50 55 60

ttg cgt gag gtc gat tcc atc aat atg cgt cgt cgc gac cgt gtg gtg 240  
 Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val  
 65 70 75 80

cag ctg gcc aaa gag atg tgt ggc ggt tcg ctg ctg ggc aag cgg gtt 288  
 Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val  
 85 90 95

aca gtg ctc ggc gcc gca ttc aaa ccc aac tcg gac gat gtc cgc gat 336  
 Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp  
 100 105 110

tct ccg gcg ctg tcg gtc gcg ggt tcg ctg tcg ctc cag ggt gcg gcg 384  
 Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala  
 115 120 125

gtc tcg gtc tac gac ccg gaa gct atg gac aac gct cga cgc gtc ttc 432  
 Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe  
 130 135 140

ccg acg ctc agc tat gcg tcc agc act aaa gag gcg ctt atc gac gcc 480

Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala  
 145 150 155 160

cac ctc gtc gtt ctt gcc act gaa tgg caa gaa ttc cgc gac ctt gac 528  
 His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp  
 165 170 175

ccc gaa gtg gcg gga ggg gtc gtc gag aag cgc gct att att gat ggc 576  
 Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly  
 180 185 190

cga aac gtc ctc gat gtt gcc aaa tgg aag gcc gcc ggt tgg gaa atg 624  
 Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met  
 195 200 205

gaa gcg ctc ggc cgc aac ctt tagtgcggtg gatcaggcgg ggc 668  
 Glu Ala Leu Gly Arg Asn Leu  
 210 215

&lt;210&gt; 262

&lt;211&gt; 215

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 262

Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu  
 1 5 10 15

Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly  
 20 25 30

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala  
 35 40 45

Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe  
 50 55 60

Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val  
 65 70 75 80

Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val  
 85 90 95

Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp  
 100 105 110

Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala  
 115 120 125

Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe  
 130 135 140

Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala  
 145 150 155 160

His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp  
 165 170 175

Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly  
 180 185 190

Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met  
 195 200 205

Glu Ala Leu Gly Arg Asn Leu  
 210 215

<210> 263

<211> 1224

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1201)

<223> RXA02485

<400> 263

cggtggtcag tgcttggtgc accttgccga cgggctgatt gatcgtaatg gtgttttctg 60

tacgcgttgc catgaggata agactaccgt tagtgggggtg ttg gat tca tcg cta 115  
 Leu Asp Ser Ser Leu  
 1 5

gcc cag gaa atc gcc gcg atc gac ggc gtc gaa ctc gat tcg gaa gtc 163  
 Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu Leu Asp Ser Glu Val  
 10 15 20

act ttc gcc gat ctg acg acc ctc cgc atc ggc gga aaa ccc cgc agc 211  
 Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly Gly Lys Pro Arg Ser  
 25 30 35

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg 259  
 Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu  
 40 45 50

ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat 307  
 Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn  
 55 60 65

ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa 355  
 Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu  
 70 75 80 85

acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat 403  
 Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp  
 90 95 100

gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc 451  
 Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly  
 105 110 115

ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc 499  
 Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala  
 120 125 130

acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta 547  
 Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val  
 135 140 145



ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg	595
Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr His Gln Val Ser Trp	
150 155 160 165	
gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa	643
Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys	
170 175 180	
ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc	691
Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr	
185 190 195	
gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta	739
Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu	
200 205 210	
gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc	787
Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val	
215 220 225	
cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa	835
Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu	
230 235 240 245	
cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca	883
His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro	
250 255 260	
atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa	931
Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu	
265 270 275	
ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc	979
Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser	
280 285 290	
gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc	1027
Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly	
295 300 305	
gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc	1075
Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr	
310 315 320 325	
aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa	1123
Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu	
330 335 340	
atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa	1171
Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu	
345 350 355	
ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg	1221
Pro Val Trp Ile Gly Ile Ser Ile Asp Asp	
360 365	
gca	1224

&lt;210&gt; 264

&lt;211&gt; 367

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 264

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Leu Asp Ser Ser Leu Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu
 1           5           10           15

Leu Asp Ser Glu Val Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly
          20           25           30

Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val
          35           40           45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val
 50           55           60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile
 65           70           75           80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly
          85           90           95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu
          100          105          110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro
          115          120          125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr
          130          135          140

Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr
145           150           155           160

His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg
          165          170          175

Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu
          180          185          190

Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu
          195          200          205

Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg
210           215           220

Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys
225           230           235           240

Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser
          245           250           255

Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe
          260          265          270

Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly
          275          280           285

Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys
290           295           300

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Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His  
305 310 315 320

Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val  
325 330 335

Ala Leu Ala Lys Glu Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val  
340 345 350

Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp  
355 360 365

<210> 265

<211> 1124

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1101)

<223> RXA01216

<400> 265

acc gac cac act ctg tct gca ctg ctg gat gca cac gtg gaa gtt cca 48  
Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro  
1 5 10 15

acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac 96  
Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr  
20 25 30

ggc cgc atc gtg cgc aac gaa gaa ggc gaa gtc acc gcc atc gtt gag 144  
Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu  
35 40 45

caa aaa gat gct tca gca gaa gtc caa gcc atc gat gag gtc aac tcc 192  
Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser  
50 55 60

ggt gtc ttt gct ttc gac gcc gcc atc ttg cgt tcc gca ctg gct gaa 240  
Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu  
65 70 75 80

ctg aag tcc gac aac gct cag ggc gag ctg tac ctg acc gac gtt ttg 288  
Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu  
85 90 95

ggc att gct cgt ggc gag ggc cac cca gtg cgc gcc cac acc gcc gcc 336  
Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala  
100 105 110

gat gct cgt gaa ctc gcc ggc gtc aac gat cgt gtg cag ctc gca gaa 384  
Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu  
115 120 125

gcc ggc gcc gaa cta aac cgt cgc acc gtc atc gcc gct atg cgt ggt 432  
Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly  
130 135 140

ggc gca acc atc gtt gat cca gca acc acc tgg atc gat gtg gag gtt 480

Gly 145	Ala	Thr	Ile	Val	Asp 150	Pro	Ala	Thr	Thr	Trp 155	Ile	Asp	Val	Glu	Val 160	
tct Ser	atc Ile	gga Gly	cgc Arg	gac Asp	gtg Val	atc Ile	atc Ile	cac His	cct Pro	ggc Gly	acc Thr	cag Gln	ctc Leu	aag Lys	ggc Gly	528
gaa Glu	act Thr	gtc Val	atc Ile	gga Gly	gac Asp	cgc Arg	gtt Val	gaa Glu	gtt Val	ggc Gly	cca Pro	gac Asp	acc Thr	acc Thr	ttg Leu	576
acc Thr	aac Asn	atg Met	acc Thr	atc Ile	ggc Gly	gac Asp	ggc Gly	gca Ala	tcc Ser	gta Val	atc Ile	cgc Arg	acc Thr	cac His	ggc Gly	624
ttc Phe	gac Asp	tcc Ser	acc Thr	atc Ile	ggc Gly	gaa Glu	aac Asn	gcc Ala	acc Thr	gtt Val	ggc Gly	ccc Pro	ttc Phe	acc Thr	tac Tyr	672
atc Ile	cgc Arg	cca Pro	gga Gly	acc Thr	aca Thr	ctg Leu	gga Gly	cca Pro	gaa Glu	ggc Gly	aag Lys	ctc Leu	ggc Gly	ttc Phe		720
gta Val	gaa Glu	acc Thr	aag Lys	aag Lys	gcc Ala	aca Thr	atc Ile	ggc Gly	cgt Arg	ggc Gly	tcc Ser	aag Lys	gtt Val	cca Pro	cac His	768
ctc Leu	acc Thr	tat Tyr	gtc Val	ggc Gly	gac Asp	gcc Ala	acc Thr	atc Ile	ggc Gly	gag Glu	gaa Glu	tcc Ser	aac Asn	atc Ile	gga Gly	816
gcc Ala	tcc Ser	tct Ser	gtc Val	ttc Phe	gtg Val	aac Asn	tac Tyr	gac Asp	ggc Gly	gaa Glu	aac Asn	aag Lys	cac His	cac His	acc Thr	864
acc Thr	atc Ile	ggc Gly	agc Ser	cac His	gtt Val	cgc Arg	act Thr	ggc Gly	tct Ser	gac Asp	acc Thr	atg Met	ttt Phe	atc Ile	gct Ala	912
cca Pro	gtg Val	acc Thr	gtg Val	ggc Gly	gac Asp	gga Gly	gag Ala	tat Tyr	tcc Ser	gga Gly	gcc Ala	ggc Gly	aca Thr	gta Val	att Ile	960
aaa Lys	gac Asp	gat Asp	gtt Val	ccg Pro	cca Pro	gga Gly	gcc Ala	ctt Leu	gcc Ala	gtg Val	tcc Ser	ggc Gly	gga Gly	cgc Arg	caa Gln	1008
cga Arg	aac Asn	atc Ile	gaa Glu	ggc Gly	tgg Trp	gtg Val	caa Gln	aag Lys	aag Lys	cgc Arg	cct Pro	gga Gly	acc Thr	gct Ala	gca Ala	1056
gca Ala	caa Gln	gcc Ala	gca Ala	gaa Glu	gcc Ala	gcc Ala	caa Gln	aac Asn	gtc Val	cac His	aac Asn	cag Gln	gaa Glu	ggc Gly		1101
taagcaggat cctcatgact gct																1124

<210> 266  
 <211> 367  
 <212> PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 266

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Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro
 1          5          10          15

Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr
          20          25          30

Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu
          35          40          45

Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser
          50          55          60

Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu
          65          70          75          80

Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu
          85          90          95

Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala
          100          105          110

Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu
          115          120          125

Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly
          130          135          140

Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val
          145          150          155          160

Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly
          165          170          175

Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu
          180          185          190

Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly
          195          200          205

Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr
          210          215          220

Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe
          225          230          235          240

Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His
          245          250          255

Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly
          260          265          270

Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr
          275          280          285

Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala
          290          295          300

Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile

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305		310		315		320
Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln						
		325		330		335
Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala						
		340		345		350
Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly						
		355		360		365

<210> 267  
 <211> 981  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(958)  
 <223> RXA01259

<400> 267  
 aagagaatta tttctaaaat tcggtatcgt ctaagaaatg agtttgccaa tagctcagca 60  
 tcaaaatgct gtaaaaactg tcgtggtacc agctgcagga atg gga aca cgg ttc 115  
 Met Gly Thr Arg Phe  
 1 5  
 ctt cct gca acg aag aca att cca aag gag ctt ctt cct gta gtt gat 163  
 Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu Leu Pro Val Val Asp  
 10 15 20  
 acc ccg ggt att gaa ctt gtt gcc aaa gag gct gct gat ctt ggt gca 211  
 Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala Ala Asp Leu Gly Ala  
 25 30 35  
 act cgg tta gca att atc act gct ccg aac aaa gac gga att ctt aaa 259  
 Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys Asp Gly Ile Leu Lys  
 40 45 50  
 cac ttc gag gag ttc cct gag ctt gag gca act ctt gag gct cgc ggt 307  
 His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr Leu Glu Ala Arg Gly  
 55 60 65  
 aag act gat caa ctg aat aaa gtt cga gca gct cga gaa ttg att gca 355  
 Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala Arg Glu Leu Ile Ala  
 70 75 80 85  
 aca gtt cca gtg gtt caa gaa aag cca ttg ggg ctt ggt cac gct gtt 403  
 Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly Leu Gly His Ala Val  
 90 95 100  
 ggc ctt gct gag tct gtg ctc gat gat gat gaa gat gtt gtg gct gtc 451  
 Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu Asp Val Val Ala Val  
 105 110 115  
 atg ctg cca gac gat ttg gtg ctg cca ttt ggt gtg acc gag aga atg 499  
 Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly Val Thr Glu Arg Met  
 120 125 130

gca gaa gtt cgc gct aag ttt ggc gga tct gtt ctt gca gca att gag 547  
 Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val Leu Ala Ala Ile Glu  
 135 140 145

gtg gct gaa gat gaa gtc tca aat tac gga gta ttt aag ctc ggt gaa 595  
 Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val Phe Lys Leu Gly Glu  
 150 155 160 165

ctc gat gca gag tcc gaa agt gaa ggc att agg cgt gtt gta gga atg 643  
 Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg Arg Val Val Gly Met  
 170 175 180

gtt gaa aag cct gcg cct gaa gat gca cca tca agg ttt gcc gca acg 691  
 Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Arg Phe Ala Ala Thr  
 185 190 195

ggc cgt tat cta ctt gat cga gct att ttt gat gca ctg cgt cga att 739  
 Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp Ala Leu Arg Arg Ile  
 200 205 210

gag cct ggt gct ggt gga gaa ctg caa tta aca gat gcc atc gca tta 787  
 Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr Asp Ala Ile Ala Leu  
 215 220 225

ttg atc gaa gaa ggc cat ccg gta cac att gtg gtt cat gaa gga aag 835  
 Leu Ile Glu Glu Gly His Pro Val His Ile Val Val His Glu Gly Lys  
 230 235 240 245

cgc cat gac ctt ggt aat cca gct ggg tac att cct gct gtt gtg tac 883  
 Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile Pro Ala Val Val Tyr  
 250 255 260

ttc gga ctt cgt cat gca gag tac ggt tcc aag att cac cgt gcg gtg 931  
 Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys Ile His Arg Ala Val  
 265 270 275

aag gaa ata ctc gct gag ttt gaa tct taaaaaggaa accgccttcc 978  
 Lys Glu Ile Leu Ala Glu Phe Glu Ser  
 280 285

aca 981

&lt;210&gt; 268

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 268

Met Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu  
 1 5 10 15

Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala  
 20 25 30

Ala Asp Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys  
 35 40 45

Asp Gly Ile Leu Lys His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr  
 50 55 60

Leu Glu Ala Arg Gly Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala  
 65 70 75 80  
 Arg Glu Leu Ile Ala Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly  
 85 90 95  
 Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu  
 100 105 110  
 Asp Val Val Ala Val Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly  
 115 120 125  
 Val Thr Glu Arg Met Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val  
 130 135 140  
 Leu Ala Ala Ile Glu Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val  
 145 150 155 160  
 Phe Lys Leu Gly Glu Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg  
 165 170 175  
 Arg Val Val Gly Met Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser  
 180 185 190  
 Arg Phe Ala Ala Thr Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp  
 195 200 205  
 Ala Leu Arg Arg Ile Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr  
 210 215 220  
 Asp Ala Ile Ala Leu Leu Ile Glu Glu Gly His Pro Val His Ile Val  
 225 230 235 240  
 Val His Glu Gly Lys Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile  
 245 250 255  
 Pro Ala Val Val Tyr Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys  
 260 265 270  
 Ile His Arg Ala Val Lys Glu Ile Leu Ala Glu Phe Glu Ser  
 275 280 285

&lt;210&gt; 269

&lt;211&gt; 526

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(526)

&lt;223&gt; RXA02028

&lt;400&gt; 269

tgcgaggttc ctgcttagtt tggctcataa atctaaggat aaccgttatt ttcggagggg 60

 tacgacgatt ggggttgcgg gggcaggtac tcttggttcc atg agt ttg cct atc 115  
 Met Ser Leu Pro Ile  
 1 5

gat gag cac gtg aac gcg gtt aaa acc gtc gta gtg cct gct gca gga 163



```

Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly
      10                      15                      20

ctg gga acc cga ttc ctt ccg gcc acc aaa acc gta ccc aag gag ttg 211
Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu
      25                      30                      35

ctg ccg gtt gtc gat acc cca ggt att gag ctg att gct gct gag gct 259
Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala
      40                      45                      50

gcc gaa ctt ggt gcg acc agg ctg gcg atc atc act gcg cca aac aaa 307
Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
      55                      60                      65

gct ggg gta ctt gca cac ttt gag cgt tct tct gaa ttg gaa gaa acg 355
Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr
      70                      75                      80                      85

ctg atg gag cgt ggc aag act gac cag gtg gag ata atc cgc cgc gcc 403
Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala
      90                      95                      100

gcc gat tta atc aag gca gtt cca gta acc cag gac aag ccg ctg ggg 451
Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly
      105                      110                      115

cta ggt cat gct gtt ggt ttg gct gag tct gtg ttg gat gat gat gaa 499
Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
      120                      125                      130

gat gtc gta gcg gtg atg ttg ccg cac
Asp Val Val Ala Val Met Leu Pro His
      135                      140

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&lt;210&gt; 270

&lt;211&gt; 142

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 270

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Met Ser Leu Pro Ile Asp Glu His Val Asn Ala Val Lys Thr Val Val
  1                      5                      10                      15

Val Pro Ala Ala Gly Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr
      20                      25                      30

Val Pro Lys Glu Leu Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu
      35                      40                      45

Ile Ala Ala Glu Ala Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile
      50                      55                      60

Thr Ala Pro Asn Lys Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser
      65                      70                      75                      80

Glu Leu Glu Glu Thr Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu
      85                      90                      95

Ile Ile Arg Arg Ala Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln

```

100	105	110
Asp Lys Pro Leu Gly Leu Gly His Ala Val Gly Leu Ala Glu Ser Val		
115	120	125
Leu Asp Asp Asp Glu Asp Val Val Ala Val Met Leu Pro His		
130	135	140

<210> 271  
 <211> 1284  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
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 <222> (101)..(1261)  
 <223> RXA01262  
  
 <400> 271  
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 aaacttgctg tatcaataaa acacgaaaag gaatactttt atg aaa att gcc gtc 115  
 Met Lys Ile Ala Val  
 1 5  
  
 gca ggg ctc gga tat gtt ggg ctt tca aat gca gct ctc ctc tct aaa 163  
 Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys  
 10 15 20  
  
 aat cat aaa gtt gtt gca gtt gac att gat gaa gaa cga gtg aaa cta 211  
 Asn His Lys Val Val Ala Val Asp Ile Asp Glu Glu Arg Val Lys Leu  
 25 30 35  
  
 gtt caa gaa ttt cgt tcg cca att gtc gat agc gat ctc gaa gaa tat 259  
 Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser Asp Leu Glu Glu Tyr  
 40 45 50  
  
 ctg tcc act aag cct caa aac tta act gcc aca acg gac gcc gaa gcc 307  
 Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr Thr Asp Ala Glu Ala  
 55 60 65  
  
 gct tac aaa ggc gca gat ttt att gtt att gca acg cca act aat tac 355  
 Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala Thr Pro Thr Asn Tyr  
 70 75 80 85  
  
 gac cca gag tca aac ttt ttt gat act tcc agc gtt gag tcc gta att 403  
 Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser Val Glu Ser Val Ile  
 90 95 100  
  
 gag ata gtc ctt aag gtt tct cct gga tcc aca atc gta att aaa tcg 451  
 Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr Ile Val Ile Lys Ser  
 105 110 115  
  
 act atc cct gtt ggt ttt aca tcg gaa cta cgc att aag cat cca gaa 499  
 Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg Ile Lys His Pro Glu  
 120 125 130  
  
 gct tcg att att ttt tca cct gag ttc ctg cgt gaa ggc cga gca ttc 547  
 Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg Glu Gly Arg Ala Phe  
 135 140 145

tac gac aat ctc tac cca tcc aga gtt gtc gtt ggt gat cgc agt cct	595
Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val Gly Asp Arg Ser Pro	
150 155 160 165	
ctg ggg gaa gaa ttt gcg act ctg tta gct gag ggg gca aaa gaa aag	643
Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu Gly Ala Lys Glu Lys	
170 175 180	
cct ccg att cta ctt acg gac tca act gag gca gag gcg att aaa tta	691
Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala Glu Ala Ile Lys Leu	
185 190 195	
ttt tct aat aca tat ctt gca ctg cga gtt gct ttt ttc aac gaa ctg	739
Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala Phe Phe Asn Glu Leu	
200 205 210	
gat act tat gcg tct gtt cga agc ttg gat act aag cag att att gaa	787
Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr Lys Gln Ile Ile Glu	
215 220 225	
ggg gta ggg ctc gat cca cgt att gga tct cat tac aat aat cct tca	835
Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His Tyr Asn Asn Pro Ser	
230 235 240 245	
ttt gga tat ggc gga tat tgt ctt ccg aaa gat acg aaa cag ctt ctc	883
Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp Thr Lys Gln Leu Leu	
250 255 260	
gcc aac tat aag gat gtc ccg cag aat cta atc tct gca gta gtc caa	931
Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile Ser Ala Val Val Gln	
265 270 275	
gca aat aag act cgt aag gac ttt att gca gag gat atc ctc agt aaa	979
Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu Asp Ile Leu Ser Lys	
280 285 290	
tca cct act gta gtt gga att tac cgc ctt gta atg aag tct gga tca	1027
Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val Met Lys Ser Gly Ser	
295 300 305	
gat aac ttt cgt tct tct tct att caa gga gtc atg aaa cga att aag	1075
Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val Met Lys Arg Ile Lys	
310 315 320 325	
gcc aag gga atc gaa att gta gta ttt gaa ccg aat ctc gga gaa gaa	1123
Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro Asn Leu Gly Glu Glu	
330 335 340	
act ttc tac aat tcg aag atc ctt aat gac atc gaa gag ttt aag gat	1171
Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile Glu Glu Phe Lys Asp	
345 350 355	
tac tgc gac atc att att gca aat cgt cca acc gat gag ctt tct gat	1219
Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr Asp Glu Leu Ser Asp	
360 365 370	
gta cca gaa aaa gtt tat aca cgt gat att ttc cag cgt gac	1261
Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe Gln Arg Asp	
375 380 385	

taagtggaaa gaatcttttg ttg

1284

<210> 272

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Met Lys Ile Ala Val Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala  
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Ala Leu Leu Ser Lys Asn His Lys Val Val Ala Val Asp Ile Asp Glu  
20 25 30

Glu Arg Val Lys Leu Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser  
35 40 45

Asp Leu Glu Glu Tyr Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr  
50 55 60

Thr Asp Ala Glu Ala Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala  
65 70 75 80

Thr Pro Thr Asn Tyr Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser  
85 90 95

Val Glu Ser Val Ile Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr  
100 105 110

Ile Val Ile Lys Ser Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg  
115 120 125

Ile Lys His Pro Glu Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg  
130 135 140

Glu Gly Arg Ala Phe Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val  
145 150 155 160

Gly Asp Arg Ser Pro Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu  
165 170 175

Gly Ala Lys Glu Lys Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala  
180 185 190

Glu Ala Ile Lys Leu Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala  
195 200 205

Phe Phe Asn Glu Leu Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr  
210 215 220

Lys Gln Ile Ile Glu Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His  
225 230 235 240

Tyr Asn Asn Pro Ser Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp  
245 250 255

Thr Lys Gln Leu Leu Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile  
260 265 270

Ser Ala Val Val Gln Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu

275	280	285
Asp Ile Leu Ser Lys Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val 290	295	300
Met Lys Ser Gly Ser Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val 305	310	315 320
Met Lys Arg Ile Lys Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro 325	330	335
Asn Leu Gly Glu Glu Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile 340	345	350
Glu Glu Phe Lys Asp Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr 355	360	365
Asp Glu Leu Ser Asp Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe 370	375	380
Gln Arg Asp 385		

<210> 273  
 <211> 1209  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1186)  
 <223> RXA01377

<400> 273  
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 ccccttaaag acaccctaaa caccagtgaa ataggaacac atg act tta act gac 115  
 Met Thr Leu Thr Asp  
 1 5  
 aac agc aaa aac gtt gat gct gtc atc ttg gtc ggt ggc aaa ggt acc 163  
 Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val Gly Gly Lys Gly Thr  
 10 15 20  
 cga ctg cgc ccc ctg acc gtc aat act cca aag cca atg ctg cca act 211  
 Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys Pro Met Leu Pro Thr  
 25 30 35  
 gct ggc cac cca ttc ttg acc cac ctt ttg gcc cgc atc aag gcc gca 259  
 Ala Gly His Pro Phe Leu Thr His Leu Leu Ala Arg Ile Lys Ala Ala  
 40 45 50  
 ggc atc aca cac gtc gtg ctg gga acg tca ttc aaa gct gaa gtc ttc 307  
 Gly Ile Thr His Val Val Leu Gly Thr Ser Phe Lys Ala Glu Val Phe  
 55 60 65  
 gag gaa tac ttc gga gat ggc tcc gaa atg ggc ttg gaa att gaa tat 355  
 Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly Leu Glu Ile Glu Tyr  
 70 75 80 85

gtc gtc gag gat cag cct ttg ggc act ggt ggt ggc atc cga aac gtc	403
Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly Gly Ile Arg Asn Val	
90 95 100	
tac gac aag ctg cgt cac gat act gcg att gtg ttc aac ggc gat gtg	451
Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val Phe Asn Gly Asp Val	
105 110 115	
ctc tcc ggt gcg gat ctc aac agc att ctg gac acc cac cgc gaa aag	499
Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp Thr His Arg Glu Lys	
120 125 130	
gac gca gat ctg acc atg cat ctc gtg cgc gta gct aac cct cgt gcg	547
Asp Ala Asp Leu Thr Met His Leu Val Arg Val Ala Asn Pro Arg Ala	
135 140 145	
ttt ggt tgc gtc ccc acc gat gag gat ggt cgc gtc agc gaa ttc ctt	595
Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg Val Ser Glu Phe Leu	
150 155 160 165	
gaa aag acc gaa gat cca cca acc gat cag atc aac gcc ggc tgc tac	643
Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile Asn Ala Gly Cys Tyr	
170 175 180	
gtg ttc aag aag gaa ctc atc gag cag atc ccg gca ggc cga gca gtt	691
Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro Ala Gly Arg Ala Val	
185 190 195	
tcc gtc gag cgc gaa acc ttc cct cag ctg ttg gaa gaa ggc aag cga	739
Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu Glu Glu Gly Lys Arg	
200 205 210	
gtc ttc ggc cac gtc gac gct tcc tac tgg cgc gac atg ggc acc cca	787
Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg Asp Met Gly Thr Pro	
215 220 225	
agc gac ttc gtc cgc ggc tcg gct gac ctg gtc cgc ggc att gcg tac	835
Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val Arg Gly Ile Ala Tyr	
230 235 240 245	
tcc cca ttg ctc gaa ggc aaa aca gga gag tcg ctt gtc gac gcc tcc	883
Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser Leu Val Asp Ala Ser	
250 255 260	
gcc ggc gtt cgc gac ggc gtc ctg ctg ctc ggc gga acc gta gtc ggc	931
Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly Gly Thr Val Val Gly	
265 270 275	
cgc ggc act gag atc ggt gcc ggc tgc cgc gtt gac aac act gtt att	979
Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val Asp Asn Thr Val Ile	
280 285 290	
ttc gac ggc gtc acc att gaa cca ggt gcg gtc att gaa aat tcc atc	1027
Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val Ile Glu Asn Ser Ile	
295 300 305	
att tcc tcg gga gca cgc atc ggt gct aat gcg cac atc tcc ggt tgc	1075
Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala His Ile Ser Gly Cys	
310 315 320 325	
atc att ggc gag ggc gca cag gtt ggt gct cgg tgt gaa ctc aac gca	1123

<210> 274  
<211> 362  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 274															
Met	Thr	Leu	Thr	Asp	Asn	Ser	Lys	Asn	Val	Asp	Ala	Val	Ile	Leu	Val
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Gly	Gly	Lys	Gly	Thr	Arg	Leu	Arg	Pro	Leu	Thr	Val	Asn	Thr	Pro	Lys
			20					25					30		
Pro	Met	Leu	Pro	Thr	Ala	Gly	His	Pro	Phe	Leu	Thr	His	Leu	Leu	Ala
		35					40					45			
Arg	Ile	Lys	Ala	Ala	Gly	Ile	Thr	His	Val	Val	Leu	Gly	Thr	Ser	Phe
	50					55					60				
Lys	Ala	Glu	Val	Phe	Glu	Glu	Tyr	Phe	Gly	Asp	Gly	Ser	Glu	Met	Gly
65					70					75					80
Leu	Glu	Ile	Glu	Tyr	Val	Val	Glu	Asp	Gln	Pro	Leu	Gly	Thr	Gly	Gly
				85					90					95	
Gly	Ile	Arg	Asn	Val	Tyr	Asp	Lys	Leu	Arg	His	Asp	Thr	Ala	Ile	Val
			100					105					110		
Phe	Asn	Gly	Asp	Val	Leu	Ser	Gly	Ala	Asp	Leu	Asn	Ser	Ile	Leu	Asp
		115					120					125			
Thr	His	Arg	Glu	Lys	Asp	Ala	Asp	Leu	Thr	Met	His	Leu	Val	Arg	Val
	130					135					140				
Ala	Asn	Pro	Arg	Ala	Phe	Gly	Cys	Val	Pro	Thr	Asp	Glu	Asp	Gly	Arg
145					150					155					160
Val	Ser	Glu	Phe	Leu	Glu	Lys	Thr	Glu	Asp	Pro	Pro	Thr	Asp	Gln	Ile
				165					170					175	
Asn	Ala	Gly	Cys	Tyr	Val	Phe	Lys	Lys	Glu	Leu	Ile	Glu	Gln	Ile	Pro
			180					185					190		
Ala	Gly	Arg	Ala	Val	Ser	Val	Glu	Arg	Glu	Thr	Phe	Pro	Gln	Leu	Leu
		195					200					205			
Glu	Glu	Gly	Lys	Arg	Val	Phe	Gly	His	Val	Asp	Ala	Ser	Tyr	Trp	Arg
	210					215					220				
Asp	Met	Gly	Thr	Pro	Ser	Asp	Phe	Val	Arg	Gly	Ser	Ala	Asp	Leu	Val

225	230	235	240
Arg Gly Ile Ala Tyr Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser	245	250	255
Leu Val Asp Ala Ser Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly	260	265	270
Gly Thr Val Val Gly Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val	275	280	285
Asp Asn Thr Val Ile Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val	290	295	300
Ile Glu Asn Ser Ile Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala	305	310	315
His Ile Ser Gly Cys Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg	325	330	335
Cys Glu Leu Asn Ala Gly Met Arg Val Phe Pro Gly Val Val Ile Pro	340	345	350
Asp Ser Gly Ile Arg Phe Ser Ser Asp Gln	355	360	

&lt;210&gt; 275

&lt;211&gt; 1350

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1327)

&lt;223&gt; RXA02063

&lt;400&gt; 275

accgaaatgg gggcattaata aggggctatc attcggaccc caaaacgatg tttagacaat 60

ttgttaccca gctttcatgc gggatagtta ttttgcttt	atg gtt aag ggt gtg	115
	Met Val Lys Gly Val	
	1 5	

aag ggt aga cca aat gtt cta gca atc gtt ctc gca ggt ggc gag ggc	163
Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu Ala Gly Gly Glu Gly	
10 15 20	

aaa cga ctt ttt ccg ttg acg gag gac cga gct aag cct gcg gtc cca	211
Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala Lys Pro Ala Val Pro	
25 30 35	

ttc ggc gga act tac aga ttg atc gac ttt gtt ttg tcg aac ctg gtg	259
Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val Leu Ser Asn Leu Val	
40 45 50	

aac tcc gga ttc ctc aag atc gcg gta ctg act cag tac aag tcg cat	307
Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr Gln Tyr Lys Ser His	
55 60 65	

tca ttg gat agg cat att tca ttg tcg tgg aac gtg tct ggt cca acg	355
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Ser 70	Leu	Asp	Arg	His	Ile 75	Ser	Leu	Ser	Trp	Asn 80	Val	Ser	Gly	Pro	Thr 85	
ggg Gly	cag Gln	tac Tyr	att Ile	gct Ala	tct Ser	ggt Val	cct Pro	gcg Ala	cag Gln	cag Gln	cgc Arg	ctg Leu	ggc Gly	aag Lys	cga Arg	403
tgg Trp	ttc Phe	act Thr	ggt Gly	tcc Ser	gcg Ala	gat Asp	gca Ala	att Ile	ttg Leu	cag Gln	tct Ser	ctg Leu	aac Asn	ttg Leu	atc Ile	451
tct Ser	gat Asp	gag Glu	aaa Lys	ccg Pro	gat Asp	tat Tyr	gtc Val	atc Ile	ggt Val	ttc Phe	ggc Gly	gcg Ala	gac Asp	cac His	gtg Val	499
tat Tyr	cg Arg	atg Met	gac Asp	cca Pro	agc Ser	cag Gln	atg Met	cta Leu	gat Asp	gag Glu	cac His	att Ile	gca Ala	tct Ser	ggt Gly	547
cg Arg	gcg Ala	gtg Val	tct Ser	gtg Val	gca Ala	ggt Gly	att Ile	cg Arg	ggt Val	cca Pro	cgt Arg	gag Glu	gaa Glu	gca Ala	act Thr	595
gcg Ala	ttt Phe	ggt Gly	tgc Cys	atc Ile	cag Gln	tcc Ser	gat Asp	gtc Val	gac Asp	ggc Gly	aac Asn	ata Ile	acc Thr	gag Glu	ttc Phe	643
ttg Leu	gaa Glu	aag Lys	cca Pro	gct Ala	gac Asp	cct Pro	ccg Pro	gga Gly	acc Thr	cct Pro	gat Asp	gat Asp	cct Pro	gac Asp	atg Met	691
act Thr	tac Tyr	gcg Ala	tcg Ser	atg Met	ggt Gly	aac Asn	tac Tyr	att Ile	ttc Phe	acc Thr	act Thr	gaa Glu	gcc Ala	ctg Leu	atc Ile	739
cag Gln	gcg Ala	ctg Leu	aaa Lys	gat Asp	gat Asp	gaa Glu	aac Asn	aac Asn	gag Glu	aac Asn	agt Ser	gat Asp	cat His	gac Asp	atg Met	787
ggc Gly	gga Gly	gac Asp	atc Ile	att Ile	ccg Pro	tac Tyr	ttc Phe	gtc Val	tct Ser	cg Arg	aac Asn	gat Asp	gcg Ala	cat His	gtt Val	835
tat Tyr	gat Asp	ttc Phe	tcc Ser	gga Gly	aac Asn	att Ile	ggt Val	cct Pro	ggc Gly	gca Ala	act Thr	gag Glu	cgt Arg	gac Asp	aag Lys	883
ggc Gly	tac Tyr	tgg Trp	cg Arg	gac Asp	gtc Val	ggt Gly	acc Thr	att Ile	gat Asp	gcg Ala	ttc Phe	tac Tyr	gag Glu	tgc Cys	cac His	931
atg Met	gac Asp	ctg Leu	att Ile	tcc Ser	gtg Val	cac His	cca Pro	atc Ile	ttc Phe	aac Asn	ctg Leu	tat Tyr	aac Asn	tct Ser	gag Glu	979
tgg Trp	cca Pro	atc Ile	cac His	acg Thr	acc Thr	tct Ser	gaa Glu	ggt Gly	aac Asn	ttg Leu	cct Pro	ccg Pro	gct Ala	aag Lys	ttc Phe	1027
gtt Val	cg Arg	ggc Gly	ggt Gly	atc Ile	gcg Ala	cag Gln	tcg Ser	tcg Ser	atg Met	gtg Val	tct Ser	tca Ser	ggt Gly	tcc Ser	atc Ile	1075

310	315	320	325	
att tct gct ggg act gtt cgc aac tcc gtg ctg tcc aac aac gtt gtc				1123
Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu Ser Asn Asn Val Val	330	335	340	
gtc gaa gag ggc gca acg gtg gaa ggt gca gtg ctg atg cca ggc gtg				1171
Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val Leu Met Pro Gly Val	345	350	355	
cgc atc ggt aag ggt gct gtt gtc cgc cat gcg att ctg gac aag aac				1219
Arg Ile Gly Lys Gly Ala Val Val Arg His Ala Ile Leu Asp Lys Asn	360	365	370	
gtg gtt gtc cgc gac gga gag ctc atc ggt gtc gac caa gtg cgc gat				1267
Val Val Val Arg Asp Gly Glu Leu Ile Gly Val Asp Gln Val Arg Asp	375	380	385	
gcg cag cgc ttc aag gtg agc gcc ggc ggc gtc gtg gtt gtc ggt aag				1315
Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val Val Val Val Gly Lys	390	395	400	405
aac cag gta gtc taaacgggaa agggacctta aaa				1350
Asn Gln Val Val				

&lt;210&gt; 276

&lt;211&gt; 409

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 276

Met Val Lys Gly Val Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu	1	5	10	15
Ala Gly Gly Glu Gly Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala	20	25	30	
Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val	35	40	45	
Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr	50	55	60	
Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn	65	70	75	80
Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln	85	90	95	
Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln	100	105	110	
Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe	115	120	125	
Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu	130	135	140	
His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro				

145		150		155		160									
Arg	Glu	Glu	Ala	Thr	Ala	Phe	Gly	Cys	Ile	Gln	Ser	Asp	Val	Asp	Gly
				165					170					175	
Asn	Ile	Thr	Glu	Phe	Leu	Glu	Lys	Pro	Ala	Asp	Pro	Pro	Gly	Thr	Pro
			180					185					190		
Asp	Asp	Pro	Asp	Met	Thr	Tyr	Ala	Ser	Met	Gly	Asn	Tyr	Ile	Phe	Thr
		195					200					205			
Thr	Glu	Ala	Leu	Ile	Gln	Ala	Leu	Lys	Asp	Asp	Glu	Asn	Asn	Glu	Asn
	210					215					220				
Ser	Asp	His	Asp	Met	Gly	Gly	Asp	Ile	Ile	Pro	Tyr	Phe	Val	Ser	Arg
225					230					235					240
Asn	Asp	Ala	His	Val	Tyr	Asp	Phe	Ser	Gly	Asn	Ile	Val	Pro	Gly	Ala
				245					250					255	
Thr	Glu	Arg	Asp	Lys	Gly	Tyr	Trp	Arg	Asp	Val	Gly	Thr	Ile	Asp	Ala
			260					265					270		
Phe	Tyr	Glu	Cys	His	Met	Asp	Leu	Ile	Ser	Val	His	Pro	Ile	Phe	Asn
		275					280					285			
Leu	Tyr	Asn	Ser	Glu	Trp	Pro	Ile	His	Thr	Thr	Ser	Glu	Gly	Asn	Leu
	290					295					300				
Pro	Pro	Ala	Lys	Phe	Val	Arg	Gly	Gly	Ile	Ala	Gln	Ser	Ser	Met	Val
305					310					315					320
Ser	Ser	Gly	Ser	Ile	Ile	Ser	Ala	Gly	Thr	Val	Arg	Asn	Ser	Val	Leu
				325					330					335	
Ser	Asn	Asn	Val	Val	Val	Glu	Glu	Gly	Ala	Thr	Val	Glu	Gly	Ala	Val
			340					345					350		
Leu	Met	Pro	Gly	Val	Arg	Ile	Gly	Lys	Gly	Ala	Val	Val	Arg	His	Ala
		355					360					365			
Ile	Leu	Asp	Lys	Asn	Val	Val	Val	Arg	Asp	Gly	Glu	Leu	Ile	Gly	Val
	370					375					380				
Asp	Gln	Val	Arg	Asp	Ala	Gln	Arg	Phe	Lys	Val	Ser	Ala	Gly	Gly	Val
385					390					395					400
Val	Val	Val	Gly	Lys	Asn	Gln	Val	Val							
				405											

&lt;210&gt; 277

&lt;211&gt; 903

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(880)

&lt;223&gt; RXN00014

&lt;400&gt; 277

catcaaagtg accgccggcg gcgtcgaaatg gtccgttgca ggaaacgcgg aagcagttag 60

tgagatctcc gaaacttttaa gcgcactaga ctaacaacac atg agc aaa tat gca 115  
Met Ser Lys Tyr Ala  
1 5

gac gat tta gcc tta gcc ctc gaa ctt gcc gaa ctt gcc gat tcc atc 163  
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile  
10 15 20

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211  
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro  
25 30 35

gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc 259  
Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Ala Leu  
40 45 50

cgt gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa 307  
Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu  
55 60 65

gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac 355  
Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp  
70 75 80 85

ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca 403  
Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala  
90 95 100

acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc 451  
Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile  
105 110 115

tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc 499  
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly  
120 125 130

gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc 547  
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser  
135 140 145

cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc 595  
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser  
150 155 160 165

ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat 643  
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp  
170 175 180

acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc 691  
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu  
185 190 195

gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc 739  
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu  
200 205 210

tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag 787  
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys

```

      215              220              225
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta 835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val
230              235              240              245

gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa 880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys
      250              255              260

tagactcccg gggttttgctt ggt 903

```

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<210> 278
<211> 260
<212> PRT
<213> Corynebacterium glutamicum

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<400> 278
Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu
  1              5              10              15

Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu
      20              25              30

Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala
      35              40              45

Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp
      50              55              60

Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg
      65              70              75              80

Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly
      85              90              95

Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro
      100             105             110

Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala
      115             120             125

Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg
      130             135             140

Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser
      145             150             155             160

Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe
      165             170             175

Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe
      180             185             190

Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu
      195             200             205

Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr
      210             215             220

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Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His  
 225 230 235 240

Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu  
 245 250 255

Asp Arg Leu Lys  
 260

<210> 279

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> FRXA00014

<400> 279

catcaaagtg accgccggcg gcgtcgatg gtccgttgca ggaaacgcgg aagcagttag 60

tgagatctcc gaaacttta ggcactaga ctagcaacac atg agc aaa tat gca 115  
 Met Ser Lys Tyr Ala  
 1 5

gac gat tta gcc tta gcc ctc gaa ctc gcc gaa ctt gcc gat tcc atc 163  
 Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile  
 10 15 20

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211  
 Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro  
 25 30 35

gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc 259  
 Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu  
 40 45 50

cgc gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa 307  
 Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu  
 55 60 65

gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac 355  
 Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp  
 70 75 80 85

ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca 403  
 Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala  
 90 95 100

acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc 451  
 Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile  
 105 110 115

tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc 499  
 Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly  
 120 125 130

gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc 547  
 Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser

135	140	145	
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc			595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser			
150	155	160	165
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat			643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp			
	170	175	180
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc			691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu			
	185	190	195
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc			739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu			
	200	205	210
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag			787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys			
	215	220	225
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta			835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val			
	230	235	240
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa			880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys			
	250	255	260
tagactcccg gggttttgctt ggt			903
<210> 280			
<211> 260			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 280			
Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu			
1	5	10	15
Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu			
	20	25	30
Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala			
	35	40	45
Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp			
	50	55	60
Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg			
	65	70	75
Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly			
	85	90	95
Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro			
	100	105	110
Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala			

115	120	125
Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg 130 135 140		
Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser 145 150 155 160		
Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe 165 170 175		
Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe 180 185 190		
Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu 195 200 205		
Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr 210 215 220		
Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His 225 230 235 240		
Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu 245 250 255		
Asp Arg Leu Lys 260		

<210> 281  
 <211> 978  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(955)  
 <223> RXA01570

<400> 281  
 cactgaactc cgttttggat ctcggcaaaa tcgaagccac cggatttagc gcaccgacct 60  
 ggcagacccg cctcaacgac tacctcaagg aactctcaaa gtg aaa ggc atc atc 115  
 Val Lys Gly Ile Ile  
 1 5  
 ctc gca ggt ggc tcc ggc acc cgg ctc tac ccc atc acc aag ggc atc 163  
 Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro Ile Thr Lys Gly Ile  
 10 15 20  
 tcc aag caa ctg atg ccg att tac gac aaa ccc atg gtc tac tac cca 211  
 Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro Met Val Tyr Tyr Pro  
 25 30 35  
 ctg acc acg ctc att cag gcc ggc atc aaa gac atc ctg att atc acc 259  
 Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp Ile Leu Ile Ile Thr  
 40 45 50  
 acc cct gaa gac agc gcc tcc ttt gaa cgc ttg ctt ggc gac ggc tcc 307  
 Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu Leu Gly Asp Gly Ser



55	60	65	
tcc tgg ggc atc aac ctc acc tac gcc gtc caa ccc tcc ccc gac gga			355
Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln Pro Ser Pro Asp Gly			
70	75	80	85
cta gcc caa gca ttc atc atc ggc gag gaa ttc atc ggt gac gac gac			403
Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe Ile Gly Asp Asp Asp			
	90	95	100
gtc gcg ttg gtg ctt ggc gat aac atc ttc gac ggc gca caa ctt ggc			451
Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp Gly Ala Gln Leu Gly			
	105	110	115
cac gca cta aag cag tgc tcc aac ccc gac ggt ggc att gtc ttt gct			499
His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly Gly Ile Val Phe Ala			
	120	125	130
tat gag gtc tcc gat cct gag cgt tat ggc gtg gtg gaa ttt gat gct			547
Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val Val Glu Phe Asp Ala			
	135	140	145
gct aat aag gcg gtg tct att gaa gaa aag ccc acc gcg cca aaa tcc			595
Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro Thr Ala Pro Lys Ser			
	150	155	160
aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac			643
Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp			
	170	175	180
atc gcc aag tca atc aag cct tcc tcg cgt ggc gaa ctg gaa atc acc			691
Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly Glu Leu Glu Ile Thr			
	185	190	195
tcc gtt aac gat gcc tac ctc cag caa ggt gct tta act gtg cag cgc			739
Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala Leu Thr Val Gln Arg			
	200	205	210
ctg gac cgt ggc gat gtc tgg tta gat acc ggc aca atc gat tcc atg			787
Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly Thr Ile Asp Ser Met			
	215	220	225
tcc gag gcg tct tcc tat gtt gag gtc ctg caa aaa cgt acc ggc aac			835
Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln Lys Arg Thr Gly Asn			
	230	235	240
atc atc gga tcc ccc gaa gtc gct gcg tac cgc gaa ggt ttc atc aca			883
Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg Glu Gly Phe Ile Thr			
	250	255	260
gct gaa gaa ctc aca gtg ctt ggt gag gaa ctg aag aaa tca ggc tac			931
Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu Lys Lys Ser Gly Tyr			
	265	270	275
gga aac tac ctg ctg aga gct ttg taattttacgg tgtggttgag gag			978
Gly Asn Tyr Leu Leu Arg Ala Leu			
	280	285	

&lt;210&gt; 282

&lt;211&gt; 285

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 282

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Val Lys Gly Ile Ile Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro
 1           5           10           15

Ile Thr Lys Gly Ile Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro
          20           25           30

Met Val Tyr Tyr Pro Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp
          35           40           45

Ile Leu Ile Ile Thr Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu
 50           55           60

Leu Gly Asp Gly Ser Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln
 65           70           75           80

Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
          85           90           95

Ile Gly Asp Asp Asp Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp
          100           105           110

Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly
          115           120           125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val
          130           135           140

Val Glu Phe Asp Ala Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro
          145           150           155           160

Thr Ala Pro Lys Ser Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp
          165           170           175

Asn Arg Val Val Asp Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly
          180           185           190

Glu Leu Glu Ile Thr Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala
          195           200           205

Leu Thr Val Gln Arg Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly
          210           215           220

Thr Ile Asp Ser Met Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln
          225           230           235           240

Lys Arg Thr Gly Asn Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg
          245           250           255

Glu Gly Phe Ile Thr Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu
          260           265           270

Lys Lys Ser Gly Tyr Gly Asn Tyr Leu Leu Arg Ala Leu
          275           280           285

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&lt;210&gt; 283

&lt;211&gt; 891

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(868)

&lt;223&gt; RXA02666

&lt;400&gt; 283

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gctcggcgcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga 60
tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga 115
                                         Met Ser Ser Thr Arg
                                         1 5
atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163
Ile Pro Val Ile Ala Leu Leu Ala Ala Gly Arg Gly Thr Arg Leu
                        10 15 20
ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211
Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu
                        25 30 35
tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259
Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu
                        40 45 50
atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307
Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu
                        55 60 65
ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg 355
Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg
                        70 75 80 85
ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt 403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu
                        90 95 100
cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc 451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile
                        105 110 115
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg 499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val
                        120 125 130
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca 547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro
                        135 140 145
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc 595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val
                        150 155 160 165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc 643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly
                        170 175 180
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac 691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp

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                185                190                195
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg 739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp
      200                205                210

tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa 787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys
      215                220                225

gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa 835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu
      230                235                240                245

gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg 888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
      250                255

tag 891

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<210> 284
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

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<400> 284
Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly
  1          5          10          15

Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu
      20          25          30

Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser
      35          40          45

Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr
      50          55          60

Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu
      65          70          75          80

Gly Val Arg Val Arg Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser
      85          90          95

Val Trp Ala Gly Leu Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp
      100         105         110

Ala Ile Val Leu Ile His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly
      115         120         125

Met Ile Ala Arg Val Val Arg Lys Val His Glu Gly Ala Thr Ala Val
      130         135         140

Ile Pro Val Leu Pro Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp
      145         150         155         160

Gly Gly Val Val Val Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val
      165         170         175

Gln Thr Pro Gln Gly Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu

```

	180		185		190										
Lys	Phe	Phe	Ala	Asp	Pro	Asn	Pro	Gly	Phe	Ile	Pro	Thr	Asp	Asp	Ala
	195					200						205			
Ser	Leu	Met	Glu	Trp	Tyr	Gly	Ala	Asp	Val	Val	Cys	Val	Gln	Gly	Asp
	210					215					220				
Pro	Met	Ala	Phe	Lys	Val	Thr	Thr	Pro	Ile	Asp	Met	Met	Leu	Ala	Gln
	225				230					235					240
Arg	Ile	Thr	Asp	Glu	Ala	Glu	Pro	Thr	Ile	Phe	Glu	Val	Pro	Gly	Asp
			245						250					255	

&lt;210&gt; 285

&lt;211&gt; 1056

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1033)

&lt;223&gt; RXA00825

&lt;400&gt; 285

cccgttcacg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60

tagtgcacgc	cgattctgag	aaacaactaa	agtgagccac	atg	cgc	aca	gta	gtt	115
				Met	Arg	Thr	Val	Val	
				1				5	

acc	ggc	ggt	gcc	ggc	ttc	atc	gga	tcc	cat	ctc	gtt	gac	ctt	ttg	atc	163
Thr	Gly	Gly	Ala	Gly	Phe	Ile	Gly	Ser	His	Leu	Val	Asp	Leu	Leu	Ile	
			10					15					20			

aag	gaa	ggc	cac	gag	gtc	gtt	gtg	atc	gat	aac	ctc	tcc	cgc	gga	cgc	211
Lys	Glu	Gly	His	Glu	Val	Val	Val	Ile	Asp	Asn	Leu	Ser	Arg	Gly	Arg	
			25					30					35			

ctg	gag	aat	ctc	tcc	gat	gcg	gaa	gcc	acc	gga	aaa	ctc	acc	ttt	gtg	259
Leu	Glu	Asn	Leu	Ser	Asp	Ala	Glu	Ala	Thr	Gly	Lys	Leu	Thr	Phe	Val	
		40				45						50				

gaa	gcc	gat	ctt	ctc	gac	gtt	gat	ttc	aac	gag	ttt	cta	gga	acc	cac	307
Glu	Ala	Asp	Leu	Leu	Asp	Val	Asp	Phe	Asn	Glu	Phe	Leu	Gly	Thr	His	
	55					60					65					

aag	cct	gag	gtt	att	ttc	cac	ctg	gca	gcg	caa	atc	gat	gtg	cgc	cac	355
Lys	Pro	Glu	Val	Ile	Phe	His	Leu	Ala	Ala	Gln	Ile	Asp	Val	Arg	His	
	70				75					80					85	

tct	gtt	gta	gat	cct	ctt	cac	gac	gcc	gaa	acc	aac	att	ttg	tcc	acc	403
Ser	Val	Val	Asp	Pro	Leu	His	Asp	Ala	Glu	Thr	Asn	Ile	Leu	Ser	Thr	
				90				95					100			

atc	cgc	atc	gct	gac	gct	gcc	cgc	cag	cac	ggt	gtt	cgc	aag	gtt	gtc	451
Ile	Arg	Ile	Ala	Asp	Ala	Ala	Arg	Gln	His	Gly	Val	Arg	Lys	Val	Val	

105	110	115	
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca			499
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro			
120	125	130	
ggt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc			547
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser			
135	140	145	
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc			595
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly			
150	155	160	165
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa			643
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln			
170	175	180	
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt			691
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu			
185	190	195	
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc			739
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg			
200	205	210	
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct			787
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser			
215	220	225	
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa			835
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu			
230	235	240	245
acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc			883
Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser			
250	255	260	
aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc			931
Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg			
265	270	275	
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct			979
Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro			
280	285	290	
gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc			1027
Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg			
295	300	305	
act cac taggggaaaa tccaccacaa atc			1056
Thr His			
310			

&lt;210&gt; 286

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 286

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu  
 1 5 10 15  
 Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn  
 20 25 30  
 Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly  
 35 40 45  
 Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu  
 50 55 60  
 Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln  
 65 70 75 80  
 Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr  
 85 90 95  
 Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly  
 100 105 110  
 Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu  
 115 120 125  
 Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser  
 130 135 140  
 Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe  
 145 150 155 160  
 Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val  
 165 170 175  
 Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile  
 180 185 190  
 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp  
 195 200 205  
 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala  
 210 215 220  
 Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile  
 225 230 235 240  
 Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala  
 245 250 255  
 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu  
 260 265 270  
 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val  
 275 280 285  
 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr  
 290 295 300  
 Val Glu Tyr Phe Arg Thr His  
 305 310

<210> 287  
 <211> 1134  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1111)  
 <223> RXA01887

<400> 287  
 catctttaca ggaaaccctt tgacggcatc aatgggtggt atctagtatc tactagaacg 60  
 ttatagtaga acgttctagt aaaacttgga aggatgaaaa atg tca gtc aaa ctt 115  
 Met Ser Val Lys Leu  
 1 5  
 gcc ctc atc ggt gct gga cgc atc gga tca aat cac gca cgc ctg atc 163  
 Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn His Ala Arg Leu Ile  
 10 15 20  
 aca aac cac gtg atc ggc tct gaa ctg gtc gcc gtc gtt gac cca act 211  
 Thr Asn His Val Ile Gly Ser Glu Leu Val Ala Val Val Asp Pro Thr  
 25 30 35  
 ccc aac gca gaa acc ctc gct gat gaa ttg ggc gcc gtt gcg ttc tct 259  
 Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly Ala Val Ala Phe Ser  
 40 45 50  
 aac cca gat gac gtc ctg acc cgc gat gac att gac gcg gtt ttg att 307  
 Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile Asp Ala Val Leu Ile  
 55 60 65  
 gct aca cca gca cga acc cac gcg gat ctc gtg gtc aaa gca gcg gca 355  
 Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val Val Lys Ala Ala Ala  
 70 75 80 85  
 gcg ggc aag cac gtg ttt gtg gaa aag ccc atg gcc gtc acc ctc gag 403  
 Ala Gly Lys His Val Phe Val Glu Lys Pro Met Ala Val Thr Leu Glu  
 90 95 100  
 gac gca gat cgt gcc atc aac gca gca cgc gaa gca aac act gtc ctg 451  
 Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu Ala Asn Thr Val Leu  
 105 110 115  
 cag gtg ggc ttc aat cgt cgt ttc gcg gca ggt ttc gct gca gca cgc 499  
 Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly Phe Ala Ala Ala Arg  
 120 125 130  
 gca cgc att gac gca ggc gat atc ggc acc cca cag ctg ctt cgt tcc 547  
 Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro Gln Leu Leu Arg Ser  
 135 140 145  
 gtg acc cgc gat cca gga cca ttc acc gct gac ccc aac aag atc cct 595  
 Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp Pro Asn Lys Ile Pro  
 150 155 160 165  
 cag tgg acc atc ttc ctg gaa acc ctc atc cac gat ttc gat gcg ctg 643  
 Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His Asp Phe Asp Ala Leu  
 170 175 180



tgc tac ctc aac cca ggc gca acc cca gtg gaa gta acc gct cac gct 691  
 Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu Val Thr Ala His Ala  
 185 190 195

gat tgc ctc gtc gtt cca gaa gct gct ggc act ggc ttc ctc gac acc 739  
 Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr Gly Phe Leu Asp Thr  
 200 205 210

gca gtg gtg act gtc cgt ttt gat aac gga gca att ggt act gca gaa 787  
 Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala Ile Gly Thr Ala Glu  
 215 220 225

gca agc ttc agc gca gcc tat ggt tat gac gtt cgc ggt gaa gtc ttc 835  
 Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val Arg Gly Glu Val Phe  
 230 235 240 245

gga tcc aag ggc atg atg acc gca ggc gac gcg cgc gca acc aac atg 883  
 Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala Arg Ala Thr Asn Met  
 250 255 260

act ttc tac ggc gct gag ggc atc gcg gct gcc acc tca cgc gcg gat 931  
 Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala Thr Ser Arg Ala Asp  
 265 270 275

acc gat ctg ctc tcc gat gct tac cga gct gaa ttc caa gct ttc gtc 979  
 Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu Phe Gln Ala Phe Val  
 280 285 290

gac tcc atc cgt acc aac acc cct tcc aag gtt cca ggc gaa gct gca 1027  
 Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val Pro Gly Glu Ala Ala  
 295 300 305

cgc acc gca cta ctc atc gca ctc ggc gcc atc cga agc gta gaa acc 1075  
 Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile Arg Ser Val Glu Thr  
 310 315 320 325

ggc gca acc atc aac ctt gct gaa agc atc gag gtt taaccatgac 1121  
 Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu Val  
 330 335

ttttaaactc gca 1134

&lt;210&gt; 288

&lt;211&gt; 337

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 288

Met Ser Val Lys Leu Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn  
 1 5 10 15

His Ala Arg Leu Ile Thr Asn His Val Ile Gly Ser Glu Leu Val Ala  
 20 25 30

Val Val Asp Pro Thr Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly  
 35 40 45

Ala Val Ala Phe Ser Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile  
 50 55 60

Asp Ala Val Leu Ile Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val  
 65 70 75 80  
 Val Lys Ala Ala Ala Gly Lys His Val Phe Val Glu Lys Pro Met  
 85 90 95  
 Ala Val Thr Leu Glu Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu  
 100 105 110  
 Ala Asn Thr Val Leu Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly  
 115 120 125  
 Phe Ala Ala Ala Arg Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro  
 130 135 140  
 Gln Leu Leu Arg Ser Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp  
 145 150 155 160  
 Pro Asn Lys Ile Pro Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His  
 165 170 175  
 Asp Phe Asp Ala Leu Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu  
 180 185 190  
 Val Thr Ala His Ala Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr /  
 195 200 205  
 Gly Phe Leu Asp Thr Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala  
 210 215 220  
 Ile Gly Thr Ala Glu Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val  
 225 230 235 240  
 Arg Gly Glu Val Phe Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala  
 245 250 255  
 Arg Ala Thr Asn Met Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala  
 260 265 270  
 Thr Ser Arg Ala Asp Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu  
 275 280 285  
 Phe Gln Ala Phe Val Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val  
 290 295 300  
 Pro Gly Glu Ala Ala Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile  
 305 310 315 320  
 Arg Ser Val Glu Thr Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu  
 325 330 335  
 Val

&lt;210&gt; 289

&lt;211&gt; 996

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(973)

&lt;223&gt; RXN00013

&lt;400&gt; 289

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ctgcagaaaa ttcgggacgc atgattgcac atattacccg caccgattgt gattottaga 60

acgccacctt attcagcaca cttggccgac ggcatgcaca atg gaa ggc atg act 115
Met Glu Gly Met Thr
1 5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163
Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
10 15 20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211
Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu
25 30 35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259
His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
40 45 50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307
Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
55 60 65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355
Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403
Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala
90 95 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp
105 110 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu
120 125 130

gcg ctg gtc gag ggc gat cca tec gcg cca tcg cgc gtg ctt ttc ggc 547
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly
135 140 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly
150 155 160 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala
170 175 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691
Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile
185 190 195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct 739
Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro

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200	205	210	
gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc			787
Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile			
215	220	225	
gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg			835
Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp			
230	235	240	245
gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gca tgc			883
Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys			
250	255	260	
atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg			931
Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala			
265	270	275	
gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac			973
Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp			
280	285	290	
taacaacaca tgagcaaata tgc			996

&lt;210&gt; 290

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 290

Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu	
1 5 10 15	
Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp	
20 25 30	
Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly	
35 40 45	
Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys	
50 55 60	
Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala	
65 70 75 80	
Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu	
85 90 95	
Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val	
100 105 110	
Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr	
115 120 125	
Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser	
130 135 140	
Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp	
145 150 155 160	

<400> 291																
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acgccacctt	attcagcaca	cttggccgac	ggcatgcaca	atg	gaa	ggc	atg	act								115
				Met	Glu	Gly	Met	Thr								
				1				5								
aat	cca	gag	cag	aca	cat	ccc	gct	gca	agc	ctc	gaa	gac	atg	atc	aaa	163
Asn	Pro	Glu	Gln	Thr	His	Pro	Ala	Ala	Ser	Leu	Glu	Asp	Met	Ile	Lys	
				10				15						20		
acc	atc	aca	aag	acc	ttc	gtg	att	gct	cac	gat	cag	gat	tct	gat	gag	211
Thr	Ile	Thr	Lys	Thr	Phe	Val	Ile	Ala	His	Asp	Gln	Asp	Ser	Asp	Glu	
			25					30					35			
cat	ctt	gcg	cag	gca	ctg	gtg	tac	aac	gct	gga	cgt	ttg	gca	tgg	cgc	259
His	Leu	Ala	Gln	Ala	Leu	Val	Tyr	Asn	Ala	Gly	Arg	Leu	Ala	Trp	Arg	
		40					45					50				
atg	cgc	gaa	aac	ggt	gtg	gat	acg	gat	tac	aag	act	tct	gtg	tct	gat	307
Met	Arg	Glu	Asn	Gly	Val	Asp	Thr	Asp	Tyr	Lys	Thr	Ser	Val	Ser	Asp	
	55					60					65					

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355  
Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val  
70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403  
Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala  
90 95 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451  
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp  
105 110 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499  
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu  
120 125 130

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc 547  
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly  
135 140 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595  
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly  
150 155 160 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643  
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala  
170 175 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691  
Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile  
185 190 195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct 739  
Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro  
200 205 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc 787  
Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile  
215 220 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg 835  
Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp  
230 235 240 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc 883  
Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys  
250 255 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg 931  
Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala  
265 270 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac 973  
Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp  
280 285 290

tagcaacaca tgagcaaata tgc 996

&lt;210&gt; 292

&lt;211&gt; 291

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 292

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Met Glu Gly Met Thr Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu
 1          5          10          15

Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
      20          25          30

Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
      35          40          45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50          55          60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65          70          75          80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
      85          90          95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
      100          105          110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
      115          120          125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
      130          135          140

Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
      145          150          155          160

Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp
      165          170          175

Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile
      180          185          190

His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser
      195          200          205

Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile
      210          215          220

Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His
      225          230          235          240

Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly
      245          250          255

Val Gly Gly Ala Cys Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser
      260          265          270

Val Ala Gly Asn Ala Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser
      275          280          285

Ala Leu Asp
      290

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<400> 293																60
ggatgagggc attgattccg tcatcattgg caaggcactt tatgagcaca agttcaccct																
cgaagaggct ttggctgcag tagaaaagct cggттаатаc atg gat gct cgt ggg																115
Met Asp Ala Arg Gly																5
1																
atg ttg gcc att gcg gag gcc gtt gta gat gat gcc gaa gcc ctc ttc																163
Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp Ala Glu Ala Leu Phe																20
10 15																
atg cag gcc ttc gga gct gca cct gcc cat atg aaa tcc ccg ggg gat																211
Met Gln Gly Phe Gly Ala Ala Pro Ala His Met Lys Ser Pro Gly Asp																35
25 30																
ttt gcc acg gaa gtg gat atg gcc atc gaa tcc cat atg cgt tcg atg																259
Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser His Met Arg Ser Met																50
40 45																
ctg aac atg atg aca ggc att gct gtc atc ggt gaa gaa ggt ggc ggt																307
Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly Glu Glu Gly Gly Gly																65
55 60																
gcg acc tcc ggc acg cgc tgg gtg att gat ccc atc gac ggc acc gcc																355
Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro Ile Asp Gly Thr Ala																85
70 75 80																
aac ttc gcg gcg tcc aac ccg atg agc gcg atc ctg gtg tct ttg ctt																403
Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile Leu Val Ser Leu Leu																100
90 95																
gtc gac gac cag ccc gtc ctg ggt att acc tcc atg ccc atg ctg ggt																451
Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser Met Pro Met Leu Gly																115
105 110																
aaa cgc ctc acc gct ttt gaa ggt tca ccg ctg atg atc aac ggt gaa																499
Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu Met Ile Asn Gly Glu																130
120 125																
cct cag gaa cca ttg caa gaa caa tcc agt ttg gta tcc cac att ggt																547
Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu Val Ser His Ile Gly																145
135 140																
ttt agt tcc atg gcc tcc ccg cgc aat aca gcg ttt cct gtg gag ttg																595
Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala Phe Pro Val Glu Leu																165
150 155 160																
cgt cgg gat ctt ctg acc gag ctc acg gaa tcg tat ctt cgt ccc cgc																643
Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser Tyr Leu Arg Pro Arg																180
170 175																



att aca ggt tcg gtg ggt gtt gat ctc gcg ttc act gcg cag ggc att 691  
 Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe Thr Ala Gln Gly Ile  
 185 190 195

ttt gga gca tgc gta tcg ttt agt cct cat gtt tgg gac aat tcc gca 739  
 Phe Gly Ala Cys Val Ser Phe Ser Pro His Val Trp Asp Asn Ser Ala  
 200 205 210

ggc gtg atg ttg atg cgc gct gct ggt gca caa gtt act gac acc gaa 787  
 Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln Val Thr Asp Thr Glu  
 215 220 225

ggc cat ccg tgg gca cca ggt agg gga gtc gtg gcc gga aca aaa agg 835  
 Gly His Pro Trp Ala Pro Gly Arg Gly Val Val Ala Gly Thr Lys Arg  
 230 235 240 245

gct cac gat gtg ctg tta agt aag att gaa aaa gtt cgg ttg atg cat 883  
 Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys Val Arg Leu Met His  
 250 255 260

gca gat gca ggt aat gac cag tcg tta aat gag gag tac aag 925  
 Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu Glu Tyr Lys  
 265 270 275

taaaatgggc gtggcaattc gag 948

&lt;210&gt; 294

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 294

Met Asp Ala Arg Gly Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp  
 1 5 10 15

Ala Glu Ala Leu Phe Met Gln Gly Phe Gly Ala Ala Pro Ala His Met  
 20 25 30

Lys Ser Pro Gly Asp Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser  
 35 40 45

His Met Arg Ser Met Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly  
 50 55 60

Glu Glu Gly Gly Gly Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro  
 65 70 75 80

Ile Asp Gly Thr Ala Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile  
 85 90 95

Leu Val Ser Leu Leu Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser  
 100 105 110

Met Pro Met Leu Gly Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu  
 115 120 125

Met Ile Asn Gly Glu Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu  
 130 135 140

Val Ser His Ile Gly Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala  
 145 150 155 160

Phe Pro Val Glu Leu Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser  
 165 170 175

Tyr Leu Arg Pro Arg Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe  
 180 185 190

Thr Ala Gln Gly Ile Phe Gly Ala Cys Val Ser Phe Ser Pro His Val  
 195 200 205

Trp Asp Asn Ser Ala Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln  
 210 215 220

Val Thr Asp Thr Glu Gly His Pro Trp Ala Pro Gly Arg Gly Val Val  
 225 230 235 240

Ala Gly Thr Lys Arg Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys  
 245 250 255

Val Arg Leu Met His Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu  
 260 265 270

Glu Tyr Lys  
 275

&lt;210&gt; 295

&lt;211&gt; 576

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(576)

&lt;223&gt; RXN01332

&lt;400&gt; 295

cac atc tct gcc att att gag ccc gac gca gca cgt gcc gct gca gct	48
His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala	
1 5 10 15	
gca gaa gac gcg ccg ggt gca cag gcc ttc act cgc att gaa gat gct	96
Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala	
20 25 30	
atc gca gcc gat gct gtc gac gca gtg ctg atc gcc gta cca ggt cag	144
Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln	
35 40 45	
ttc cat gag cca gta ctt gtc cca gca cta gaa gca ggc ctt ccc atc	192
Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile	
50 55 60	
ctg tgt gaa aag cca ctg acc cca gat tct gaa tcc tca ctg cgc atc	240
Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile	
65 70 75 80	
gtc gag ctg gag cag aag ctg gac aag cca cac atc cag gtt ggt ttc	288
Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe	

	85	90	95	
atg cgc cgc ttc gac cct gag tac aac aac ttg cgc aaa ttg gtg gaa				336
Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu				
	100	105	110	
tcc ggc gaa gct ggc gaa ctg ctc atg ctc cgc ggc ctg cac cgc aac				384
Ser Gly Glu Ala Gly Glu Leu Met Leu Arg Gly Leu His Arg Asn				
	115	120	125	
cca agt gtt ggt gag agc tac acc cag tcc atg ctg atc acc gac tcc				432
Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser				
	130	135	140	
gtc gtc cac gaa ttc gat gtc atc cca tgg ctc gca ggc tcc cga gtt				480
Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val				
	145	150	155	160
gtc tcc gtt gaa gtg aag tac cca aag acc tcc tca ctg gcg cac tcc				528
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser				
	165	170	175	
ggc ctc aag gaa cca atc ctg gtg atc atg gag ctc gaa aac ggc gtg				576
Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val				
	180	185	190	

&lt;210&gt; 296

&lt;211&gt; 192

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 296

His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala				
1	5	10	15	
Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala				
20	25	30		
Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln				
35	40	45		
Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile				
50	55	60		
Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile				
65	70	75	80	
Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe				
85	90	95		
Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu				
100	105	110		
Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn				
115	120	125		
Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser				
130	135	140		
Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val				

145		150		155		160
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser						
		165		170		175
Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val						
		180		185		190

<210> 297  
 <211> 549  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(549)  
 <223> FRXA01332

<400> 297	
gca gca cgt gcc gct gca gct gca gaa gac gcg ccg ggt gca cag gcc	48
Ala Ala Arg Ala Ala Ala Ala Glu Asp Ala Pro Gly Ala Gln Ala	
1 5 10 15	
ttc act cgc att gaa gat gct atc gca gcc gat gct gtc gac gca gtg	96
Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val	
20 25 30	
ctg atc gcc gta cca ggt cag ttc cat gag cca gta ctt gtc cca gca	144
Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala	
35 40 45	
cta gaa gca ggc ctt ccc atc ctg tgt gaa aag cca ctg acc cca gat	192
Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp	
50 55 60	
tct gaa tcc tca ctg cgc atc gtc gag ctg gag cag aag ctg gac aag	240
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys	
65 70 75 80	
cca cac atc cag gtt ggt ttc atg cgc cgc ttc gac cct gag tac aac	288
Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn	
85 90 95	
aac ttg cgc aaa ttg gtg gaa tcc ggc gaa gct ggc gaa ctg ctc atg	336
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met	
100 105 110	
ctc cgc ggc ctg cac cgc aac cca agt gtt ggt gag agc tac acc cag	384
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln	
115 120 125	
tcc atg ctg atc acc gac tcc gtc gtc cac gaa ttc gat gtc atc cca	432
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro	
130 135 140	
tgg ctc gca ggc tcc cga gtt gtc tcc gtt gaa gtg aag tac cca aag	480
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys	

atg gag ctc gaa aac ggc gtg 549  
Met Glu Leu Glu Asn Gly Val  
180

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<210> 298
<211> 183
<212> PRT
<213> Corynebacterium glutamicum
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[illegible]

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<210> 299
<211> 1128
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS

&lt;222&gt; (101)..(1105)

&lt;223&gt; RXA01632

&lt;400&gt; 299

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aagggctgca acgtgctttc gacaccacca tcgcagcggt tgaacaagct gctcgtctcg 60

ccccctccac taactgatct ttgaaaggct gaaaaaactc atg act ctt cgt atc 115
                                         Met Thr Leu Arg Ile
                                         1 5

gcc ctt ttc ggc gct ggc cgc atc ggt cac gtc cac gct gcc aac att 163
Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val His Ala Ala Asn Ile
                        10 15 20

gct gca aac cct gat ctt gaa ctc gtt gtt atc gcc gat cct ttc att 211
Ala Ala Asn Pro Asp Leu Glu Leu Val Ile Ala Asp Pro Phe Ile
                        25 30 35

gaa ggc gca cag cgt ttg gca gaa gcc aat ggg gca gaa gcg gtt gca 259
Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly Ala Glu Ala Val Ala
                        40 45 50

tca cca gat gag gtg ttc gcc cgc gat gat atc gat ggc atc gtg atc 307
Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile Asp Gly Ile Val Ile
                        55 60 65

ggt tca cca acc agc acc cac gtt gat ctg atc acc cgc gcc gtg gaa 355
Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile Thr Arg Ala Val Glu
                        70 75 80 85

cgt ggc att cct gca ctg tgc gaa aaa ccc att gat tta gac att gaa 403
Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile Asp Leu Asp Ile Glu
                        90 95 100

atg gtg cgt gcc tgc aaa gag aag atc ggc gac ggc gct tcc aag gtg 451
Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp Gly Ala Ser Lys Val
                        105 110 115

atg ctg ggg ttt aac cga cgc ttc gat cct tct ttc gct gcc atc aat 499
Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser Phe Ala Ala Ile Asn
                        120 125 130

gcg cga gtg gca aac cag gag atc ggc aac ctg gag cag ttg gtg atc 547
Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu Glu Gln Leu Val Ile
                        135 140 145

atc agc cgc gat cca gcg ccc gca ccg aag gac tac atc gca ggt tcc 595
Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp Tyr Ile Ala Gly Ser
                        150 155 160 165

ggt gga atc ttc cgc gat atg acc atc cac gat ctg gat atg gcg cgt 643
Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp Leu Asp Met Ala Arg
                        170 175 180

ttc ttt gtg ccc aat atc gtg gaa gtg act gca acc ggc gcc aat gtt 691
Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala Thr Gly Ala Asn Val
                        185 190 195

ttc agc cag gaa atc gcg gag ttc aat gac tac gac cag gtt atc gtc 739
Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr Asp Gln Val Ile Val
                        200 205 210

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acg ctt cgt ggc tca aag ggc gag ttg atc aac atc gtg aac tcc cgc 787  
 Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn Ile Val Asn Ser Arg  
 215 220 225

cac tgc tcc tac ggc tac gac cag cga ctt gag gct ttc ggc tct aag 835  
 His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu Ala Phe Gly Ser Lys  
 230 235 240 245

ggc atg ctc gcc gcc gac aac atc agg ccc acc acg gtg cgc aag cac 883  
 Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr Thr Val Arg Lys His  
 250 255 260

aat gcg gaa agc acc gag cag gca gat ccg att ttc aac ttc ttc ctc 931  
 Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile Phe Asn Phe Phe Leu  
 265 270 275

gag cgc tac gac gcc gct tac aag gca gag ctc gca act ttt gct caa 979  
 Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu Ala Thr Phe Ala Gln  
 280 285 290

gga atc cgc gac ggc caa ggc ttc tca cca aac ttc gag gac ggc gtc 1027  
 Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn Phe Glu Asp Gly Val  
 295 300 305

atc gcc ctt gaa cta gcg aat gca tgc ctt gaa tca gct caa acc ggc 1075  
 Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu Ser Ala Gln Thr Gly  
 310 315 320 325

cgc acc gtc acc ctc aac cct gcc aac gtt tagtcaacgt ctagttaatg 1125  
 Arg Thr Val Thr Leu Asn Pro Ala Asn Val  
 330 335

cct 1128

<210> 300  
 <211> 335  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 300  
 Met Thr Leu Arg Ile Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val  
 1 5 10 15

His Ala Ala Asn Ile Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile  
 20 25 30

Ala Asp Pro Phe Ile Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly  
 35 40 45

Ala Glu Ala Val Ala Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile  
 50 55 60

Asp Gly Ile Val Ile Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile  
 65 70 75 80

Thr Arg Ala Val Glu Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile  
 85 90 95

Asp Leu Asp Ile Glu Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp

100					105					110					
Gly	Ala	Ser	Lys	Val	Met	Leu	Gly	Phe	Asn	Arg	Arg	Phe	Asp	Pro	Ser
	115						120					125			
Phe	Ala	Ala	Ile	Asn	Ala	Arg	Val	Ala	Asn	Gln	Glu	Ile	Gly	Asn	Leu
	130					135					140				
Glu	Gln	Leu	Val	Ile	Ile	Ser	Arg	Asp	Pro	Ala	Pro	Ala	Pro	Lys	Asp
145					150					155					160
Tyr	Ile	Ala	Gly	Ser	Gly	Gly	Ile	Phe	Arg	Asp	Met	Thr	Ile	His	Asp
			165						170					175	
Leu	Asp	Met	Ala	Arg	Phe	Phe	Val	Pro	Asn	Ile	Val	Glu	Val	Thr	Ala
			180					185					190		
Thr	Gly	Ala	Asn	Val	Phe	Ser	Gln	Glu	Ile	Ala	Glu	Phe	Asn	Asp	Tyr
	195						200					205			
Asp	Gln	Val	Ile	Val	Thr	Leu	Arg	Gly	Ser	Lys	Gly	Glu	Leu	Ile	Asn
	210					215					220				
Ile	Val	Asn	Ser	Arg	His	Cys	Ser	Tyr	Gly	Tyr	Asp	Gln	Arg	Leu	Glu
225					230					235					240
Ala	Phe	Gly	Ser	Lys	Gly	Met	Leu	Ala	Ala	Asp	Asn	Ile	Arg	Pro	Thr
				245					250					255	
Thr	Val	Arg	Lys	His	Asn	Ala	Glu	Ser	Thr	Glu	Gln	Ala	Asp	Pro	Ile
			260					265					270		
Phe	Asn	Phe	Phe	Leu	Glu	Arg	Tyr	Asp	Ala	Ala	Tyr	Lys	Ala	Glu	Leu
	275						280					285			
Ala	Thr	Phe	Ala	Gln	Gly	Ile	Arg	Asp	Gly	Gln	Gly	Phe	Ser	Pro	Asn
	290					295					300				
Phe	Glu	Asp	Gly	Val	Ile	Ala	Leu	Glu	Leu	Ala	Asn	Ala	Cys	Leu	Glu
305					310					315					320
Ser	Ala	Gln	Thr	Gly	Arg	Thr	Val	Thr	Leu	Asn	Pro	Ala	Asn	Val	
				325					330					335	

&lt;210&gt; 301

&lt;211&gt; 1206

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1183)

&lt;223&gt; RXA01633

&lt;400&gt; 301

gcgaatgcat gccttgaatc agctcaaacc ggccgcaccg tcaccctcaa ccctgccaac 60

gtttagtcaa cgtctagtta atgcctaagg agaaaacctc atg aaa aac atc acc 115

Met Lys Asn Ile Thr

1

5



atc gga atg gtc ggc gtc ggc cgc att ggc cgc atg cac gtc gcc aac	163
Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg Met His Val Ala Asn	
10 15 20	
atg ctt gcc gtt gct gaa act ttg aag gaa cgc gac ctc aac att gag	211
Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg Asp Leu Asn Ile Glu	
25 30 35	
atc gtg ctc gca gac gca atg ccc ggt ttt gcg gag cag gtg ggc gcg	259
Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala Glu Gln Val Gly Ala	
40 45 50	
gac atg ggc gtg aag gcg gcg gca agc gtc gat aag ctt att gag gac	307
Asp Met Gly Val Lys Ala Ala Ser Val Asp Lys Leu Ile Glu Asp	
55 60 65	
ggg gtg gat gcc ctt ttc att gcc acc agc acc gct ggc cac gtc gat	355
Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr Ala Gly His Val Asp	
70 75 80 85	
gtt ttg cgc aag ggc atc gcg gca aag ctg ccg atg ttc tgc gag aag	403
Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys	
90 95 100	
ccg atc gcg tcg gat gtg cct gag tcg ctg aac atc atc cgc gaa att	451
Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn Ile Ile Arg Glu Ile	
105 110 115	
gat gcg gct ggc gcg acg gtt cag gtc ggc cac cag cgc cgt ttt gac	499
Asp Ala Ala Gly Ala Thr Val Gln Val Gly His Gln Arg Arg Phe Asp	
120 125 130	
ctc ggt tac cag gaa gct aaa cga cgc cta gat gca ggc gac ctc ggc	547
Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp Ala Gly Asp Leu Gly	
135 140 145	
tgg ctt cat tcg ctc aag gcc gta tcg agc gat gcg ttt ccg cca ccg	595
Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp Ala Phe Pro Pro Pro	
150 155 160 165	
gtg tcc tac tgc gct acc tct ggt gga ctt ttc cgc gat gtg tcg ctg	643
Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe Arg Asp Val Ser Leu	
170 175 180	
cac gat ttc gac atc att cgc tgg ctg acc ggc cag gat att gtc gag	691
His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly Gln Asp Ile Val Glu	
185 190 195	
gtg tac gcc aag ggc agc aac aac ggc gac cca gaa atc ggc gca gtc	739
Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro Glu Ile Gly Ala Val	
200 205 210	
ggt gac atc gat acc gga gcg gcc cta ctc acg ctt gcc gac ggc acc	787
Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr Leu Ala Asp Gly Thr	
215 220 225	
ctc gcc acc gcc atc gcc act cgt tac aac ggt gca ggc cac gac gtt	835
Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly Ala Gly His Asp Val	
230 235 240 245	

cgc ctc gat gtt atg ggc tct aaa gat tcc acg atc gtt ggc ctg gat 883  
 Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr Ile Val Gly Leu Asp  
 250 255 260

gaa aag tct gcg ttc gct tct gcg gag gag ggc atc gat ttc cca acc 931  
 Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly Ile Asp Phe Pro Thr  
 265 270 275

ggc gaa tcg cac cca acg ttt gcc gag cgc ttc gcc gac gca tac aag 979  
 Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe Ala Asp Ala Tyr Lys  
 280 285 290

aat gag tgc att gcg ttc gtg gag ttg atc ctg gga gag cgg gaa aac 1027  
 Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu Gly Glu Arg Glu Asn  
 295 300 305

cct tgt acc cct gca gac gct gtg gct gcg gcg att gtt gcc gat gca 1075  
 Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ile Val Ala Asp Ala  
 310 315 320 325

gct cag ctg tcg ctg gtc act ggc gag cca gtg aag att cct act gta 1123  
 Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val Lys Ile Pro Thr Val  
 330 335 340

cgg gaa att ctt gaa ggt tct gcg cag cca gtt gag gtg cgt gcg ctg 1171  
 Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val Glu Val Arg Ala Leu  
 345 350 355

gtt cca tct gct taaaacctta ctgcttatct aaa 1206  
 Val Pro Ser Ala  
 360

&lt;210&gt; 302

&lt;211&gt; 361

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 302

Met Lys Asn Ile Thr Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg  
 1 5 10 15

Met His Val Ala Asn Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg  
 20 25 30

Asp Leu Asn Ile Glu Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala  
 35 40 45

Glu Gln Val Gly Ala Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp  
 50 55 60

Lys Leu Ile Glu Asp Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr  
 65 70 75 80

Ala Gly His Val Asp Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro  
 85 90 95

Met Phe Cys Glu Lys Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn  
 100 105 110

Ile Ile Arg Glu Ile Asp Ala Ala Gly Ala Thr Val Gln Val Gly His

115					120					125					
Gln	Arg	Arg	Phe	Asp	Leu	Gly	Tyr	Gln	Glu	Ala	Lys	Arg	Arg	Leu	Asp
130						135					140				
Ala	Gly	Asp	Leu	Gly	Trp	Leu	His	Ser	Leu	Lys	Ala	Val	Ser	Ser	Asp
145					150					155					160
Ala	Phe	Pro	Pro	Pro	Val	Ser	Tyr	Cys	Ala	Thr	Ser	Gly	Gly	Leu	Phe
				165					170					175	
Arg	Asp	Val	Ser	Leu	His	Asp	Phe	Asp	Ile	Ile	Arg	Trp	Leu	Thr	Gly
		180						185					190		
Gln	Asp	Ile	Val	Glu	Val	Tyr	Ala	Lys	Gly	Ser	Asn	Asn	Gly	Asp	Pro
	195						200					205			
Glu	Ile	Gly	Ala	Val	Gly	Asp	Ile	Asp	Thr	Gly	Ala	Ala	Leu	Leu	Thr
210					215						220				
Leu	Ala	Asp	Gly	Thr	Leu	Ala	Thr	Ala	Ile	Ala	Thr	Arg	Tyr	Asn	Gly
225					230					235					240
Ala	Gly	His	Asp	Val	Arg	Leu	Asp	Val	Met	Gly	Ser	Lys	Asp	Ser	Thr
				245					250					255	
Ile	Val	Gly	Leu	Asp	Glu	Lys	Ser	Ala	Phe	Ala	Ser	Ala	Glu	Glu	Gly
			260					265					270		
Ile	Asp	Phe	Pro	Thr	Gly	Glu	Ser	His	Pro	Thr	Phe	Ala	Glu	Arg	Phe
		275					280					285			
Ala	Asp	Ala	Tyr	Lys	Asn	Glu	Cys	Ile	Ala	Phe	Val	Glu	Leu	Ile	Leu
	290					295					300				
Gly	Glu	Arg	Glu	Asn	Pro	Cys	Thr	Pro	Ala	Asp	Ala	Val	Ala	Ala	Ala
305					310					315					320
Ile	Val	Ala	Asp	Ala	Ala	Gln	Leu	Ser	Leu	Val	Thr	Gly	Glu	Pro	Val
			325						330					335	
Lys	Ile	Pro	Thr	Val	Arg	Glu	Ile	Leu	Glu	Gly	Ser	Ala	Gln	Pro	Val
			340					345					350		
Glu	Val	Arg	Ala	Leu	Val	Pro	Ser	Ala							
	355					360									

&lt;210&gt; 303

&lt;211&gt; 1146

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1123)

&lt;223&gt; RXN01406

&lt;400&gt; 303

gttcctcatt cctctaatacg ggcactatc tttgcctcgc gacggcgggtg cccgagcctt 60

ttcctcctct tagaaaccca cttctgaaag gtataaaaac	atg act att cga atc	115
	Met Thr Ile Arg Ile	
	1 5	
gga ctc gtt ggc tac ggt gtc ggc ggc agg ctc ttt cac acc cct tac	163	
Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu Phe His Thr Pro Tyr		
10 15 20		
atc caa gct tct acg cac tgc gaa tta gta ggc gta gtt gct cgt tcc	211	
Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly Val Val Ala Arg Ser		
25 30 35		
gaa ggc acc aaa gca gcc gtt gca gaa gat ctt cca gat gtt gcc atc	259	
Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu Pro Asp Val Ala Ile		
40 45 50		
gtg gga tcg ctg aca gaa ctc ctc gaa ctg ggc gtc gat gca gtg gtg	307	
Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly Val Asp Ala Val Val		
55 60 65		
atc tcc acc cct cca gcc acg cgc cgg gaa ctg gcc ttg gaa gca atc	355	
Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu Ala Leu Glu Ala Ile		
70 75 80 85		
aac gca ggt gtc gca gtg gtt gcc gat aaa ccg ttt gca cca tca gcc	403	
Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro Phe Ala Pro Ser Ala		
90 95 100		
gca gat gcc atg gaa ctt gtc gaa gcc gcc gaa aag gct gga gtg ctg	451	
Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu Lys Ala Gly Val Leu		
105 110 115		
ctc aac gtc ttc cac aac agg cgc aac gac acc cac att gtc acg gca	499	
Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr His Ile Val Thr Ala		
120 125 130		
ctg gga atc caa gaa gaa ctt ggt gcg atg cgt gga ctg gac ctg cga	547	
Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg Gly Leu Asp Leu Arg		
135 140 145		
cta gac ctg atc gaa cct gat tcc ttg gag gca ggt cct gaa ggt ggt	595	
Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala Gly Pro Glu Gly Gly		
150 155 160 165		
ttg ctg cgc gat ctg ggc tca cac gta gtc gat cag acc ctg gtt ctc	643	
Leu Leu Arg Asp Leu Gly Ser His Val Val Asp Gln Thr Leu Val Leu		
170 175 180		
atg ggg ccg gct acc tct gtc acc gcc caa ctt gga tcc atc gac ctt	691	
Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu Gly Ser Ile Asp Leu		
185 190 195		
cca gaa ggc cca acc aac gca agg ttc cgc atc gtg ttg gaa cat gaa	739	
Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile Val Leu Glu His Glu		
200 205 210		
tcg ggc gcc gta tcg cac att tct gcc agc aag att gac cgc ttg gag	787	
Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys Ile Asp Arg Leu Glu		
215 220 225		
tcc tgg gaa atc cgc ttg gtg ggc gag cgc ggc tcc tac gta tcc aac	835	

Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly Ser Tyr Val Ser Asn  
 230 235 240 245  
 tac acc gac gtg cag acc gtg gcg atc aaa cag gga ctt cga cca acc 883  
 Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln Gly Leu Arg Pro Thr  
 250 255 260  
 aat gac cgc gaa cac tgg ggc tac gaa tcg gag gag cgg tgg ggc acc 931  
 Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu Glu Arg Trp Gly Thr  
 265 270 275  
 ttg gtt acc gat gaa ggc tca aag gtg att cct tca gca caa ggc gat 979  
 Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro Ser Ala Gln Gly Asp  
 280 285 290  
 tac acc cgc ttc tac gat gcc ttt gcc ttg gct gtg gaa aac ggt ggc 1027  
 Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala Val Glu Asn Gly Gly  
 295 300 305  
 gca ggg ccg gtg cct gca cgt gaa ggt gtt gca gtg ctc aag gtg ttg 1075  
 Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala Val Leu Lys Val Leu  
 310 315 320 325  
 gat gct gta gcc cag agc gct gcg gaa aaa cgc acc att gag ttg agc 1123  
 Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg Thr Ile Glu Leu Ser  
 330 335 340  
 taaggagaag tgctgctggc tgc 1146

&lt;210&gt; 304

&lt;211&gt; 341

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 304

Met Thr Ile Arg Ile Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu  
 1 5 10 15  
 Phe His Thr Pro Tyr Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly  
 20 25 30  
 Val Val Ala Arg Ser Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu  
 35 40 45  
 Pro Asp Val Ala Ile Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly  
 50 55 60  
 Val Asp Ala Val Val Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu  
 65 70 75 80  
 Ala Leu Glu Ala Ile Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro  
 85 90 95  
 Phe Ala Pro Ser Ala Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu  
 100 105 110  
 Lys Ala Gly Val Leu Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr  
 115 120 125  
 His Ile Val Thr Ala Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg

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<400> 305
gtaggtgagt cttcgtgaga taccctccggc cagtcataca gttcaaccaa gctccaccac 60
ccagataaaa acctgcgggt tgcgttttag gagaattccc atg agt gat caa aaa 115
                                         Met Ser Asp Gln Lys
                                         1                               5
att gtt gtt ggc ctg cta ggc atc acc cac ccg cat gcg tcg gcg cgg 163
Ile Val Val Gly Leu Leu Gly Ile Thr His Pro His Ala Ser Ala Arg

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10					15					20						
gtg	cgt	gcc	ctc	cgt	gaa	att	gat	ggg	gta	gag	gtc	gtc	gcc	gcc	gcg	211
Val	Arg	Ala	Leu	Arg	Glu	Ile	Asp	Gly	Val	Glu	Val	Val	Ala	Ala	Ala	
			25					30					35			
gat	act	gat	tcc	cgc	ctc	cag	tac	ttc	acc	gac	aaa	tat	gat	gtt	gaa	259
Asp	Thr	Asp	Ser	Arg	Leu	Gln	Tyr	Phe	Thr	Asp	Lys	Tyr	Asp	Val	Glu	
		40					45					50				
ccc	cgc	gag	atc	gat	gac	gtc	ttg	aac	gac	gat	cgc	atc	aac	gcc	atc	307
Pro	Arg	Glu	Ile	Asp	Asp	Val	Leu	Asn	Asp	Asp	Arg	Ile	Asn	Ala	Ile	
		55				60					65					
atg	gtt	cac	tcc	aag	agc	aag	gac	atg	gtc	cct	cac	gcc	aag	cgc	gcg	355
Met	Val	His	Ser	Lys	Ser	Lys	Asp	Met	Val	Pro	His	Ala	Lys	Arg	Ala	
	70				75					80					85	
ctc	gcg	gcc	gga	aaa	tcc	gtc	gtc	gtg	gag	aag	ccc	ggc	ggg	gga	aca	403
Leu	Ala	Ala	Gly	Lys	Ser	Val	Val	Val	Glu	Lys	Pro	Gly	Gly	Gly	Thr	
				90					95					100		
gtg	gcg	gat	ctt	gag	gag	ctc	ctg	gcc	ctc	aaa	gaa	gct	gcc	gat	cct	451
Val	Ala	Asp	Leu	Glu	Glu	Leu	Leu	Ala	Leu	Lys	Glu	Ala	Ala	Asp	Pro	
			105					110					115			
cag	cga	atc	gtg	cag	gtc	ggg	tac	aac	gtc	cgc	ctg	tct	gaa	tcg	gtt	499
Gln	Arg	Ile	Val	Gln	Val	Gly	Tyr	Asn	Val	Arg	Leu	Ser	Glu	Ser	Val	
		120					125					130				
cag	aga	tta	aaa	gag	ctt	ctc	gac	gcc	ggc	ctc	atc	ggc	gaa	gtc	gtc	547
Gln	Arg	Leu	Lys	Glu	Leu	Leu	Asp	Ala	Gly	Leu	Ile	Gly	Glu	Val	Val	
		135				140					145					
agc	gtg	caa	gca	cgc	ggc	gcc	gca	aaa	gta	ggt	gag	cat	atc	acc	gag	595
Ser	Val	Gln	Ala	Arg	Gly	Ala	Ala	Lys	Val	Gly	Glu	His	Ile	Thr	Glu	
	150				155					160					165	
cac	ctc	aac	caa	ccc	gca	gac	atg	ggc	ggt	gtg	ttg	tgg	att	ctt	ggc	643
His	Leu	Asn	Gln	Pro	Ala	Asp	Met	Gly	Gly	Val	Leu	Trp	Ile	Leu	Gly	
				170					175					180		
tgc	cac	atg	ctc	gat	gca	ttg	gtg	gaa	gtc	ttc	gga	gct	cca	gaa	tcc	691
Cys	His	Met	Leu	Asp	Ala	Leu	Val	Glu	Val	Phe	Gly	Ala	Pro	Glu	Ser	
			185					190					195			
gtg	aac	gcc	cga	gtg	cat	aag	acc	gca	aaa	ctc	tct	gac	gac	acc	agc	739
Val	Asn	Ala	Arg	Val	His	Lys	Thr	Ala	Lys	Leu	Ser	Asp	Asp	Thr	Ser	
		200					205					210				
cgc	gaa	gac	tca	gcc	tcc	gca	ctg	ctg	tac	tac	cca	gat	ttc	tcc	gtc	787
Arg	Glu	Asp	Ser	Ala	Ser	Ala	Leu	Leu	Tyr	Tyr	Pro	Asp	Phe	Ser	Val	
	215					220					225					
agc	ttc	agc	ttc	gac	ggc	cac	gat	gat	ctg	gaa	tgg	ttc	gaa	agc	tcc	835
Ser	Phe	Ser	Phe	Asp	Gly	His	Asp	Asp	Leu	Glu	Trp	Phe	Glu	Ser	Ser	
	230				235					240					245	
cga	ctc	acg	gtc	tat	gga	acc	aag	ggc	atg	atc	gaa	gcc	gga	atc	ctc	883
Arg	Leu	Thr	Val	Tyr	Gly	Thr	Lys	Gly	Met	Ile	Glu	Ala	Gly	Ile	Leu	
			250						255					260		

cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca 931  
 Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro  
                   265                                  270                                  275

cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct 979  
 Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Phe Ala  
                   280                                  285                                  290

cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc 1027  
 Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile  
                   295                                  300                                  305

agc aac ttc cgc aca gaa atg cag ggg tgg gtg aat tcc att cgc act 1075  
 Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr  
 310                                  315                                  320                                  325

gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc 1123  
 Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg  
                   330                                  335                                  340

att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta 1171  
 Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val  
                   345                                  350                                  355

aac atc taagaggagc actccatgaa acc 1200  
 Asn Ile

&lt;210&gt; 306

&lt;211&gt; 359

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 306

Met Ser Asp Gln Lys Ile Val Val Gly Leu Leu Gly Ile Thr His Pro  
   1                                  5                                  10                                  15

His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu  
                   20                                  25                                  30

Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp  
                   35                                  40                                  45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp  
                   50                                  55                                  60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro  
   65                                  70                                  75                                  80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys  
                   85                                  90                                  95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys  
                   100                                  105                                  110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg  
                   115                                  120                                  125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu



130	135	140
Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly 145	150	155 160
Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val 165	170	175
Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe 180	185	190
Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu 195	200	205
Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr 210	215	220
Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu 225	230	235 240
Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile 245	250	255
Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser 260	265	270
Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe 275	280	285
Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro 290	295	300
Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val 305	310	315 320
Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala 325	330	335
Leu Thr Val Ala Arg Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn 340	345	350
Gln Gly Ile Ser Val Asn Ile 355		

&lt;210&gt; 307

&lt;211&gt; 1212

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1189)

&lt;223&gt; RXN00528

&lt;400&gt; 307

ttctgctggg aatccccaca ttttgaacg tagcgtcgat aagcgtgcgg cgaagctttt 60

tcggtcgcgg ccgttatctt ttttaagagga gaaattttag atg agc acg tcc acc 115

Met Ser Thr Ser Thr

1

5

atc	agg	gtt	gcc	att	gcc	gga	gtc	gga	aac	tgc	gcg	acc	tcc	ctc	att	163
Ile	Arg	Val	Ala	Ile	Ala	Gly	Val	Gly	Asn	Cys	Ala	Thr	Ser	Leu	Ile	
			10						15					20		
cag	ggt	gtg	gaa	tat	tac	cga	aat	gcg	gat	cct	tcc	gaa	act	gtc	ccg	211
Gln	Gly	Val	Glu	Tyr	Tyr	Arg	Asn	Ala	Asp	Pro	Ser	Glu	Thr	Val	Pro	
			25					30					35			
ggt	ttg	atg	cac	gtc	aaa	ttc	ggt	gat	tac	cac	gtt	ggc	gac	att	gaa	259
Gly	Leu	Met	His	Val	Lys	Phe	Gly	Asp	Tyr	His	Val	Gly	Asp	Ile	Glu	
		40					45					50				
ttc	gtg	gcc	gcg	ttc	gac	gtc	gac	gcc	gaa	aaa	gta	ggc	atc	gat	ctt	307
Phe	Val	Ala	Ala	Phe	Asp	Val	Asp	Ala	Glu	Lys	Val	Gly	Ile	Asp	Leu	
	55					60					65					
gcc	gac	gcc	acc	gag	gct	tca	caa	aac	tgc	act	atc	aaa	atc	gcc	gat	355
Ala	Asp	Ala	Thr	Glu	Ala	Ser	Gln	Asn	Cys	Thr	Ile	Lys	Ile	Ala	Asp	
	70				75					80					85	
gtc	cca	cag	acc	ggc	atc	aac	gtg	ctg	cgt	ggc	ccg	act	ctc	gac	ggc	403
Val	Pro	Gln	Thr	Gly	Ile	Asn	Val	Leu	Arg	Gly	Pro	Thr	Leu	Asp	Gly	
				90					95					100		
ctg	ggc	gat	cat	tac	cgc	gcg	acc	atc	gac	gag	tcc	acc	gcc	gag	cca	451
Leu	Gly	Asp	His	Tyr	Arg	Ala	Thr	Ile	Asp	Glu	Ser	Thr	Ala	Glu	Pro	
			105					110					115			
gtc	gac	gtt	gtc	cag	gcg	ctt	atc	gac	gca	aaa	gcc	gat	gtt	ttg	gtg	499
Val	Asp	Val	Val	Gln	Ala	Leu	Ile	Asp	Ala	Lys	Ala	Asp	Val	Leu	Val	
		120				125						130				
tcc	tac	ctc	cca	gtg	ggc	tcc	gaa	gaa	gcc	gac	aaa	ttc	tac	gca	caa	547
Ser	Tyr	Leu	Pro	Val	Gly	Ser	Glu	Glu	Ala	Asp	Lys	Phe	Tyr	Ala	Gln	
	135					140					145					
gcc	gcc	atc	gat	gca	ggc	tgc	gcc	ttt	gtc	aac	gct	ctc	cca	gta	ttc	595
Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Phe	Val	Asn	Ala	Leu	Pro	Val	Phe	
	150				155					160					165	
atc	gcc	tcc	gac	cct	gag	tgg	gct	aag	aag	ttc	act	gac	gct	ggc	atc	643
Ile	Ala	Ser	Asp	Pro	Glu	Trp	Ala	Lys	Lys	Phe	Thr	Asp	Ala	Gly	Ile	
				170					175					180		
cca	att	gtt	ggc	gat	gac	atc	aaa	tcc	cag	atc	ggt	gca	acc	atc	acc	691
Pro	Ile	Val	Gly	Asp	Asp	Ile	Lys	Ser	Gln	Ile	Gly	Ala	Thr	Ile	Thr	
			185					190					195			
cac	cgt	gtc	ctc	gca	cgc	ctt	ttt	gaa	gaa	cgt	ggc	gtt	cgc	gta	gat	739
His	Arg	Val	Leu	Ala	Arg	Leu	Phe	Glu	Glu	Arg	Gly	Val	Arg	Val	Asp	
		200				205						210				
cgc	acc	atg	cag	ctc	aac	gtc	ggc	ggc	aac	atg	gac	ttc	aaa	aac	atg	787
Arg	Thr	Met	Gln	Leu	Asn	Val	Gly	Gly	Asn	Met	Asp	Phe	Lys	Asn	Met	
	215					220					225					
ctt	gac	cgc	aat	cgc	ttg	gaa	tcc	aag	aag	gtc	tcc	aaa	acc	caa	gca	835
Leu	Asp	Arg	Asn	Arg	Leu	Glu	Ser	Lys	Lys	Val	Ser	Lys	Thr	Gln	Ala	
	230				235					240					245	

gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac 883  
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp  
250 255 260

cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac 931  
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp  
265 270 275

cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt 979  
Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val  
280 285 290

ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct 1027  
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser  
295 300 305

gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat 1075  
Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp  
310 315 320 325

cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag 1123  
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys  
330 335 340

tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag 1171  
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu  
345 350 355

gca ttc atc atc gag gcg taaaattagg ctaaaaattt ggg 1212  
Ala Phe Ile Ile Glu Ala  
360

&lt;210&gt; 308

&lt;211&gt; 363

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 308

Met Ser Thr Ser Thr Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys  
1 5 10 15

Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro  
20 25 30

Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His  
35 40 45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys  
50 55 60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr  
65 70 75 80

Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly  
85 90 95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu  
100 105 110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys

115					120					125						
Ala	Asp	Val	Leu	Val	Ser	Tyr	Leu	Pro	Val	Gly	Ser	Glu	Glu	Ala	Asp	
130					135					140						
Lys	Phe	Tyr	Ala	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Phe	Val	Asn	
145					150					155					160	
Ala	Leu	Pro	Val	Phe	Ile	Ala	Ser	Asp	Pro	Glu	Trp	Ala	Lys	Lys	Phe	
165					170					175						
Thr	Asp	Ala	Gly	Ile	Pro	Ile	Val	Gly	Asp	Asp	Ile	Lys	Ser	Gln	Ile	
180					185					190						
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Lys	Ile	Ala	Leu	Asp	Arg	Gly	Ile	Gly	Gly	Pro	Ile	Met	Pro	Ala	Ser	
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&lt;210&gt; 309

&lt;211&gt; 795

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(772)

&lt;223&gt; RXN03057

&lt;400&gt; 309

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Lys	Phe	Ala	Thr	Gly	Leu	Gly	Ala	Ala	Gly	Asp	Ser	Ser	Glu	Ser	Ser	
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Asn	Pro	Asp	Gly	Pro	Lys	Ile	Ala	Val	Cys	Tyr	Gln	Asn	Arg	Tyr	Asn	
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Val	Ser	Ser	Gln	Glu	Leu	Arg	Arg	Leu	Leu	Asp	Ser	Gly	Asp	Leu	Gly	
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Ala	Ile	Asn	Gly	Ala	Tyr	Ser	Ser	Val	Val	Trp	Thr	Arg	Thr	Pro	Gly	
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tac	tac	acc	cag	aaa	cct	tgg	cgt	ggc	cag	caa	gca	cac	tcc	ggg	ggg	595
Tyr	Tyr	Thr	Gln	Lys	Pro	Trp	Arg	Gly	Gln	Gln	Ala	His	Ser	Gly	Gly	
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Gly	Leu	Leu	Met	Asn	Gln	Ala	Ile	His	Thr	Leu	Asp	Leu	Leu	Gln	Trp	
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Phe	Leu	Gly	Lys	Ala	Thr	Glu	Val	Lys	Gly	Thr	Val	Ser	Thr	Asp	Lys	
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 <213> Corynebacterium glutamicum

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 His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile  
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 Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp  
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 Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp  
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 Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln  
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 Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu  
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 Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr  
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 Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala  
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&lt;222&gt; (101)..(772)

&lt;223&gt; FRXA02902

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Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
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Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
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Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
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Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
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Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
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Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
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Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
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gcc atc aat ggt gca tat tcc tct gtg gtg tgg acc cgc acc cca ggc 547
Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
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tac tac acc cag aaa cct tgg cgt ggc cag caa gca cac tcc ggt ggt 595
Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
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ggc ctg ctg atg aac caa gca att cac acc ctg gat ctg ctg cag tgg 643
Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
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ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
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tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
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aca

795

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<211> 224

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 312

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 35 40 45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln  
 50 55 60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile  
 65 70 75 80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile  
 85 90 95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr  
 100 105 110

Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp  
 115 120 125

Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp  
 130 135 140

Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln  
 145 150 155 160

Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu  
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Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr  
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Val Ser Thr Asp Lys Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala  
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His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser  
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                                         Met Lys Lys Lys Ile
                                         1 5

gcg gtc gtt acc gga gcg acc gga ggc atg gga att gag atc gtc aaa 163
Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly Ile Glu Ile Val Lys
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cat ctg gca gct ctc gca gag atc gag gga gta gag cct atc gag tcc 259
His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val Glu Pro Ile Glu Ser
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Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly Val Asp Lys Leu Lys
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Asn Leu Asp His Val Asp Thr Leu Val His Ala Ala Ala Val Ala Arg
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gac acg acc atc gaa gcc ggc agt gtg gcc gaa tgg cac gca cac ctt 403
Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu Trp His Ala His Leu
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Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser Arg Gln Leu Leu Pro
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Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr Ile Asn Ser Gly Ala
                        120                        125                        130

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Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr Ala Ala Ser Lys His
                        135                        140                        145

gcc ctc cgc gga ctc gcc gac gcc ttc cgc aaa gaa gaa gcc aac aac 595
Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys Glu Glu Ala Asn Asn
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ggc atc cgc gtc agc act gtc agc ccc ggc ccc acc aac acc ccc atg 643
Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro Thr Asn Thr Pro Met
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 200 205 210  
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 Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp Val Arg Pro Arg Ile  
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 Glu Leu Ala Asp Arg Lys Asp  
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 Glu Pro Ile Glu Ser Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly  
 50 55 60  
 Val Asp Lys Leu Lys Asn Leu Asp His Val Asp Thr Leu Val His Ala  
 65 70 75 80  
 Ala Ala Val Ala Arg Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu  
 85 90 95  
 Trp His Ala His Leu Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser  
 100 105 110  
 Arg Gln Leu Leu Pro Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr  
 115 120 125  
 Ile Asn Ser Gly Ala Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr  
 130 135 140  
 Ala Ala Ser Lys His Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys  
 145 150 155 160  
 Glu Glu Ala Asn Asn Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro  
 165 170 175  
 Thr Asn Thr Pro Met Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn  
 180 185 190  
 Phe Arg Pro Glu Ile Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile  
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Arg Phe Val Ile Asp Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp  
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Val Arg Pro Arg Ile Glu Leu Ala Asp Arg Lys Asp  
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<223> RXN02654

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 Met Ile Ser Leu Leu  
 1 5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163  
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser  
 10 15 20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211  
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile  
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ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259  
 Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala  
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ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct 307  
 Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala  
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 70 75 80 85

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 Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln  
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 Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu  
 120 125 130

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 Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile  
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acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt 595

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Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu		
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Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala		
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Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln		
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Thr	Pro																
	295																

&lt;210&gt; 316

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 316

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Ala	Val	Ala	Ile	Ala	Tyr	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ala	Ile	Ala	
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70					75				80						85	
caa	gcc	gat	gct	gac	aga	gtg	ctc	caa	gca	atc	gag	gaa	aca	ggc	caa	403
Gln	Ala	Asp	Ala	Asp	Arg	Val	Leu	Gln	Ala	Ile	Glu	Glu	Thr	Gly	Gln	
				90					95					100		
aaa	gct	ttt	tct	ttc	cct	ggc	gat	ctc	cgt	gat	cca	gaa	tac	tgt	cgc	451
Lys	Ala	Phe	Ser	Phe	Pro	Gly	Asp	Leu	Arg	Asp	Pro	Glu	Tyr	Cys	Arg	
			105					110					115			
tcg	ctg	gtc	caa	gag	acg	gtg	aac	gct	tta	ggc	ggc	cta	gac	atc	ttg	499
Ser	Leu	Val	Gln	Glu	Thr	Val	Asn	Ala	Leu	Gly	Gly	Leu	Asp	Ile	Leu	
		120					125					130				
gtc	aac	aac	gcg	tca	cgt	cag	gtg	tgg	gca	cct	ggc	ttg	acc	gaa	att	547
Val	Asn	Asn	Ala	Ser	Arg	Gln	Val	Trp	Ala	Pro	Gly	Leu	Thr	Glu	Ile	
	135					140				145						
acc	gac	gaa	aac	ttc	gac	cag	act	ttg	cag	gtt	aac	ctc	tat	ggc	agt	595
Thr	Asp	Glu	Asn	Phe	Asp	Gln	Thr	Leu	Gln	Val	Asn	Leu	Tyr	Gly	Ser	
150					155					160					165	
ttt	cgg	gtt	acc	aaa	gca	gct	ata	cct	cat	ctg	aag	ccc	gga	tca	tcg	643
Phe	Arg	Val	Thr	Lys	Ala	Ala	Ile	Pro	His	Leu	Lys	Pro	Gly	Ser	Ser	
				170					175					180		
ata	atc	ttt	aca	tcg	tcc	att	cag	gcg	tac	caa	cct	tcg	gaa	acc	ctc	691
Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu	
			185					190					195			
ttg	gat	tac	gcc	atg	act	aag	gcg	gca	ttg	aac	aat	ttg	tca	aag	ggc	739
Leu	Asp	Tyr	Ala	Met	Thr	Lys	Ala	Ala	Leu	Asn	Asn	Leu	Ser	Lys	Gly	
		200					205					210				
ttg	gca	agt	agt	ctg	ata	ggc	gat	ggc	att	cgg	gta	aat	tct	gta	gcc	787
Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala	
	215					220					225					
cca	ggc	cct	ttc	tgg	acg	ccg	ttg	caa	ccc	agc	cat	ggc	cag	cca	caa	835
Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln	
230					235					240					245	
gag	aaa	ata	gaa	gga	ttt	ggc	cag	cac	gct	ccg	att	gga	aga	gcg	ggc	883
Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro	Ile	Gly	Arg	Ala	Gly	

	250	255	260	
cac cct gtt gag ttg gca ggt gcg tac gtt ttt ctc gct tct gac gaa				931
His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu				
	265	270	275	
gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc				979
Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro				
	280	285	290	
acc cca tagtcggtac aagcgggaatc act				1008
Thr Pro				
	295			

&lt;210&gt; 318

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 318

Met Ile Ser Leu Leu Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp	
1 5 10 15	

Pro Pro Lys Gln Ser Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser	
20 25 30	

Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu	
35 40 45	

Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala	
50 55 60	

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala	
65 70 75 80	

Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile	
85 90 95	

Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp	
100 105 110	

Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly	
115 120 125	

Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro	
130 135 140	

Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val	
145 150 155 160	

Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu	
165 170 175	

Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln	
180 185 190	

Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn	
195 200 205	

Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg	
---	--

210	215	220
Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser		
225	230	235 240
His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro		
	245	250 255
Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe		
	260	265 270
Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val		
	275	280 285
Thr Gly Gly Thr Pro Thr Pro		
290	295	

<210> 319  
 <211> 1605  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1582)  
 <223> RXN01049

<400> 319  
 aagcacagca attgagcaat actcccatgc atgttttcgc gtgatcacgc tatatcctta 60  
  
 aagaatattc tttattagtc agaccttttaa aggaaacctt atg gga tca att cca 115  
 Met Gly Ser Ile Pro  
 1 5  
  
 aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct 163  
 Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala  
 10 15 20  
  
 atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc 211  
 Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser  
 25 30 35  
  
 ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc 259  
 Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr  
 40 45 50  
  
 acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag 307  
 Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu  
 55 60 65  
  
 atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac 355  
 Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn  
 70 75 80 85  
  
 atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca 403  
 Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser  
 90 95 100  
  
 tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc 451  
 Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr



105	110	115	
tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa			499
Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu			
120	125	130	
atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc			547
Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr			
135	140	145	
tcc tac cac cca tcg cgc ttg ctg tgg ctg aaa act gag ttc gag aaa			595
Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys Thr Glu Phe Glu Lys			
150	155	160	165
gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag tac gtc tac			643
Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu Tyr Val Tyr			
170	175	180	
ttc aaa ctt gca ggc atc acc gga atg gct act tcg att gcc gcg tgg			691
Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile Ala Ala Trp			
185	190	195	
agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg act atc ttg			739
Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu Thr Ile Leu			
200	205	210	
gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc aga aac cct			787
Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile Arg Asn Pro			
215	220	225	
gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag tgg aag cac			835
Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys Trp Lys His			
230	235	240	245
ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc tgg cct tcc			883
Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly Trp Pro Ser			
250	255	260	
aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca gtc gcc gcc			931
Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala Val Ala Ala			
265	270	275	
gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt ccc gaa cag			979
Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val Pro Glu Gln			
280	285	290	
atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac cag tgc atc			1027
Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp Gln Cys Ile			
295	300	305	
gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc tgg ctg gaa			1075
Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr Trp Leu Glu			
310	315	320	325
cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg atc cgc gaa			1123
Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu Ile Arg Glu			
330	335	340	
ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc ggg gaa cgc			1171
Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser Gly Glu Arg			
345	350	355	

tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc aac att cag 1219  
 Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr Asn Ile Gln  
 360 365 370

gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc gaa gcc ctc 1267  
 Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe Glu Ala Leu  
 375 380 385

gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa gcc ggc gca 1315  
 Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys Ala Gly Ala  
 390 395 400 405

gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc gac cac cca 1363  
 Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr Asp His Pro  
 410 415 420

gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca gtc atc cct 1411  
 Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro Val Ile Pro  
 425 430 435

ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt atc gtc ctt 1459  
 Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu Ile Val Leu  
 440 445 450

gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca ttc ggc acg 1507  
 Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro Phe Gly Thr  
 455 460 465

acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca aga gag ctt 1555  
 Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala Arg Glu Leu  
 470 475 480 485

ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg cagtggaacg 1602  
 Phe Asp Ala Leu Tyr Leu Lys Leu Val  
 490

cgc 1605

&lt;210&gt; 320

&lt;211&gt; 494

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 320

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly  
 1 5 10 15

Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly  
 20 25 30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu  
 35 40 45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp  
 50 55 60

Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala  
 65 70 75 80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp  
 85 90 95  
 Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu  
 100 105 110  
 Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu  
 115 120 125  
 Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly  
 130 135 140  
 Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys  
 145 150 155 160  
 Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile  
 165 170 175  
 Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr  
 180 185 190  
 Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu  
 195 200 205  
 Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly  
 210 215 220  
 Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp  
 225 230 235 240  
 Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro  
 245 250 255  
 Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr  
 260 265 270  
 Val Ala Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro  
 275 280 285  
 Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser  
 290 295 300  
 Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala  
 305 310 315 320  
 Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu  
 325 330 335  
 Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe  
 340 345 350  
 Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr  
 355 360 365  
 Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly  
 370 375 380  
 Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met  
 385 390 395 400  
 Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val

	405		410		415
Ser Thr Asp	His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp				
	420		425		430
Thr Pro Val	Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr				
	435		440		445
Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr					
	450		455		460
Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser					
465		470		475	480
Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val					
	485		490		

&lt;210&gt; 321

&lt;211&gt; 1134

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1111)

&lt;223&gt; FRXA01049

&lt;400&gt; 321

cacagtatgt ggagcagctg cgcgcgga aa tcgatgagaa ggcctaccac ggccgcaccg 60

gcgtctgctt gcacacctcc taccacccat cgcgcttgct	gtg gtg aaa act gag	115
	Val Val Lys Thr Glu	
	1 5	

ttc gag aaa gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag	163
Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu	
	10 15 20

tac gtc tac ttc aaa ctt gca ggc atc acc gga atg gct act tcg att	211
Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile	
	25 30 35

gcc gcg tgg agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg	259
Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu	
	40 45 50

act atc ttg gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc	307
Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile	
	55 60 65

aga aac cct gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag	355
Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys	
	70 75 80 85

tgg aag cac ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc	403
Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly	
	90 95 100

tgg cct tcc aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca	451
Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala	

				105				110				115							
gtc	gcc	gcc	gct	aca	tcc	ggc	gcc	atg	cgc	gtg	atc	ctt	ccg	agc	gtt	499			
Val	Ala	Ala	Ala	Thr	Ser	Gly	Ala	Met	Arg	Val	Ile	Leu	Pro	Ser	Val				
120								125				130							
ccc	gaa	cag	atc	ccc	tct	ggc	ctg	tgg	tgt	tac	cgc	gtt	tcc	cgc	gac	547			
Pro	Glu	Gln	Ile	Pro	Ser	Gly	Leu	Trp	Cys	Tyr	Arg	Val	Ser	Arg	Asp				
135								140				145							
cag	tgc	atc	gtt	ggg	ggc	gca	ctc	aac	gac	gtc	gga	cgc	gcc	gtc	acc	595			
Gln	Cys	Ile	Val	Gly	Gly	Ala	Leu	Asn	Asp	Val	Gly	Arg	Ala	Val	Thr				
150				155				160				165							
tgg	ctg	gaa	cgc	acc	att	atc	aag	cct	gaa	aac	ctc	gac	gaa	gtg	ctg	643			
Trp	Leu	Glu	Arg	Thr	Ile	Ile	Lys	Pro	Glu	Asn	Leu	Asp	Glu	Val	Leu				
				170				175				180							
atc	cgc	gaa	ccc	ctc	gaa	ggc	acc	cca	gct	gtc	ctg	ccg	ttc	ttc	tcc	691			
Ile	Arg	Glu	Pro	Leu	Glu	Gly	Thr	Pro	Ala	Val	Leu	Pro	Phe	Phe	Ser				
185								190				195							
ggg	gaa	cgc	tcc	atc	ggc	tgg	gca	gcc	tca	gcg	cag	gcc	acg	atc	acc	739			
Gly	Glu	Arg	Ser	Ile	Gly	Trp	Ala	Ala	Ser	Ala	Gln	Ala	Thr	Ile	Thr				
200								205				210							
aac	att	cag	gaa	caa	acc	ggc	cct	gaa	cac	ttg	tgg	cgc	ggc	gtt	ttc	787			
Asn	Ile	Gln	Glu	Gln	Thr	Gly	Pro	Glu	His	Leu	Trp	Arg	Gly	Val	Phe				
215								220				225							
gaa	gcc	ctc	gca	ctc	tcc	tac	cag	cgc	gtt	tgg	gaa	cac	atg	ggg	aaa	835			
Glu	Ala	Leu	Ala	Leu	Ser	Tyr	Gln	Arg	Val	Trp	Glu	His	Met	Gly	Lys				
230				235				240				245							
gcc	ggc	gca	gcc	cct	gaa	cgg	gtc	atc	gca	tca	gga	cga	gtc	tcc	acc	883			
Ala	Gly	Ala	Ala	Pro	Glu	Arg	Val	Ile	Ala	Ser	Gly	Arg	Val	Ser	Thr				
				250				255				260							
gac	cac	cca	gaa	ttc	ctc	gcg	atg	ctt	tcc	gac	gcc	ctc	gac	acc	cca	931			
Asp	His	Pro	Glu	Phe	Leu	Ala	Met	Leu	Ser	Asp	Ala	Leu	Asp	Thr	Pro				
265								270				275							
gtc	atc	cct	ctg	gaa	atg	aag	cgc	gcc	acc	ctc	cgc	ggc	acc	gca	ctt	979			
Val	Ile	Pro	Leu	Glu	Met	Lys	Arg	Ala	Thr	Leu	Arg	Gly	Thr	Ala	Leu				
280								285				290							
atc	gtc	ctt	gag	cag	ctc	gaa	cca	ggc	ggc	acg	cgc	gcg	acg	cca	cca	1027			
Ile	Val	Leu	Glu	Gln	Leu	Glu	Pro	Gly	Gly	Thr	Arg	Ala	Thr	Pro	Pro				
295				300				305											
ttc	ggc	acg	acg	cat	cag	ccg	cgc	ttt	gcg	cac	cat	tac	tcc	aag	gca	1075			
Phe	Gly	Thr	Thr	His	Gln	Pro	Arg	Phe	Ala	His	His	Tyr	Ser	Lys	Ala				
310				315				320				325							
aga	gag	ctt	ttc	gac	gcc	ctc	tac	ctc	aag	ttg	gtc	tagcttttcg					1121		
Arg	Glu	Leu	Phe																

&lt;210&gt; 322

&lt;211&gt; 337

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 322

Val	Val	Lys	Thr	Glu	Phe	Glu	Lys	Glu	Phe	Asn	Lys	Ala	Lys	Tyr	Val
1				5					10					15	

Met	Thr	Ile	Gly	Glu	Tyr	Val	Tyr	Phe	Lys	Leu	Ala	Gly	Ile	Thr	Gly
			20					25					30		

Met	Ala	Thr	Ser	Ile	Ala	Ala	Trp	Ser	Gly	Ile	Leu	Asp	Ala	His	Thr
		35					40					45			

Gly	Glu	Leu	Asp	Leu	Thr	Ile	Leu	Glu	His	Ile	Gly	Val	Asp	Pro	Ala
	50					55					60				

Leu	Phe	Gly	Glu	Ile	Arg	Asn	Pro	Asp	Glu	Pro	Ala	Thr	Asp	Ala	Lys
65					70					75					80

Val	Val	Asp	Lys	Lys	Trp	Lys	His	Leu	Glu	Glu	Ile	Pro	Trp	Phe	His
				85					90					95	

Ala	Ile	Pro	Asp	Gly	Trp	Pro	Ser	Asn	Ile	Gly	Pro	Gly	Ala	Val	Asp
			100					105					110		

Ser	Lys	Thr	Val	Ala	Val	Ala	Ala	Ala	Thr	Ser	Gly	Ala	Met	Arg	Val
		115					120					125			

Ile	Leu	Pro	Ser	Val	Pro	Glu	Gln	Ile	Pro	Ser	Gly	Leu	Trp	Cys	Tyr
	130					135					140				

Arg	Val	Ser	Arg	Asp	Gln	Cys	Ile	Val	Gly	Gly	Ala	Leu	Asn	Asp	Val
145					150					155					160

Gly	Arg	Ala	Val	Thr	Trp	Leu	Glu	Arg	Thr	Ile	Ile	Lys	Pro	Glu	Asn
				165					170					175	

Leu	Asp	Glu	Val	Leu	Ile	Arg	Glu	Pro	Leu	Glu	Gly	Thr	Pro	Ala	Val
			180					185					190		

Leu	Pro	Phe	Phe	Ser	Gly	Glu	Arg	Ser	Ile	Gly	Trp	Ala	Ala	Ser	Ala
		195					200					205			

Gln	Ala	Thr	Ile	Thr	Asn	Ile	Gln	Glu	Gln	Thr	Gly	Pro	Glu	His	Leu
	210					215					220				

Trp	Arg	Gly	Val	Phe	Glu	Ala	Leu	Ala	Leu	Ser	Tyr	Gln	Arg	Val	Trp
225					230					235					240

Glu	His	Met	Gly	Lys	Ala	Gly	Ala	Ala	Pro	Glu	Arg	Val	Ile	Ala	Ser
				245					250					255	

Gly	Arg	Val	Ser	Thr	Asp	His	Pro	Glu	Phe	Leu	Ala	Met	Leu	Ser	Asp
			260					265					270		

Ala	Leu	Asp	Thr	Pro	Val	Ile	Pro	Leu	Glu	Met	Lys	Arg	Ala	Thr	Leu
		275					280					285			

Arg	Gly	Thr	Ala	Leu	Ile	Val	Leu	Glu	Gln	Leu	Glu	Pro	Gly	Gly	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

290	295	300
Arg Ala Thr Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His		
305	310	315 320
His Tyr Ser Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu		
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Val		

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 Met Gly Ser Ile Pro 5  
 1  
 aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct 163  
 Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala 20  
 10 15  
 atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc 211  
 Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser 35  
 25 30  
 ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc 259  
 Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr 50  
 40 45  
 acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag 307  
 Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu 65  
 55 60  
 atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac 355  
 Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn 85  
 70 75 80  
 atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca 403  
 Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser 100  
 90 95  
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 Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr 115  
 105 110  
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 Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu 130  
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atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc 547  
 Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr  
 135 140 145

tcc tac cac cca tcg cgc ttg ctg tgg tgaaaactga gttcgagaaa 594  
 Ser Tyr His Pro Ser Arg Leu Leu Trp  
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gag 597

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<212> PRT

<213> Corynebacterium glutamicum

<400> 324

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Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly  
 20 25 30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu  
 35 40 45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp  
 50 55 60

Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala  
 65 70 75 80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp  
 85 90 95

Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu  
 100 105 110

Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu  
 115 120 125

Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly  
 130 135 140

Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp  
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<210> 325

<211> 1065

<212> DNA

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<220>

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<222> (101)..(1042)

<223> RXA00202

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				Met	Tyr	Ala	Arg	Lys	
				1				5	
ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct	163								
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala									
	10	15	20						
tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat	211								
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp									
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ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg	259								
Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val									
	40	45	50						
cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc	307								
Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr									
	55	60	65						
ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag	355								
Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln									
	70	75	80	85					
ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca	403								
Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro									
	90	95	100						
act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct	451								
Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala									
	105	110	115						
gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg	499								
Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val									
	120	125	130						
gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct	547								
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala									
	135	140	145						
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg	595								
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu									
	150	155	160	165					
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt	643								
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe									
	170	175	180						
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag	691								
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln									
	185	190	195						
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg	739								
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu									
	200	205	210						
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag	787								
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu									
	215	220	225						
atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat	835								

Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp  
 230 235 240 245

gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt 883  
 Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val  
 250 255 260

gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg 931  
 Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu  
 265 270 275

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac 979  
 Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp  
 280 285 290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac 1027  
 Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn  
 295 300 305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt 1065  
 Val Ala Asp Phe Lys  
 310

&lt;210&gt; 326

&lt;211&gt; 314

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 326

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Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp  
 20 25 30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr  
 35 40 45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp  
 50 55 60

Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala  
 65 70 75 80

Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val  
 85 90 95

Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu  
 100 105 110

Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser  
 115 120 125

Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly  
 130 135 140

Gly Ala Gln Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly  
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Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp

<400> 327																	
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<div style="display: flex; justify-content: space-between;"> <span>atg act aac ttg acg</span> <span>115</span> </div> <div style="display: flex; justify-content: space-between;"> <span>Met Thr Asn Leu Thr</span> </div> <div style="display: flex; justify-content: space-between;"> <span>1</span> <span>5</span> </div>																	
agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac																	163
<div style="display: flex; justify-content: space-between;"> <span>Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr</span> </div> <div style="display: flex; justify-content: space-between;"> <span>10</span> <span>15</span> <span>20</span> </div>																	
cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag																	211
<div style="display: flex; justify-content: space-between;"> <span>Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys</span> </div> <div style="display: flex; justify-content: space-between;"> <span>25</span> <span>30</span> <span>35</span> </div>																	
tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat																	259
<div style="display: flex; justify-content: space-between;"> <span>Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His</span> </div> <div style="display: flex; justify-content: space-between;"> <span>40</span> <span>45</span> <span>50</span> </div>																	
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ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala 105 110 115	451		
ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg 120 125 130	499		
gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro 135 140 145	547		
agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg 150 155 160 165	595		
cac acc atc ttt gat ctg gac tac cga cca atg ttc tgg gaa tcc cca His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met Phe Trp Glu Ser Pro 170 175 180	643		
gaa gag gcc acc aag cag gcg gaa tgg gcg ttg cag cat tcc acg gtg Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu Gln His Ser Thr Val 185 190 195	691		
gcg gtt ggc aac aag gaa gaa tgc gaa atc gca gtg ggc gag acc gag Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala Val Gly Glu Thr Glu 200 205 210	739		
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acc gta gaa gtt cct ccg ttc ttc gtc gat gtc atc aac ggt ctt ggt Thr Val Glu Val Pro Pro Phe Phe Val Asp Val Ile Asn Gly Leu Gly 250 255 260	883		
gcc ggc gat gca ttc ggc ggc gcg ctg tgc cac ggt ctg ctc tct gaa Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His Gly Leu Leu Ser Glu 265 270 275	931		
tgg ccg ttg gaa aag gtt ctc cgt ttt gcc aac acc gcg ggt gcg ctt Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn Thr Ala Gly Ala Leu 280 285 290	979		
gtg gcg tcc cgt ctt gaa tgc tcc acc gca atg cct act acc gat gag Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met Pro Thr Thr Asp Glu 295 300 305	1027		

gtg gaa gcc tcc ctc aac cag aaa gtc tgatatgact cctccgatta 1074  
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tct 1077

<210> 328

<211> 318

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

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Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val  
 35 40 45

Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly  
 50 55 60

Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly  
 65 70 75 80

Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val  
 85 90 95

Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr  
 100 105 110

Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser  
 115 120 125

Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly  
 130 135 140

Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr  
 145 150 155 160

Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met  
 165 170 175

Phe Trp Glu Ser Pro Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu  
 180 185 190

Gln His Ser Thr Val Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala  
 195 200 205

Val Gly Glu Thr Glu Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg  
 210 215 220

Gly Val Glu Leu Ala Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala  
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Met Thr Lys Asp Glu Thr Val Glu Val Pro Pro Phe Phe Val Asp Val  
 245 250 255

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agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac																163	
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr 10 15 20																	
cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag																211	
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys 25 30 35																	
tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat																259	
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His 40 45 50																	
gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc																307	
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly 55 60 65																	
gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac																355	
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr 70 75 80 85																	
gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att																403	
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile 90 95 100																	
ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct																451	
Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala 105 110 115																	
ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc																499	
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg																	

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gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca			547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro			
135	140	145	
agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc			595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg			
150	155	160	165
cac acc atc ttt gat ctg gac tac cga			622
His Thr Ile Phe Asp Leu Asp Tyr Arg			
170			

&lt;210&gt; 330

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 330

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Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val	
20 25 30	
Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val	
35 40 45	
Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly	
50 55 60	
Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly	
65 70 75 80	
Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val	
85 90 95	
Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr	
100 105 110	
Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser	
115 120 125	
Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly	
130 135 140	
Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr	
145 150 155 160	
Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg	
165 170	

&lt;210&gt; 331

&lt;211&gt; 1767

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1744)

&lt;223&gt; RXN00799

&lt;400&gt; 331

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Met Ser Gln Glu Arg
1 5

cct caa atc ggc tcc cgc ctc tct cgt gtc att gaa caa gac ggc cta 163
Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile Glu Gln Asp Gly Leu
10 15 20

caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa gat 211
Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu Ala Pro Tyr Glu Asp
25 30 35

tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt atg 259
Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg Met
40 45 50

aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac ccc 307
Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr Pro
55 60 65

gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa aag 355
Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu Lys
70 75 80 85

tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac ccg 403
Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn Pro
90 95 100

atc acg ggt gtt cct ttc acc gag cct gtg ctg gca act tct tcc act 451
Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser Thr
105 110 115

gaa aat gcc att aac ctg cgc aat cag cgt tac tta att gtt cgt gac 499
Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg Asp
120 125 130

aac ctg cca gct cgt ggg ctt gct act tgg acc aat gct gtt cag gaa 547
Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln Glu
135 140 145

gtc gcg gag cga tcc cgt ttg ggt att cct gtt gcg ttt gcg tcg aat 595
Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser Asn
150 155 160 165

cct cgt aac cac gtc gcg ctc gtt gcg cag ttc ggt gtg aac gag tcc 643
Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu Ser
170 175 180

gcg ggt gtg ttc tct gag tgg cct ggc gag ctg ggt ctt gct gcg ctt 691
Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala Leu
185 190 195

cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa gaa 739
Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys Glu

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200						205						210						
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Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His	Trp			
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Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr	His			
	295					300					305							
ctg	cct	cct	ttc	cag	gca	gct	atc	gac	gct	ggc	tgc	gcc	tcg	atc	atg	1075		
Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile	Met			
310					315					320					325			
cct	tac	tac	gca	cgg	cca	atg	aac	aac	tcc	gcc	aac	cag	ctc	gat	cag	1123		
Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp	Gln			
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cag	ctg	tgg	caa	aac	ccg	acc	acg	cag	ttc	gaa	gag	gtt	gcg	ttt	gcc	1171		
Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe	Ala			
			345					350					355					
tac	aac	cgc	acc	ttc	att	cag	gat	ttg	ctt	cgc	gac	gcc	atg	ggc	cac	1219		
Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly	His			
		360					365					370						
cgt	ggg	tac	gtc	aac	tcc	gac	tcc	ggc	gtc	atc	gac	gcc	atg	atg	tgg	1267		
Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met	Trp			
	375					380					385							
ggc	gtg	gag	gaa	ctc	agc	gag	cca	gaa	cgc	ttc	gcc	gca	gca	gtg	cgt	1315		
Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val	Arg			
390					395					400					405			
gca	ggc	acc	gac	att	ttc	tcc	gac	atg	gct	aac	cca	cgt	cga	ctg	ctc	1363		
Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu	Leu			
				410					415					420				
gaa	gca	gtt	gct	gag	gga	cac	ctt	gat	gag	tca	gag	ctg	aat	cag	cca	1411		
Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln	Pro			
		425						430					435					
gtc	cag	cga	ctc	ctg	gag	gaa	atc	ttc	cag	ctt	ggt	ctg	ttt	gag	aac	1459		
Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu	Asn			
		440					445					450						

cca tat gtc tct gaa gat gaa gca gaa aag atc att ggt gcg cca gag 1507  
 Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro Glu  
 455 460 465

gtt tct gca ttg ggc aac aaa gca cag ctt gat tcc gtc acc ttg ctg 1555  
 Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu Leu  
 470 475 480 485

cgt aac aac ccc atc cgt gct gcc act gga tcc tgc agc aag cct gaa 1603  
 Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro Glu  
 490 495 500

gat cta ccc att ggt tac tgg ccg tac caa gat cga cga ggt tca act 1651  
 Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser Thr  
 505 510 515

aca gct gga agc agc cat tcg cgc aga act ccc agg ggt aac ctt ggt 1699  
 Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro Arg Gly Asn Leu Gly  
 520 525 530

gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc 1744  
 Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg Val Gly Ser Pro  
 535 540 545

tgaaattgca ctgtttgaag atg 1767

&lt;210&gt; 332

&lt;211&gt; 548

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 332

Met Ser Gln Glu Arg Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile  
 1 5 10 15

Glu Gln Asp Gly Leu Gln Phe Arg Asp Leu Asp Gly Asp Gly Val Leu  
 20 25 30

Ala Pro Tyr Glu Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp  
 35 40 45

Leu Val Lys Arg Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile  
 50 55 60

Gly Ser His Tyr Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly  
 65 70 75 80

Lys Asp Ala Glu Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp  
 85 90 95

Arg Glu Asp Asn Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu  
 100 105 110

Ala Thr Ser Ser Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr  
 115 120 125

Leu Ile Val Arg Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr  
 130 135 140

Asn Ala Val Gln Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val  
 145 150 155 160  
 Ala Phe Ala Ser Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe  
 165 170 175  
 Gly Val Asn Glu Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu  
 180 185 190  
 Gly Leu Ala Ala Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr  
 195 200 205  
 Glu Ala Ala Lys Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly  
 210 215 220  
 Tyr Met Ala Asp Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly  
 225 230 235 240  
 Thr Phe Gly Glu Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val  
 245 250 255  
 Val Arg Gly Leu Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr  
 260 265 270  
 Thr Ile Lys His Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp  
 275 280 285  
 Pro His Phe His Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala  
 290 295 300  
 Leu Gly Lys Tyr His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly  
 305 310 315 320  
 Cys Ala Ser Ile Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala  
 325 330 335  
 Asn Gln Leu Asp Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu  
 340 345 350  
 Glu Val Ala Phe Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg  
 355 360 365  
 Asp Ala Met Gly His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile  
 370 375 380  
 Asp Ala Met Met Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe  
 385 390 395 400  
 Ala Ala Ala Val Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn  
 405 410 415  
 Pro Arg Arg Leu Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser  
 420 425 430  
 Glu Leu Asn Gln Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu  
 435 440 445  
 Gly Leu Phe Glu Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile  
 450 455 460  
 Ile Gly Ala Pro Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp

<400> 333																
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Leu	Gln	Phe	Arg	Asp	Leu	Asp	Gly	Asp	Gly	Val	Leu	Ala	Pro	Tyr	Glu	
1				5					10					15		
gat	tgg	cgt	cta	acc	cca	gca	gag	cgt	gcc	gct	gac	ctg	gtg	aaa	cgt	96
Asp	Trp	Arg	Leu	Thr	Pro	Ala	Glu	Arg	Ala	Ala	Asp	Leu	Val	Lys	Arg	
			20					25					30			
atg	aat	gtg	gaa	gaa	aaa	gcg	ggc	ctg	atg	atc	atc	ggt	tcg	cac	tac	144
Met	Asn	Val	Glu	Glu	Lys	Ala	Gly	Leu	Met	Ile	Ile	Gly	Ser	His	Tyr	
		35					40					45				
ccc	gga	tac	tcg	cct	ttg	gcg	ccg	gag	agt	gaa	ggc	aaa	gac	gcg	gaa	192
Pro	Gly	Tyr	Ser	Pro	Leu	Ala	Pro	Glu	Ser	Glu	Gly	Lys	Asp	Ala	Glu	
	50					55					60					
aag	tgc	gag	cct	ttg	ctg	aac	cct	gtc	gat	atg	tgg	cgt	gag	gat	aac	240
Lys	Cys	Glu	Pro	Leu	Leu	Asn	Pro	Val	Asp	Met	Trp	Arg	Glu	Asp	Asn	
	65				70				75						80	
ccg	atc	acg	ggt	gtt	cct	ttc	acc	gag	cct	gtg	ctg	gca	act	tct	tcc	288
Pro	Ile	Thr	Gly	Val	Pro	Phe	Thr	Glu	Pro	Val	Leu	Ala	Thr	Ser	Ser	
				85					90					95		
act	gaa	aat	gcc	att	aac	ctg	cgc	aat	cag	cgt	tac	tta	att	gtt	cgt	336
Thr	Glu	Asn	Ala	Ile	Asn	Leu	Arg	Asn	Gln	Arg	Tyr	Leu	Ile	Val	Arg	
			100					105					110			
gac	aac	ctg	cca	gct	cgt	ggg	ctt	gct	act	tgg	acc	aat	gct	gtt	cag	384
Asp	Asn	Leu	Pro	Ala	Arg	Gly	Leu	Ala	Thr	Trp	Thr	Asn	Ala	Val	Gln	
		115					120					125				

gaa gtc gcg gag cga tcc cgt ttg ggt att cct gtt gcg ttt gcg tcg Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser 130 135 140	432
aat cct cgt aac cac gtc gcg ctc gtt gcg cag ttc ggt gtg aac gag Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu 145 150 155 160	480
tcc gcg ggt gtg ttc tct gag tgg cct ggc gag ctg ggt ctt gct gcg Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala 165 170 175	528
ctt cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys 180 185 190	576
gaa tgg cgt gcc ggt ggt gtg cac aag ctg tac ggt tac atg gct gac Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp 195 200 205	624
ctc gct tct gag cct cgt tgg tcc cgc ttc aac ggt act ttt ggt gag Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu 210 215 220	672
gat ccg gag ttg atc tct gat tac atc gct gct gtt gtg cgt ggt ttg Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu 225 230 235 240	720
cag ggc cct gag ctg tcc aag aat tcc gtg tcg acc acc att aag cac Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His 245 250 255	768
ttc cca ggt ggc ggc gtg cgc ctc gac ggc cac gat cct cac ttc cac Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp Pro His Phe His 260 265 270	816
tgg ggt cag acc aat gag tac cca acc gaa gat gcg ctg ggc aag tac Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala Leu Gly Lys Tyr 275 280 285	864
cat ctg cct cct ttc cag gca gct atc gac gct ggc tgc gcc tcg atc His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly Cys Ala Ser Ile 290 295 300	912
atg cct tac tac gca cgg cca atg aac aac tcc gcc aac cag ctc gat Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala Asn Gln Leu Asp 305 310 315 320	960
cag cag ctg tgg caa aac ccg acc acg cag ttc gaa gag gtt gcg ttt Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe 325 330 335	1008
gcc tac aac cgc acc ttc att cag gat ttg ctt cgc gac gcc atg ggc Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly 340 345 350	1056
cac cgt ggg tac gtc aac tcc gac tcc ggc gtc atc gac gcc atg atg His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met 355 360 365	1104
tgg ggc gtg gag gaa ctc agc gag cca gaa cgc ttc gcc gca gca gtg	1152

Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val		
370						375					380						
cgt	gca	ggc	acc	gac	att	ttc	tcc	gac	atg	gct	aac	cca	cgt	cga	ctg	1200	
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu		
385					390					395					400		
ctc	gaa	gca	gtt	gct	gag	gga	cac	ctt	gat	gag	tca	gag	ctg	aat	cag	1248	
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln		
				405					410					415			
cca	gtc	cag	cga	ctc	ctg	gag	gaa	atc	ttc	cag	ctt	ggc	ctg	ttt	gag	1296	
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu		
			420					425					430				
aac	cca	tat	gtc	tct	gaa	gat	gaa	gca	gaa	aag	atc	att	ggc	gcg	cca	1344	
Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro		
		435					440					445					
gag	gtt	tct	gca	ttg	ggc	aac	aaa	gca	cag	ctt	gat	tcc	gtc	acc	ttg	1392	
Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu		
	450					455					460						
ctg	cgt	aac	aac	ccc	atc	cgt	gct	gcc	act	gga	tcc	tgc	agc	aag	cct	1440	
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro		
465					470					475					480		
gaa	gat	cta	ccc	att	ggc	tac	tgg	ccg	tac	caa	gat	cga	cga	ggc	tca	1488	
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp	Pro	Tyr	Gln	Asp	Arg	Arg	Gly	Ser		
				485					490					495			
act	aca	gct	gga	agc	agc	cat	tcg	cgc	aga	act	ccc	agg	ggc	aac	ctt	1536	
Thr	Thr	Ala	Gly	Ser	Ser	His	Ser	Arg	Arg	Thr	Pro	Arg	Gly	Asn	Leu		
			500					505					510				
ggc	gtc	ttc	cga	gtc	aga	agc	aga	tct	tgc	aat	cgt	gtg	ggc	tcg	ccc	1584	
Gly	Val	Phe	Arg	Val	Arg	Ser	Arg	Ser	Cys	Asn	Arg	Val	Gly	Ser	Pro		
		515					520					525					
tgaaaattgca	ctgtttgaag	atg														1607	

&lt;210&gt; 334

&lt;211&gt; 528

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 334

Leu	Gln	Phe	Arg	Asp	Leu	Asp	Gly	Asp	Gly	Val	Leu	Ala	Pro	Tyr	Glu		
1				5					10					15			
Asp	Trp	Arg	Leu	Thr	Pro	Ala	Glu	Arg	Ala	Ala	Asp	Leu	Val	Lys	Arg		
			20					25					30				
Met	Asn	Val	Glu	Glu	Lys	Ala	Gly	Leu	Met	Ile	Ile	Gly	Ser	His	Tyr		
		35					40					45					
Pro	Gly	Tyr	Ser	Pro	Leu	Ala	Pro	Glu	Ser	Glu	Gly	Lys	Asp	Ala	Glu		
	50					55					60						
Lys	Cys	Glu	Pro	Leu	Leu	Asn	Pro	Val	Asp	Met	Trp	Arg	Glu	Asp	Asn		

65		70		75		80									
Pro	Ile	Thr	Gly	Val	Pro	Phe	Thr	Glu	Pro	Val	Leu	Ala	Thr	Ser	Ser
			85						90					95	
Thr	Glu	Asn	Ala	Ile	Asn	Leu	Arg	Asn	Gln	Arg	Tyr	Leu	Ile	Val	Arg
			100					105					110		
Asp	Asn	Leu	Pro	Ala	Arg	Gly	Leu	Ala	Thr	Trp	Thr	Asn	Ala	Val	Gln
		115					120					125			
Glu	Val	Ala	Glu	Arg	Ser	Arg	Leu	Gly	Ile	Pro	Val	Ala	Phe	Ala	Ser
	130					135					140				
Asn	Pro	Arg	Asn	His	Val	Ala	Leu	Val	Ala	Gln	Phe	Gly	Val	Asn	Glu
145					150					155					160
Ser	Ala	Gly	Val	Phe	Ser	Glu	Trp	Pro	Gly	Glu	Leu	Gly	Leu	Ala	Ala
				165					170					175	
Leu	Arg	Asp	Ala	Glu	Leu	Met	Glu	Thr	Phe	Gly	Thr	Glu	Ala	Ala	Lys
			180					185					190		
Glu	Trp	Arg	Ala	Gly	Gly	Val	His	Lys	Leu	Tyr	Gly	Tyr	Met	Ala	Asp
		195					200					205			
Leu	Ala	Ser	Glu	Pro	Arg	Trp	Ser	Arg	Phe	Asn	Gly	Thr	Phe	Gly	Glu
	210					215					220				
Asp	Pro	Glu	Leu	Ile	Ser	Asp	Tyr	Ile	Ala	Ala	Val	Val	Arg	Gly	Leu
225					230					235					240
Gln	Gly	Pro	Glu	Leu	Ser	Lys	Asn	Ser	Val	Ser	Thr	Thr	Ile	Lys	His
				245					250					255	
Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His
			260					265					270		
Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr
		275					280					285			
His	Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile
	290				295						300				
Met	Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp
305					310					315					320
Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe
				325					330					335	
Ala	Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly
			340					345					350		
His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met
		355					360					365			
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val
	370					375					380				
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu
385					390					395					400

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<211> 1632
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1609)
<223> RXA00032
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ttttcgagct aaacccatcc ttgaaaggat cttttccacc atg aac acc cca ctc 115
Met Asn Thr Pro Leu
1 5

cag ctc aac act gaa aac ctg cag gaa atc gct tcg act tcc gga gtg 163
Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala Ser Thr Ser Gly Val
10 15 20

cag atc cca gcg ttc aac cgc gct gac gtc gcc ccg ggc att gtc cac 211
Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala Pro Gly Ile Val His
25 30 35

ttc ggt gtt ggc gga ttc cat cgc gct cac caa gcg atg tac ctc aat 259
Phe Gly Val Gly Gly Phe His Arg Ala His Gln Ala Met Tyr Leu Asn
40 45 50

gaa ttg atg aat gag ggc aag gcc ttg gat tgg ggc atc atc ggc atg 307
Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp Gly Ile Ile Gly Met
55 60 65

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ggt gtc atg cct tcc gat gtg cgc atg cgc gat gcc ctg gcc agc caa	355
Gly Val Met Pro Ser Asp Val Arg Met Arg Asp Ala Leu Ala Ser Gln	
70 75 80 85	
gat cac ctt tat acc ctg acc act aaa gct cct gat gga act ctt gat	403
Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro Asp Gly Thr Leu Asp	
90 95 100	
caa aaa atc atc gga tcc atc att gac tac gtg ttc gct ccc gag gac	451
Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val Phe Ala Pro Glu Asp	
105 110 115	
cca gca cgg gcc gtt gca acc ctc gcg cag gac tcc atc cgc att gtt	499
Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp Ser Ile Arg Ile Val	
120 125 130	
tcc ctc acg gtg act gaa ggc gga tac aac atc gat ccg gcg aca gaa	547
Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile Asp Pro Ala Thr Glu	
135 140 145	
gat ttc gac cac acc aac cct cga atc gtt gct gac cgc gaa gcc ctg	595
Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala Asp Arg Glu Ala Leu	
150 155 160 165	
cag gcg ggc gat act tcc act ttg cag acc ttc ttt ggg ttg atc act	643
Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe Phe Gly Leu Ile Thr	
170 175 180	
gcc gca ttg att tcc cga aaa gaa tca gga tct acg cca ttt acc atc	691
Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser Thr Pro Phe Thr Ile	
185 190 195	
atg agc tgc gat aac atc caa ggc aac ggc gat ctg gct aag cgt ttc	739
Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp Leu Ala Lys Arg Phe	
200 205 210	
ttc ctc gcc ttc gca cat tcc gtg tct tct gag ctc ggc gaa tgg gtg	787
Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu Leu Gly Glu Trp Val	
215 220 225	
gaa aac aac gtg gcc ttc ccc aac tcc atg gtg gac cgc atc acc cct	835
Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val Asp Arg Ile Thr Pro	
230 235 240 245	
gaa acc acc gac ggc gac cgc gat gac atc aag gaa atc ggc tac atc	883
Glu Thr Thr Asp Gly Asp Arg Asp Ile Lys Glu Ile Gly Tyr Ile	
250 255 260	
gat gcg tgg cca gtg gtt tct gaa gat ttc acc caa tgg gtc ctc gag	931
Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr Gln Trp Val Leu Glu	
265 270 275	
gat gcc ttc acc cag ggc cgc ccc gcg tac gag gag gtt ggc gtg cag	979
Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu Glu Val Gly Val Gln	
280 285 290	
gtc gtc tcc gac gtg gag cct tat gaa tta atg aag ctg cgc ctg ctc	1027
Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met Lys Leu Arg Leu Leu	
295 300 305	

aac gcc tcc cac cag gga ctt tgc tac ttc ggc cac ttg gct ggc cac 1075  
 Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly His Leu Ala Gly His  
 310 315 320 325  
 cac atg gtc cac gac gtc atg gcg gat acc cgc ttc cag gat ttc ctc 1123  
 His Met Val His Asp Val Met Ala Asp Thr Arg Phe Gln Asp Phe Leu  
 330 335 340  
 ctg gct tac atg gag cgc gaa gcc acc cct acc ctc aag gaa ctt cca 1171  
 Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr Leu Lys Glu Leu Pro  
 345 350 355  
 ggt gtc gat cta gat gct tat cga cgc caa ctc atc gcg cga ttc ggc 1219  
 Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu Ile Ala Arg Phe Gly  
 360 365 370  
 aac gcc gca gtc aaa gac acc gta ccg cgc ctg tgt gcg gaa tcc tcc 1267  
 Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu Cys Ala Glu Ser Ser  
 375 380 385  
 gac cgc att cca aag tgg ctg ttg cca gtc gta cgc gaa aac ctc gca 1315  
 Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val Arg Glu Asn Leu Ala  
 390 395 400 405  
 gca ggc cgc gac gtc aca ctt tct gca gcc atc gtc gca tcc tgg gcg 1363  
 Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile Val Ala Ser Trp Ala  
 410 415 420  
 cgc tac gca gaa ggc acc gac gag cag ggc aac cca ata aag att gtt 1411  
 Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn Pro Ile Lys Ile Val  
 425 430 435  
 gac cgt ttg agt gag cgc gtc caa gaa aac gca tca gga aat cgc acc 1459  
 Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala Ser Gly Asn Arg Thr  
 440 445 450  
 gat att ttg tca ttc atc cgc gac cgt gga atc ttc gga gac ttg gtc 1507  
 Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile Phe Gly Asp Leu Val  
 455 460 465  
 gat gct gaa cca ttc acc aag gca tac tcc gag aca ctg tcc tcc ctt 1555  
 Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu Thr Leu Ser Ser Leu  
 470 475 480 485  
 cat gac cgt ggc gcg gaa gca acc atc gat gca ctt ctt acg cag gta 1603  
 His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala Leu Leu Thr Gln Val  
 490 495 500  
 act gtc taaatccggt gcgcgctagg gtt 1632  
 Thr Val

&lt;210&gt; 336

&lt;211&gt; 503

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 336

Met Asn Thr Pro Leu Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala  
 1 5 10 15

Ser Thr Ser Gly Val Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala  
                   20                  25                  30  
 Pro Gly Ile Val His Phe Gly Val Gly Gly Phe His Arg Ala His Gln  
           35                  40                  45  
 Ala Met Tyr Leu Asn Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp  
       50                  55                  60  
 Gly Ile Ile Gly Met Gly Val Met Pro Ser Asp Val Arg Met Arg Asp  
   65                  70                  75                  80  
 Ala Leu Ala Ser Gln Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro  
                   85                  90                  95  
 Asp Gly Thr Leu Asp Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val  
          100                 105                 110  
 Phe Ala Pro Glu Asp Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp  
      115                 120                 125  
 Ser Ile Arg Ile Val Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile  
   130                 135                 140  
 Asp Pro Ala Thr Glu Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala  
  145                 150                 155                 160  
 Asp Arg Glu Ala Leu Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe  
          165                 170                 175  
 Phe Gly Leu Ile Thr Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser  
          180                 185                 190  
 Thr Pro Phe Thr Ile Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp  
      195                 200                 205  
 Leu Ala Lys Arg Phe Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu  
   210                 215                 220  
 Leu Gly Glu Trp Val Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val  
  225                 230                 235                 240  
 Asp Arg Ile Thr Pro Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys  
          245                 250                 255  
 Glu Ile Gly Tyr Ile Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr  
          260                 265                 270  
 Gln Trp Val Leu Glu Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu  
      275                 280                 285  
 Glu Val Gly Val Gln Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met  
   290                 295                 300  
 Lys Leu Arg Leu Leu Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly  
  305                 310                 315                 320  
 His Leu Ala Gly His His Met Val His Asp Val Met Ala Asp Thr Arg  
          325                 330                 335

Phe Gln Asp Phe Leu Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr  
 340 345 350  
 Leu Lys Glu Leu Pro Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu  
 355 360 365  
 Ile Ala Arg Phe Gly Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu  
 370 375 380  
 Cys Ala Glu Ser Ser Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val  
 385 390 395 400  
 Arg Glu Asn Leu Ala Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile  
 405 410 415  
 Val Ala Ser Trp Ala Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn  
 420 425 430  
 Pro Ile Lys Ile Val Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala  
 435 440 445  
 Ser Gly Asn Arg Thr Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile  
 450 455 460  
 Phe Gly Asp Leu Val Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu  
 465 470 475 480  
 Thr Leu Ser Ser Leu His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala  
 485 490 495  
 Leu Leu Thr Gln Val Thr Val  
 500

<210> 337  
 <211> 1098  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1075)  
 <223> RXA02528

<400> 337  
 ctggcgcggt atcgattaca atctggttgg ttatcgggtg tttgtggatg aatgtcatcg 60  
 gactctggta atcgaaaatt aaaggtaagg ggggtgtggag atg tca gca aaa tcg 115  
 Met Ser Ala Lys Ser  
 1 5  
 agc ctc aag gaa gtt gct gag tta gct gga gtc ggt tat gcc aca gcc 163  
 Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val Gly Tyr Ala Thr Ala  
 10 15 20  
 tcg agg gca cta tct ggc aag ggg tat gtg tcc ccg cag acg cgg gag 211  
 Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser Pro Gln Thr Arg Glu  
 25 30 35  
 aaa gtt cag gcg gcg gct aaa gag ctg aac tat gta cca aat cag ctg 259  
 Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr Val Pro Asn Gln Leu

40	45	50	
gcc aag gcg ttg cgg gaa cat cgc agt gcc ttg gtg ggg gtc att gtt Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu Val Gly Val Ile Val 55 60 65			307
ccg gat ttg tcc aat gag tat tat tcg gaa tcg ctg cag act att cag Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser Leu Gln Thr Ile Gln 70 75 80 85			355
cag gat ctg aaa gct gct ggc tat caa atg ctg gtt gcg gag gcc aac Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu Val Ala Glu Ala Asn 90 95 100			403
agt gtg cag gcg cag gac gtg gtg atg gaa tcg ttg atc tcg att caa Ser Val Gln Ala Gln Asp Val Val Met Glu Ser Leu Ile Ser Ile Gln 105 110 115			451
gct gca gga att atc cac gtt cca gtg gtc ggc tca att gct cct gaa Ala Ala Gly Ile Ile His Val Pro Val Val Gly Ser Ile Ala Pro Glu 120 125 130			499
gga atc ccc atg gtg cag ttg act cgt ggt gaa ttg ggt cct ggt ttc Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu Leu Gly Pro Gly Phe 135 140 145			547
cct cgg gtg ttg tgt gat gat gag gct ggg ttt ttt cag ctg acc gag Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe Phe Gln Leu Thr Glu 150 155 160 165			595
tcg gtg ctg ggc ggc agc gga atg aac att gct gct ttg gtt ggt gaa Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala Ala Leu Val Gly Glu 170 175 180			643
gaa tca ctt tcc acc acg cag gaa cga atg cgc ggt att agt cat gcg Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg Gly Ile Ser His Ala 185 190 195			691
gcg tcg ata tat ggg gct gag gtg acg ttc cat ttt ggc cac tat tct Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His Phe Gly His Tyr Ser 200 205 210			739
gtc gaa tct ggc gaa gag atg gct cag gtg gtg ttt aac aac ggc ctt Val Glu Ser Gly Glu Glu Met Ala Gln Val Val Phe Asn Asn Gly Leu 215 220 225			787
ccc gat gca ttg att gtg gcg tct cct cgg ctg atg gct ggg gtg atg Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu Met Ala Gly Val Met 230 235 240 245			835
cgt gct ttt act cgc ctg aat gtc cgc gtt ccc cac gat gtg gtg att Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro His Asp Val Val Ile 250 255 260			883
ggg ggt tat gac gat cct gag tgg tac agc ttt gtc ggc gcg ggg att Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe Val Gly Ala Gly Ile 265 270 275			931
acc acg ttt gtt cca ccg cat gag gag atg ggg aaa gag gcc gtg cgc Thr Thr Phe Val Pro Pro His Glu Glu Met Gly Lys Glu Ala Val Arg 280 285 290			979

ttg ttg gta gat ctg att gaa aat ccc gaa ctt ccc acc ggc gat gtg 1027  
 Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu Pro Thr Gly Asp Val  
 295 300 305

gtt ttg cag ggg cag gtg atc ctt cgg ggg tcg agc aca cat tcc ggg 1075  
 Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser Ser Thr His Ser Gly  
 310 315 320 325

tagaattgcc caaatgtcat caa 1098

<210> 338

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Ser Ala Lys Ser Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val  
 1 5 10 15

Gly Tyr Ala Thr Ala Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser  
 20 25 30

Pro Gln Thr Arg Glu Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr  
 35 40 45

Val Pro Asn Gln Leu Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu  
 50 55 60

Val Gly Val Ile Val Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser  
 65 70 75 80

Leu Gln Thr Ile Gln Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu  
 85 90 95

Val Ala Glu Ala Asn Ser Val Gln Ala Gln Asp Val Val Met Glu Ser  
 100 105 110

Leu Ile Ser Ile Gln Ala Ala Gly Ile Ile His Val Pro Val Val Gly  
 115 120 125

Ser Ile Ala Pro Glu Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu  
 130 135 140

Leu Gly Pro Gly Phe Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe  
 145 150 155 160

Phe Gln Leu Thr Glu Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala  
 165 170 175

Ala Leu Val Gly Glu Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg  
 180 185 190

Gly Ile Ser His Ala Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His  
 195 200 205

Phe Gly His Tyr Ser Val Glu Ser Gly Glu Glu Met Ala Gln Val Val  
 210 215 220

Phe Asn Asn Gly Leu Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu

<400> 339																
agcgcgatgat cgatgcctgc gagtccgcag ggggtccaact tggcgtgctc ttccagcgcc																60
gcttctggcc cgcggtctcaa aaaatgaaaa aggagccgctc atg ggc caa tgc acg																115
Met Gly Gln Cys Thr																5
1																
gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga																163
Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg																20
10 15																
gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc																211
Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile																35
25 30																
cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt																259
His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val																50
40 45																
ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa																307
Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu																65
55 60																
gac agc gcc gtt gcc act gtg cgt ttt gaa tgc ggc gcg ttg gcc aca																355
Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr																85
70 75 80																
att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag																403
Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln																100
90 95 100																

gtg atg gga aca aag ggt gcc acc atg acg atc ctg gaa ttc cct gaa	451
Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile Leu Glu Phe Pro Glu	
105 110 115	
ggt acc gac ggc agg ctc att gtt cgc agt gaa aac gac acc cgt cga	499
Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu Asn Asp Thr Arg Arg	
120 125 130	
aac cac ccc att cca ccc cgc gga tct tta tcc caa tgc cga tct ttc	547
Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser Gln Cys Arg Ser Phe	
135 140 145	
cat cat caa cgg tgc ttt gat ccc gta tca cac cgc cca gat cgc aga	595
His His Gln Arg Cys Phe Asp Pro Val Ser His Arg Pro Asp Arg Arg	
150 155 160 165	
ctt tat cga tgc gct caa cga agg ccg ccc acc act gat cac cgg ccg	643
Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr Thr Asp His Arg Pro	
170 175 180	
cga tgc cac cag agc tct gaa agt tct cct tgg tgt cta cga atc agc	691
Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp Cys Leu Arg Ile Ser	
185 190 195	
agc cac cca cca gcc ggt ctc ttt gat cta acg gaa gct ttt aaa acg	739
Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr Glu Ala Phe Lys Thr	
200 205 210	
tca cgc caa atc ggt ctt gca cct tta tcc tcc ctg tcc aca cca cct	787
Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser Leu Ser Thr Pro Pro	
215 220 225	
gat caa cta gtg cgc ctc gca gct gcc act ggt ttc tcc ttt gtc ggt	835
Asp Gln Leu Val Arg Leu Ala Ala Thr Gly Phe Ser Phe Val Gly	
230 235 240 245	
ctg cgc gtc atc gca gta acc ccc aac gaa cgt gta tat gac ctt tcc	883
Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg Val Tyr Asp Leu Ser	
250 255 260	
cca gga tcc cca ctg ctg gct gca acc caa caa gcg ttg aaa gaa acc	931
Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln Ala Leu Lys Glu Thr	
265 270 275	
gcc ctg tat gtg ctc gac act gaa ttc cta cag gta aac gca gac acc	979
Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln Val Asn Ala Asp Thr	
280 285 290	
acc cgc gag gcc tgg ctt ccc gca cta gaa gcc gcc gga gca ctg gga	1027
Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala Ala Gly Ala Leu Gly	
295 300 305	
gct aaa acc ttc acc atc gcc gcc ggt gat gac aac att gcg ccc ctg	1075
Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp Asn Ile Ala Pro Leu	
310 315 320 325	
acc gac acg atc ggt gcc atg gtt gac gat gcc cgt gat ttc gga gtc	1123
Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala Arg Asp Phe Gly Val	
330 335 340	



acc cca gcc cta gag cca atc tct tac cgc agc gtg cat tcc att ccg 1171  
 Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser Val His Ser Ile Pro  
                   345                  350                  355

cag gca gca gca atc gcc aga gac tcc ggc gga aaa gtc gtg gcg gac 1219  
 Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly Lys Val Val Ala Asp  
                   360                  365                  370

acc ttg cac atg gcc agg ttc gga gcc 1246  
 Thr Leu His Met Ala Arg Phe Gly Ala  
           375                  380

<210> 340

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr  
   1                  5                  10                  15

Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu  
                   20                  25                  30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly  
                   35                  40                  45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp  
                   50                  55                  60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser  
   65                  70                  75                  80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu  
                   85                  90                  95

Gly Ala Gln Val Gln Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile  
                   100                  105                  110

Leu Glu Phe Pro Glu Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu  
                   115                  120                  125

Asn Asp Thr Arg Arg Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser  
   130                  135                  140

Gln Cys Arg Ser Phe His His Gln Arg Cys Phe Asp Pro Val Ser His  
   145                  150                  155                  160

Arg Pro Asp Arg Arg Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr  
                   165                  170                  175

Thr Asp His Arg Pro Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp  
                   180                  185                  190

Cys Leu Arg Ile Ser Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr  
                   195                  200                  205

Glu Ala Phe Lys Thr Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser  
                   210                  215                  220

Leu Ser Thr Pro Pro Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly  
 225 230 235 240  
 Phe Ser Phe Val Gly Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg  
 245 250 255  
 Val Tyr Asp Leu Ser Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln  
 260 265 270  
 Ala Leu Lys Glu Thr Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln  
 275 280 285  
 Val Asn Ala Asp Thr Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala  
 290 295 300  
 Ala Gly Ala Leu Gly Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp  
 305 310 315 320  
 Asn Ile Ala Pro Leu Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala  
 325 330 335  
 Arg Asp Phe Gly Val Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser  
 340 345 350  
 Val His Ser Ile Pro Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly  
 355 360 365  
 Lys Val Val Ala Asp Thr Leu His Met Ala Arg Phe Gly Ala  
 370 375 380

&lt;210&gt; 341

&lt;211&gt; 412

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(412)

&lt;223&gt; FRXA00309

&lt;400&gt; 341

agcgcacgat cgatgcctgc gagtccgcag ggggtccaact tggcgtgctc ttccagcgcc 60

gcttctggcc cgcggctcaa aaaatgaaaa aggagccgctc atg ggc caa tgc acg 115  
 Met Gly Gln Cys Thr  
 1 5

gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163  
 Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg  
 10 15 20

gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211  
 Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile  
 25 30 35

cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259  
 His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val  
 40 45 50

ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307



tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163  
 Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile  
                   10                  15                  20

gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211  
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp  
                   25                  30                  35

gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259  
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser  
                   40                  45                  50

ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307  
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile  
                   55                  60                  65

gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355  
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala  
                   70                  75                  80                  85

gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403  
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile  
                   90                  95                  100

gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451  
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly  
                   105                  110                  115

gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499  
 Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln  
                   120                  125                  130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545  
 Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg  
                   135                  140                  145

ccgagagcat tcc 558

&lt;210&gt; 344

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 344

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile  
   1                  5                  10                  15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val  
                   20                  25                  30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala  
                   35                  40                  45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala  
                   50                  55                  60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu  
   65                  70                  75                  80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu

	85		90		95										
Lys	Pro	Ile	Ala	Ile	Glu	Leu	Asp	Ser	Ala	Gln	Arg	Met	Ile	Asp	Ala
			100					105						110	
Cys	Glu	Ser	Ala	Gly	Val	Gln	Leu	Gly	Val	Leu	Phe	Gln	Arg	Arg	Phe
		115					120					125			
Trp	Pro	Ala	Ala	Gln	Lys	Met	Lys	Lys	Glu	Pro	Ser	Trp	Ala	Asn	Ala
	130					135					140				
Arg															
145															

<210> 345  
 <211> 558  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(535)  
 <223> FRXA00310

<400> 345  
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 aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115  
 Met Ser Asp Lys Ile 5  
 1  
 tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163  
 Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile 20  
 10 15  
 gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211  
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp 35  
 25 30  
 gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259  
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser 50  
 40 45  
 ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307  
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile 65  
 55 60  
 gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355  
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala 85  
 70 75 80  
 gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403  
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile 100  
 90 95  
 gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451  
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly 115  
 105 110  
 gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499

Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln  
           120                  125                  130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545  
 Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg  
           135                  140                  145

ccgagagcat tcc 558

<210> 346

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile  
   1                  5                  10                  15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val  
           20                  25                  30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala  
           35                  40                  45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala  
           50                  55                  60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu  
           65                  70                  75                  80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu  
                   85                  90                  95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala  
           100                  105                  110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe  
           115                  120                  125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala  
           130                  135                  140

Arg

145

<210> 347

<211> 1342

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1342)

<223> RXA00041

<400> 347

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agctgcgcta gaaacaaaaa ggaaagtagt gtgtggggct atg cac aca gaa ctt 115

												Met	His	Thr	Glu	Leu	
												1				5	
tcc	agt	ttg	cgc	cct	gcg	tac	cat	gtg	act	cct	ccg	cag	ggc	agg	ctc		163
Ser	Ser	Leu	Arg	Pro	Ala	Tyr	His	Val	Thr	Pro	Pro	Gln	Gly	Arg	Leu		
				10					15					20			
aat	gat	ccc	aac	gga	atg	tac	gtc	gat	ggc	gat	acc	ctc	cac	gtc	tac		211
Asn	Asp	Pro	Asn	Gly	Met	Tyr	Val	Asp	Gly	Asp	Thr	Leu	His	Val	Tyr		
			25					30					35				
tac	cag	cac	gat	cca	ggc	ttc	ccc	ttc	gca	cca	aag	cgc	acc	ggc	tgg		259
Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	Ala	Pro	Lys	Arg	Thr	Gly	Trp		
		40					45					50					
gct	cac	acc	acc	acg	ccg	ttg	acc	gga	ccg	cag	cga	ttg	cag	tgg	acg		307
Ala	His	Thr	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp	Thr		
	55					60					65						
cac	ctg	ccc	gac	gct	ctt	tac	ccg	gat	gca	tcc	tat	gac	ctg	gat	gga		355
His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Ala	Ser	Tyr	Asp	Leu	Asp	Gly		
	70				75					80					85		
tgc	tat	tcc	ggc	gga	gcc	gta	ttt	act	gac	ggc	aca	ctt	aaa	ctt	ttc		403
Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Thr	Asp	Gly	Thr	Leu	Lys	Leu	Phe		
			90						95					100			
tac	acc	ggc	aac	cta	aaa	att	gac	ggc	aag	cgc	cgc	gcc	acc	caa	aac		451
Tyr	Thr	Gly	Asn	Leu	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln	Asn		
			105					110					115				
ctc	gtc	gaa	gtc	gag	gac	cca	act	ggg	ctg	atg	ggc	ggc	att	cat	cgc		499
Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	Arg		
		120					125					130					
cgt	tcg	cct	aaa	aat	ccg	ctt	atc	gac	gga	ccc	gcc	agc	ggc	ttc	aca		547
Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	Thr		
	135					140					145						
ccc	cat	tac	cgc	gat	ccc	atg	atc	agc	cct	gat	ggc	gat	ggc	tgg	aaa		595
Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	Lys		
	150				155					160					165		
atg	gtt	ctt	ggg	gcc	caa	cgc	gaa	aac	ctc	acc	ggc	gca	gcg	gtt	cta		643
Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	Leu		
			170						175					180			
tac	cgc	tcg	aca	gat	ctt	gaa	aac	tgg	gaa	ttc	tcc	ggc	gaa	atc	acc		691
Tyr	Arg	Ser	Thr	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	Ile	Thr		
			185					190					195				
ttt	gac	ctc	agt	gat	gca	caa	cct	ggc	tct	gct	cct	gat	ctc	gtt	ccc		739
Phe	Asp	Leu	Ser	Asp	Ala	Gln	Pro	Gly	Ser	Ala	Pro	Asp	Leu	Val	Pro		
		200					205					210					
ggc	ggc	tac	atg	tgg	gaa	tgc	ccc	aac	ctt	ttt	acg	ctt	cgc	gat	gaa		787
Gly	Gly	Tyr	Met	Trp	Glu	Cys	Pro	Asn	Leu	Phe	Thr	Leu	Arg	Asp	Glu		
	215					220					225						
gaa	act	ggc	gaa	gat	ctc	gac	gtg	ctg	att	ttc	tgt	cca	caa	gga	ttg		835
Glu	Thr	Gly	Glu	Asp	Leu	Asp	Val	Leu	Ile	Phe	Cys	Pro	Gln	Gly	Leu		

230	235	240	245	
gac cga atc cac gat gag gtt act cac tac gca agc tct gac cag tgc				883
Asp Arg Ile His Asp Glu Val Thr His Tyr Ala Ser Ser Asp Gln Cys	250	255	260	
gga tat gtc gtc ggc aag ctt gaa gga acg acc ttc cgc gtc ttg cga				931
Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr Phe Arg Val Leu Arg	265	270	275	
gga ttc agc gag ctg gat ttc ggc cat gaa ttc tac gca ccg cag gtt				979
Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe Tyr Ala Pro Gln Val	280	285	290	
gca gta aac ggt tct gat gcc tgg ctc gtg ggc tgg atg ggg ctg ccc				1027
Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly Trp Met Gly Leu Pro	295	300	305	
gcg cag gat gat cac cca aca gtt gca cgg gaa gga tgg gtg cac tgc				1075
Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu Gly Trp Val His Cys	310	315	320	325
ctg act gtg ccc cgc aag ctt cat ttg cgc aac cac gcg atc tat caa				1123
Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn His Ala Ile Tyr Gln	330	335	340	
gag ctt ctt ctc cca gag ggg gag tca ggg gta atc aga tct gta tta				1171
Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val Ile Arg Ser Val Leu	345	350	355	
ggt tct gaa cct gtc cga gta gac atc cga ggc aat att tcc ctc gag				1219
Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly Asn Ile Ser Leu Glu	360	365	370	
tgg gat ggt gtc cgt ttg tct gtg gat cgt ggt ggt gat cgt cgc gta				1267
Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val	375	380	385	
gct gag gta aaa cct ggc gaa tta gtg atc gcg gac gat aat aca gcc				1315
Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala Asp Asp Asn Thr Ala	390	395	400	405
att gag ata act gca ggt gat gga cag				1342
Ile Glu Ile Thr Ala Gly Asp Gly Gln	410			

&lt;210&gt; 348

&lt;211&gt; 414

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 348

Met	His	Thr	Glu	Leu	Ser	Ser	Leu	Arg	Pro	Ala	Tyr	His	Val	Thr	Pro
1				5					10					15	

Pro	Gln	Gly	Arg	Leu	Asn	Asp	Pro	Asn	Gly	Met	Tyr	Val	Asp	Gly	Asp
			20					25					30		

Thr	Leu	His	Val	Tyr	Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	Ala	Pro
		35					40					45			



Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln  
 50 55 60  
 Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser  
 65 70 75 80  
 Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly  
 85 90 95  
 Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg  
 100 105 110  
 Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met  
 115 120 125  
 Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro  
 130 135 140  
 Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp  
 145 150 155 160  
 Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr  
 165 170 175  
 Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe  
 180 185 190  
 Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala  
 195 200 205  
 Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe  
 210 215 220  
 Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe  
 225 230 235 240  
 Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala  
 245 250 255  
 Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr  
 260 265 270  
 Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe  
 275 280 285  
 Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly  
 290 295 300  
 Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu  
 305 310 315 320  
 Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn  
 325 330 335  
 His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val  
 340 345 350  
 Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly  
 355 360 365

Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly  
 370 375 380

Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala  
 385 390 395 400

Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln  
 405 410

<210> 349

<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(720)

<223> RXA02026

<400> 349

cca ttt cat ata caa cca gaa aca ggt tta tta aat gat ccc aac gga 48  
 Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly  
 1 5 10 15

ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca 96  
 Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro  
 20 25 30

tta ggc gca gta cat ggc tta aag tat tgg tat aac tac acg agt gat 144  
 Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp  
 35 40 45

gac tta ata aac ttt aaa cct gaa ggg cca ata tta aat cca gat act 192  
 Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr  
 50 55 60

aaa tat gac agc cat ggt gtt tat agc ggt agc gct ttt gaa tat aac 240  
 Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn  
 65 70 75 80

ggg cat tta tat tat atg tac aca gga aat cat cga gat aat cat tgg 288  
 Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp  
 85 90 95

caa cga cat gcg agt cag atg atc gca cga ttg aaa gaa gac ggt tca 336  
 Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser  
 100 105 110

gtt gaa aag ttt cca aag cca gta att agc cag caa cca gaa gga tat 384  
 Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr  
 115 120 125

aca agt cat ttt aga gat cct aaa gtt ttt aaa tat ggt gag aaa tat 432  
 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr  
 130 135 140

tat gca atc att ggc gca caa aat aat gat cag caa ggt cga tta tta 480  
 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu  
 145 150 155 160

ctt tat aat act gaa gat ata att aat tgg cat tat tta ggt gaa ata 528  
 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile  
                   165                                  170                                  175

aat aca gag tta gat gat ttt gga tat atg tgg gaa tgc cca gat tac 576  
 Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr  
                   180                                  185                                  190

ttt aat tta gat aat caa gat gtc ata ctt att tgt cca caa ggt att 624  
 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile  
                   195                                  200                                  205

gaa cca aaa ggc aat cag ttc aaa aat att tat caa agt ggt tat ata 672  
 Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile  
                   210                                  215                                  220

ctt gga aag ttt gat att gaa aag tta aca tat gaa cat gaa aat ttt 720  
 Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe  
 225                                  230                                  235                                  240

<210> 350

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly  
   1                                  5                                  10                                  15

Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro  
                   20                                  25                                  30

Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp  
                   35                                  40                                  45

Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr  
                   50                                  55                                  60

Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn  
   65                                  70                                  75                                  80

Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp  
                   85                                  90                                  95

Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser  
                   100                                  105                                  110

Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr  
                   115                                  120                                  125

Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr  
   130                                  135                                  140

Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu  
 145                                  150                                  155                                  160

Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile  
                   165                                  170                                  175

Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr

180	185	190
Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile		
195	200	205
Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile		
210	215	220
Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe		
225	230	235
		240

<210> 351  
 <211> 1617  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1594)  
 <223> RXA02061

<400> 351  
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 agacactggc gtaattgagt gaaggcagga caataaagag atg acg aac gtt tcc 115  
 Met Thr Asn Val Ser 5  
 1  
 ggg tat cac cga cca gag ctg cac atc acc gct gaa agt ggt gtt ttg 163  
 Gly Tyr His Arg Pro Glu Leu His Ile Thr Ala Glu Ser Gly Val Leu 20  
 10 15  
 ttt gca cct gca ggc gtt ctg ttg gat gac gac acg tgg cat ttc ttc 211  
 Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp Thr Trp His Phe Phe 35  
 25 30  
 cac cag tac cgt ccc tca cca gat cac ggc ccc agg tgg gcg cac caa 259  
 His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro Arg Trp Ala His Gln 50  
 40 45  
 ttc gca gag cgc act cca ttt gtg tgg gat atc tgc gat gac gtg cta 307  
 Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile Cys Asp Asp Val Leu 65  
 55 60  
 gcc cct gaa ggc gat gaa acc cag gtt cgc gct ggc tca gtg gtg tcc 355  
 Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala Gly Ser Val Val Ser 85  
 70 75 80  
 aac aac ggt ggc gtt gat ctg tac ttc acc tcg gtt gtt ggc ccc act 403  
 Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser Val Val Gly Pro Thr 100  
 90 95  
 tcc act atc cag ttg gca cac atc aac aac atc cgt ggc acc acc gaa 451  
 Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile Arg Gly Thr Thr Glu 115  
 105 110  
 ctg atc aat gag gac gag ctg ggg ctc gat cca gat gtc tcc cga atc 499

Leu	Ile	Asn	Glu	Asp	Glu	Leu	Gly	Leu	Asp	Pro	Asp	Val	Ser	Arg	Ile	
		120					125					130				
ggc	gaa	gtg	gtt	ggc	aac	act	gat	ggt	tat	gta	aag	ttc	cgc	tca	ccg	547
Gly	Glu	Val	Val	Gly	Asn	Thr	Asp	Gly	Tyr	Val	Lys	Phe	Arg	Ser	Pro	
		135				140					145					
tgc	gtt	atc	cca	ggt	tgg	gaa	gac	caa	gga	aac	cgc	gat	gaa	ggc	cac	595
Cys	Val	Ile	Pro	Gly	Trp	Glu	Asp	Gln	Gly	Asn	Arg	Asp	Glu	Gly	His	
					155					160					165	
tca	gga	tgg	ttg	atg	ctc	gca	gtt	act	ggc	cca	gtt	gaa	gcc	cca	aca	643
Ser	Gly	Trp	Leu	Met	Leu	Ala	Val	Thr	Gly	Pro	Val	Glu	Ala	Pro	Thr	
				170					175					180		
gta	gtg	gtc	ctc	gac	tcg	cca	gat	gga	aga	gaa	tgg	tcc	att	aca	ggt	691
Val	Val	Val	Leu	Asp	Ser	Pro	Asp	Gly	Arg	Glu	Trp	Ser	Ile	Thr	Gly	
			185					190					195			
ccc	ctg	tct	ctc	aac	ggc	ctc	tct	gga	tta	gag	tca	gac	gaa	gtt	cta	739
Pro	Leu	Ser	Leu	Asn	Gly	Leu	Ser	Gly	Leu	Glu	Ser	Asp	Glu	Val	Leu	
		200					205					210				
gtt	gct	cct	cgc	atg	att	cgt	ctg	cgc	gat	gaa	gtg	gat	cat	gaa	atc	787
Val	Ala	Pro	Arg	Met	Ile	Arg	Leu	Arg	Asp	Glu	Val	Asp	His	Glu	Ile	
		215				220					225					
tac	gat	gtc	ctc	att	gtc	acc	att	gaa	caa	gac	ggg	att	gac	att	tcg	835
Tyr	Asp	Val	Leu	Ile	Val	Thr	Ile	Glu	Gln	Asp	Gly	Ile	Asp	Ile	Ser	
		230			235					240					245	
gga	tac	ctg	gta	ggc	cag	ctc	aac	ggc	tca	gaa	ttc	gat	gtg	aag	act	883
Gly	Tyr	Leu	Val	Gly	Gln	Leu	Asn	Gly	Ser	Glu	Phe	Asp	Val	Lys	Thr	
				250					255					260		
cca	ttt	acc	cgc	atc	gat	ttt	ggc	cat	gat	ttc	tct	cgc	ccc	cgc	aac	931
Pro	Phe	Thr	Arg	Ile	Asp	Phe	Gly	His	Asp	Phe	Ser	Arg	Pro	Arg	Asn	
			265					270					275			
acc	aac	tac	gcc	gaa	acc	acc	atc	ggc	tac	gac	ttc	gcc	cac	atc	ttt	979
Thr	Asn	Tyr	Ala	Glu	Thr	Thr	Ile	Gly	Tyr	Asp	Phe	Ala	His	Ile	Phe	
		280					285					290				
ggt	ctc	atg	aat	ggc	gta	ggt	cgt	ttg	gac	tcc	ccc	act	gag	cat	ctc	1027
Gly	Leu	Met	Asn	Gly	Val	Gly	Arg	Leu	Asp	Ser	Pro	Thr	Glu	His	Leu	
		295				300					305					
agt	tgg	aag	gaa	gaa	ggc	tgg	gca	aac	gct	att	tct	ttc	cca	cgt	att	1075
Ser	Trp	Lys	Glu	Glu	Gly	Trp	Ala	Asn	Ala	Ile	Ser	Phe	Pro	Arg	Ile	
					315					320					325	
gtc	acg	ctc	cag	gac	ggt	acg	gtc	ttc	cag	acc	cct	cca	gaa	gga	ttg	1123
Val	Thr	Leu	Gln	Asp	Gly	Thr	Val	Phe	Gln	Thr	Pro	Pro	Glu	Gly	Leu	
				330					335					340		
ctt	gat	gcc	att	cat	gaa	tcc	gag	gca	gcg	gca	ggt	tgg	acc	gga	ctg	1171
Leu	Asp	Ala	Ile	His	Glu	Ser	Glu	Ala	Ala	Ala	Gly	Trp	Thr	Gly	Leu	
			345					350					355			
tgc	gaa	atc	cca	tca	aac	agc	gca	gtt	gaa	gtg	gcg	ttg	aag	gac	caa	1219
Cys	Glu	Ile	Pro	Ser	Asn	Ser	Ala	Val	Glu	Val	Ala	Leu	Lys	Asp	Gln	

360	365	370	
gaa ggt gaa atc gct gca aca atc act cac cgc cac aat cag cta gtc			1267
Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg His Asn Gln Leu Val			
375	380	385	
ggt gat cgg tcc atg aac ccc aac cac gcg ggt gat cca cac gcg att			1315
Val Asp Arg Ser Met Asn Pro Asn His Ala Gly Asp Pro His Ala Ile			
390	395	400	405
gca cca ttg act gat gat gaa aca gat tca ctg ttc att gtc gtt gac			1363
Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu Phe Ile Val Val Asp			
410	415		420
ggc tct aca gta gaa gtt ttt gct gat ggc ggt tat gta tca atg gca			1411
Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly Tyr Val Ser Met Ala			
425	430		435
agc cgt gtg tat ttc aac aac gga cca ttc agc gaa ttt gag gtc acc			1459
Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser Glu Phe Glu Val Thr			
440	445		450
acc acc ggt gac gca agc att att cgc cag gaa agt cac ttc cct gtt			1507
Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu Ser His Phe Pro Val			
455	460		465
gat ttc agt tcg gtg tcc cta gat ata gat gat ctc act gcg ctc atg			1555
Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp Leu Thr Ala Leu Met			
470	475	480	485
cag ttc gat gaa aac gaa ccg cat gaa ggc cca gtg aga taagagttag			1604
Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro Val Arg			
490	495		
atgcgttcca gcc			1617

&lt;210&gt; 352

&lt;211&gt; 498

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 352

Met Thr Asn Val Ser Gly Tyr His Arg Pro Glu Leu His Ile Thr Ala
1 5 10 15

Glu Ser Gly Val Leu Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp
20 25 30

Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro
35 40 45

Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile
50 55 60

Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala
65 70 75 80

Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser
85 90 95

Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile  
 100 105 110  
 Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro  
 115 120 125  
 Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val  
 130 135 140  
 Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn  
 145 150 155 160  
 Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro  
 165 170 175  
 Val Glu Ala Pro Thr Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu  
 180 185 190  
 Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu  
 195 200 205  
 Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu  
 210 215 220  
 Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp  
 225 230 235 240  
 Gly Ile Asp Ile Ser Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu  
 245 250 255  
 Phe Asp Val Lys Thr Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe  
 260 265 270  
 Ser Arg Pro Arg Asn Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp  
 275 280 285  
 Phe Ala His Ile Phe Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser  
 290 295 300  
 Pro Thr Glu His Leu Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile  
 305 310 315 320  
 Ser Phe Pro Arg Ile Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr  
 325 330 335  
 Pro Pro Glu Gly Leu Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala  
 340 345 350  
 Gly Trp Thr Gly Leu Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val  
 355 360 365  
 Ala Leu Lys Asp Gln Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg  
 370 375 380  
 His Asn Gln Leu Val Val Asp Arg Ser Met Asn Pro Asn His Ala Gly  
 385 390 395 400  
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<223> RXN01369
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Met Glu Leu Leu Glu																5
ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat																163
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp																20
ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg																211
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp																35
ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc																259
Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu																50
aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt																307
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val																65
gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca																355
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala																85
gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc																403
Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala																100
cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca																451
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala																



105	110	115	
ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val 120 125 130			499
gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn 135 140 145			547
acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr 150 155 160 165			595
cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu 170 175 180			643
ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile 185 190 195			691
gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg 200 205 210			739
gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu 215 220 225			787
cag tac ccc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg aac ttc Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu Asn Phe 230 235 240 245			835
tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca aac ctt Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala Asn Leu 250 255 260			883
cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac tcc gac His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn Ser Asp 265 270 275			931
aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc ccg gag Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val Pro Glu 280 285 290			979
ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc gtg gac Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg Val Asp 295 300 305			1027
gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc aac gaa Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile Asn Glu 310 315 320 325			1075
ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc aac cac Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala Asn His 330 335 340			1123
gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc ttg gaa Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser Leu Glu 345 350 355			1171

gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca tgg gtt 1219  
 Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala Trp Val  
 360 365 370

cca gca aac gac cca acc att gcg atg cgt tct gag gac gca gaa gta 1267  
 Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala Glu Val  
 375 380 385

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 Phe Leu Ala Arg Val  
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<210> 354

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

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Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile  
 35 40 45

Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala  
 50 55 60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu  
 65 70 75 80

Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro  
 85 90 95

Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly  
 100 105 110

Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys  
 115 120 125

Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe  
 130 135 140

Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu  
 145 150 155 160

Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu  
 165 170 175

Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys  
 180 185 190

Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu  
 195 200 205

Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile  
 210 215 220

Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala  
 225 230 235 240  
 Leu Leu Leu Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu  
 245 250 255  
 Asp Ala Ala Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile  
 260 265 270  
 Met Ala Asn Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr  
 275 280 285  
 Val Asp Val Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu  
 290 295 300  
 Asn Ala Arg Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro  
 305 310 315 320  
 Val Pro Ile Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu  
 325 330 335  
 Ala Glu Ala Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly  
 340 345 350  
 Thr Val Ser Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly  
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 370 375 380  
 Glu Asp Ala Glu Val Phe Leu Ala Arg Val  
 385 390

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 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(501)  
 <223> FRXA01369

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 1 5 10 15  
 aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca 96  
 Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala  
 20 25 30  
 aac ctt cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac 144  
 Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn  
 35 40 45  
 tcc gac aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc 192  
 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val  
 50 55 60

ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc 240  
 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg  
 65 70 75 80  
 gtg gac gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc 288  
 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile  
 85 90 95  
 aac gaa ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc 336  
 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala  
 100 105 110  
 aac cac gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc 384  
 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser  
 115 120 125  
 ttg gaa gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca 432  
 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala  
 130 135 140  
 tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca 480  
 Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala  
 145 150 155 160  
 gaa gta ttc ctc gct agg gtt tagatctttt tagattaaaa tca 524  
 Glu Val Phe Leu Ala Arg Val  
 165

<210> 356  
 <211> 167  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 356  
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 Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn  
 35 40 45  
 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val  
 50 55 60  
 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg  
 65 70 75 80  
 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile  
 85 90 95  
 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala  
 100 105 110  
 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser  
 115 120 125  
 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala

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130              135              140
Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
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Glu Val Phe Leu Ala Arg Val
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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(808)
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gtcagccacg acctattcca ttgaagaaaa ggacttgtaa atg gag cta ttg gaa 115
Met Glu Leu Leu Glu
1 5

ggc tca ctg cgc acc tac cca tgg ggt tca aga aca ctg atc gct gat 163
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp
10 15 20

ctc aaa ggc gaa gaa tca cca tcg tct cgc cca gag gcc gaa gtc tgg 211
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp
25 30 35

ttc ggt gcc cac cca gga tca cca tca acc atc ggt gga aac gca ctc 259
Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu
40 45 50

aac gaa gtc atc gca gcg aac ccc gaa gaa gca ttg ggc acg cgt gtt 307
Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val
55 60 65

gcc gaa gcg ttt gaa aat gag ctt cca ttc ctc ctc aaa atc ctc gca 355
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala
70 75 80 85

gcg gga gca ccc cta tca ctg cag gcc cac cca tcg ctg gaa cag gcc 403
Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala
90 95 100

cgt gaa gga ttc gcc cgc gaa aac tca gca gga att gac ctc ggc gca 451
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala
105 110 115

ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt 499
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val
120 125 130

gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac 547
Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn
135 140 145

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acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac 595  
 Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr  
 150 155 160 165

cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg 643  
 Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu  
 170 175 180

ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc 691  
 Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile  
 185 190 195

gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt 739  
 Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg  
 200 205 210

gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa 787  
 Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu  
 215 220 225

cag tac ccc ggc gat gtc ggc 808  
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<210> 358

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

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Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro  
 20 25 30

Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile  
 35 40 45

Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala  
 50 55 60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu  
 65 70 75 80

Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro  
 85 90 95

Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly  
 100 105 110

Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys  
 115 120 125

Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe  
 130 135 140

Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu  
 145 150 155 160

Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu  
                   165                                  170                  175

Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys  
                   180                                  185                  190

Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu  
                   195                                  200                  205

Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile  
                   210                                  215                  220

Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly  
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&lt;210&gt; 359

&lt;211&gt; 1775

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1752)

&lt;223&gt; RXA02611

&lt;400&gt; 359

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aag att gag gcc ggc cag ggt tgc gat gag ttg tat aac gac ttt gag	96
Lys Ile Glu Ala Gly Gln Gly Ser Asp Glu Leu Tyr Asn Asp Phe Glu	
20                                  25                                  30	
cac ggg gct cag ctg ttt gag cgt gct gcg gag aat ttg tct aaa gag	144
His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu	
35                                  40                                  45	
gat agg act gcg ctt ttc gac gtc gcc tcc tct ctg cgg cgc ggc ggc	192
Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly	
50                                  55                                  60	
gat gta cgc gca cgt ctc gcc cca gcg ctc acc gcg agt gtc act cat	240
Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His	
65                                  70                                  75                                  80	
ctt tta gaa ctt aac ccg ttg cgt gag ttg gtc acg atg ggt gaa aac	288
Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn	
85                                  90                                  95	
ctg cag gtt cgt gtc gag cgt cgt gcc gct ttg gtc aac tct tgg tat	336
Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr	
100                                  105                                  110	
gag ctt ttc cct cgt tcc aca ggt ggt tgg gat gag tcc ggc acc ccc	384
Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro	
115                                  120                                  125	
ggt cat ggc act ttc gct acc act gct cag gcg ttg gag cgt gtc gcg	432

Val	His	Gly	Thr	Phe	Ala	Thr	Thr	Ala	Gln	Ala	Leu	Glu	Arg	Val	Ala		
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Lys	Met	Gly	Phe	Asp	Thr	Val	Tyr	Phe	Pro	Pro	Ile	His	Pro	Ile	Gly		
145					150				155						160		
gag	gtc	aac	cgc	aag	ggc	cgc	aat	aat	acg	ctg	acc	ccg	gaa	cct	cat	528	
Glu	Val	Asn	Arg	Lys	Gly	Arg	Asn	Asn	Thr	Leu	Thr	Pro	Glu	Pro	His		
				165					170					175			
gat	gtg	ggg	tgc	ccg	tgg	gct	att	ggg	tct	aaa	gat	ggg	ggg	cat	gat	576	
Asp	Val	Gly	Ser	Pro	Trp	Ala	Ile	Gly	Ser	Lys	Asp	Gly	Gly	His	Asp		
			180					185					190				
gca	acg	cat	ccg	cgg	ttg	ggc	acc	att	gaa	gat	ttc	cag	gcg	ttg	ttg	624	
Ala	Thr	His	Pro	Arg	Leu	Gly	Thr	Ile	Glu	Asp	Phe	Gln	Ala	Leu	Leu		
		195					200					205					
gct	cgc	gca	cgg	gaa	ctc	aat	ttg	gaa	gtt	gca	ctc	gat	cta	gct	ctg	672	
Ala	Arg	Ala	Arg	Glu	Leu	Asn	Leu	Glu	Val	Ala	Leu	Asp	Leu	Ala	Leu		
	210					215					220						
cag	gct	gcc	cct	gat	cat	cca	tgg	gcg	cag	gaa	cac	cgc	gag	ttt	ttc	720	
Gln	Ala	Ala	Pro	Asp	His	Pro	Trp	Ala	Gln	Glu	His	Arg	Glu	Phe	Phe		
225					230					235					240		
acg	gtg	ttg	gct	gat	ggc	acc	att	gcg	tat	gca	gaa	aac	cca	ccg	aag	768	
Thr	Val	Leu	Ala	Asp	Gly	Thr	Ile	Ala	Tyr	Ala	Glu	Asn	Pro	Pro	Lys		
				245					250					255			
aag	tac	cag	gat	att	tat	ccc	atc	aac	ttt	gat	aat	gat	gct	ccg	aag	816	
Lys	Tyr	Gln	Asp	Ile	Tyr	Pro	Ile	Asn	Phe	Asp	Asn	Asp	Ala	Pro	Lys		
			260					265					270				
atc	tac	gaa	gag	gtc	tat	cgt	gtg	gtg	aag	ttc	tgg	gtg	gat	ttg	ggg	864	
Ile	Tyr	Glu	Glu	Val	Tyr	Arg	Val	Val	Lys	Phe	Trp	Val	Asp	Leu	Gly		
		275					280					285					
gtg	acc	aca	ttc	cgc	gtg	gat	aac	ccg	cac	act	aag	ccc	gct	aat	ttc	912	
Val	Thr	Thr	Phe	Arg	Val	Asp	Asn	Pro	His	Thr	Lys	Pro	Ala	Asn	Phe		
	290					295					300						
tgg	cag	tgg	ctt	att	tct	gcc	atc	cat	aaa	tca	aac	cct	gag	gtc	att	960	
Trp	Gln	Trp	Leu	Ile	Ser	Ala	Ile	His	Lys	Ser	Asn	Pro	Glu	Val	Ile		
305					310					315					320		
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Phe	Leu	Ala	Glu	Ala	Ser	Thr	Arg	Pro	Ala	Arg	Leu	Tyr	Phe	Leu	Ser		
				325					330					335			
aag	att	ggg	ttc	tcc	cag	tct	tac	acc	tac	ttc	acc	tgg	aag	gtc	acc	1056	
Lys	Ile	Gly	Phe	Ser	Gln	Ser	Tyr	Thr	Tyr	Phe	Thr	Trp	Lys	Val	Thr		
			340					345					350				
aac	gag	gag	ctc	acc	gag	ttc	gct	act	gag	atc	gcc	ccc	atg	gcg	gat	1104	
Asn	Glu	Glu	Leu	Thr	Glu	Phe	Ala	Thr	Glu	Ile	Ala	Pro	Met	Ala	Asp		
		355					360				365						
att	tct	cgt	ccg	aac	ctg	ttt	gtg	aac	act	ccc	gac	att	ttg	cat	gcg	1152	
Ile	Ser	Arg	Pro	Asn	Leu	Phe	Val	Asn	Thr	Pro	Asp	Ile	Leu	His	Ala		



370	375	380	
tct ctg cag cat ggt gga cgc gcc atg ttc gct atc cgc gcc gca ttg			1200
Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu			
385	390	395	400
gcc gcc acg atg tct cct gtg tgg ggc gta tat tcc gga tat gag ctc			1248
Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu			
	405	410	415
ttt gag cac gag gcc gtc aag cct ggt tgc gaa gag tac ttg gat tct			1296
Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser			
	420	425	430
gag aag tac gag ctg cgt ccc cgc gat ttc gag ggt gct ctg gaa cgt			1344
Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg			
	435	440	445
ggc gat tct ctc gag gat tac atc gct ctg ctc aac cag atc cgt cgc			1392
Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg			
	450	455	460
gcg aac cct gcc ttg cag caa cta cgc aac atc cac ttc cac gaa gcg			1440
Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala			
	465	470	475
gac aat gat cag atc atc gcc tac tcc aag gtt gat gct ttg acc gga			1488
Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly			
	485	490	495
aat acc gtg ttg att gtg gtc aac ttg gat cca cgt agt gct cgt gag			1536
Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu			
	500	505	510
gct act gtt cgc ctt gat ctt gga gcg ctt ggc tta gaa gcg ggt gca			1584
Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala			
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cag ttt gag gtg cgc gat gcg atc acc ggc tcc cgt tac ctg tgg tca			1632
Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser			
	530	535	540
gag acg aac ttt gtc cgc ctc gag ccc cta cgc gat gtc gcc cac atc			1680
Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile			
	545	550	555
ttt gtt ctt cct gaa ctt cca gcg tct cgc cgt gag cgt ctc gcg tgg			1728
Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp			
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cgc gaa atc aag acc tac cgc gcg taatttccca tctctgtacc ttc			1775
Arg Glu Ile Lys Thr Tyr Arg Ala			
	580		

&lt;210&gt; 360

&lt;211&gt; 584

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 360

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 His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu  
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 Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro  
 115 120 125  
 Val His Gly Thr Phe Ala Thr Thr Ala Gln Ala Leu Glu Arg Val Ala  
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 Lys Met Gly Phe Asp Thr Val Tyr Phe Pro Pro Ile His Pro Ile Gly  
 145 150 155 160  
 Glu Val Asn Arg Lys Gly Arg Asn Asn Thr Leu Thr Pro Glu Pro His  
 165 170 175  
 Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp  
 180 185 190  
 Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu  
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 Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe  
 225 230 235 240  
 Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys  
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 Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys  
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 Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile  
 305 310 315 320  
 Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser

325										330					335				
Lys	Ile	Gly	Phe	Ser	Gln	Ser	Tyr	Thr	Tyr	Phe	Thr	Trp	Lys	Val	Thr				
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Ser	Leu	Gln	His	Gly	Gly	Arg	Ala	Met	Phe	Ala	Ile	Arg	Ala	Ala	Leu				
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Glu	Lys	Tyr	Glu	Leu	Arg	Pro	Arg	Asp	Phe	Glu	Gly	Ala	Leu	Glu	Arg				
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Ala	Thr	Val	Arg	Leu	Asp	Leu	Gly	Ala	Leu	Gly	Leu	Glu	Ala	Gly	Ala				
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Gln	Phe	Glu	Val	Arg	Asp	Ala	Ile	Thr	Gly	Ser	Arg	Tyr	Leu	Trp	Ser				
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Glu	Thr	Asn	Phe	Val	Arg	Leu	Glu	Pro	Leu	Arg	Asp	Val	Ala	His	Ile				
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                                   Met Thr Val Asp Pro
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gcg agc cac atc acc atc cct gaa gca gat ctg gcc cgc ctg cgc cac 163
Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu Ala Arg Leu Arg His
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Cys Asn His His Asp Pro His Gly Phe Tyr Gly Trp His Glu Thr Glu
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Leu Leu Ile Asp Asp Thr Ser His Val Met Thr Pro Ile Gly Asp Asp
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Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg Ala Asp Tyr Arg Leu
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Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val Lys Ala Asp Pro Tyr
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Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly Ala Asn Ile Lys Thr
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Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr Ala Phe Thr Val Trp
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gct cca aac gca att ggc tgc gca gtg gtc ggt ggc ttc aac ggt tgg 595
Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly Gly Phe Asn Gly Trp
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Asn Ala Ser Gln His Pro Met Arg Ser Met Gly Gly Ser Gly Leu Trp
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Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu Val Tyr Lys Phe Ala
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gtc caa acc agg gaa ggc caa cgt cgt gat aag gcc gat ccg atg gct 739
Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys Ala Asp Pro Met Ala
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cgt cgc gca gaa ctg gcg ccg gca acc gga tct att gtc gct tcc tct 787
Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser Ile Val Ala Ser Ser

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Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu Val His Leu Gly Ser			
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Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala Thr Glu Leu Val Asp			
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tac gtc gca gat ctt ggc tac acc cac gtg gaa ttc ctc cct gtc gca 979			
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Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala Arg Phe Asp Gly Glu			
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gcc ctc tat gaa cac cct gac tgg agg cgc ggc gaa caa aag gat tgg 1219			
Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly Glu Gln Lys Asp Trp			
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Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu Val Arg Asn Phe Leu			
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Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe Ser Lys Asn Pro Val	
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Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met Trp Ser His Pro Gly	
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Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly Gln Arg Glu Glu Trp	
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Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp Phe Thr Gly Glu Gly	
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Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn Asn Ile Leu Ala Phe	
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act cgt ttc ggc agc gac ggc tcc cag atg ctg tgt gta ttc aac ctg	2083
Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu Cys Val Phe Asn Leu	
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Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly Val Ala Ala Gly Gly	
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<212> PRT

<213> Corynebacterium glutamicum

<400> 362

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Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr  
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Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg  
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Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val  
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Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile  
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Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly  
 115 120 125

Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr  
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Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly  
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Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly  
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Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu  
 180 185 190

Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys  
 195 200 205

Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser  
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Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg  
 225 230 235 240

Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu

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 580 585  
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 Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe  
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 Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly  
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Gly Thr Pro Met Leu Ser His Gly Asp Glu Met Ala Arg Thr Gln Asn	
325 330 335	
ggc aac aac aac gtc tac tgc caa gac aat gaa ctg gcg tgg gtg aat	1056
Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu Leu Ala Trp Val Asn	
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tgg gat cag gct gaa gaa aac gct gac ttg gtg agc ttc acc agg cgt	1104
Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val Ser Phe Thr Arg Arg	
355 360 365	
ttg ctg cgt atc cga gca aac cac cca gta ttt agg cgc agg cag ttc	1152
Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Arg Gln Phe	
370 375 380	
ctt gcc ggt ggc cct ttg ggc gcc gat gtt cgt gac cgc gat atc gca	1200
Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala	
385 390 395 400	
tgg ctg gta cca aat gga acc ttg atg act caa gat gac tgg gac ttc	1248
Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe	
405 410 415	
gct ttc ggt aaa tca ctg cag gtg ttc ttc aac ggc gat gcc atc gaa	1296
Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu	
420 425 430	
gag cct gat tat cga gga cag aaa atc cac gat gac tcc ttc atc ttg	1344
Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu	
435 440 445	
atg ttc aac gct cac ttc gaa cct atc gat ttc aat ctc cct cct gag	1392
Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu	
450 455 460	
cat ttc ggt atg aag tgg aag ctt ttg gtc gat acc acc gaa gcg gtg	1440
His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val	
465 470 475 480	
ggc cac ccg ctg gag gat ctc acc atc gaa gct ggc gga acc atc act	1488
Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr	
485 490 495	
gtt cct gcc cgt tcc acg atg ctg ctg cgc cag gtg gag gct ccg gac	1536
Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp	
500 505 510	
tac acc aag ctt gag gaa aag atc gct gct gaa aag cgt gag caa gaa	1584
Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu	
515 520 525	
ctt gcg gca gag aag gaa gct gct gag aag cgc gaa ttg gaa ctg gcg	1632
Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala	
530 535 540	
gca gca aag gaa gct gaa gat gct gct gag gct ctc cac ctt gcg gca	1680
Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala	
545 550 555 560	

gaa cgt gct tcg act cag gaa gct gaa ttg gcc cat caa cac ggt gct 1728  
 Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala  
 565 570 575  
 gat gcg att gcc gat gag gta gcg gaa gaa cca caa gag ctg cca caa 1776  
 Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln  
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 gat gaa gta gcg gca gag gtc gag act gag ccc gac acc gag cct gac 1824  
 Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp  
 595 600 605  
 act gaa tct gac tcc gag cag gct gag gta gct tca gag gag cct gaa 1872  
 Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu  
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 <213> Corynebacterium glutamicum

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 Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly  
 35 40 45  
 Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala  
 50 55 60  
 Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly  
 65 70 75 80  
 Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala  
 85 90 95  
 Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr  
 100 105 110  
 Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu  
 115 120 125  
 Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly  
 130 135 140  
 Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val  
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 Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Gln Asp Pro Val Val  
 165 170 175  
 Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly

180					185					190					
Tyr	Gln	Val	Gly	Asn	Phe	Pro	Pro	Leu	Trp	Thr	Glu	Trp	Asn	Gly	Lys
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Tyr	Arg	Asp	Thr	Val	Arg	Asp	Phe	Trp	Arg	Gly	Glu	Pro	Ala	Thr	Leu
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Gly	Glu	Phe	Ala	Ser	Arg	Leu	Thr	Gly	Ser	Ser	Asp	Leu	Tyr	Ala	Asn
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Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe	Val	Thr	Ala	His	Asp
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Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn	Glu	Lys	His	Asn	Met
			260					265					270		
Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser	His	Asn	Arg	Ser	Trp
		275					280					285			
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	290					295					300				
Arg	Ala	Gln	Gln	Arg	Arg	Asn	Phe	Leu	Thr	Thr	Leu	Leu	Leu	Ser	Gln
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Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met	Ala	Arg	Thr	Gln	Asn
				325					330					335	
Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu	Leu	Ala	Trp	Val	Asn
			340					345					350		
Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val	Ser	Phe	Thr	Arg	Arg
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Leu	Leu	Arg	Ile	Arg	Ala	Asn	His	Pro	Val	Phe	Arg	Arg	Arg	Gln	Phe
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Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg	Asp	Arg	Asp	Ile	Ala
385					390					395					400
Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln	Asp	Asp	Trp	Asp	Phe
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			420					425					430		
Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp	Asp	Ser	Phe	Ile	Leu
		435					440					445			
Met	Phe	Asn	Ala	His	Phe	Glu	Pro	Ile	Asp	Phe	Asn	Leu	Pro	Pro	Glu
	450					455					460				
His	Phe	Gly	Met	Lys	Trp	Lys	Leu	Leu	Val	Asp	Thr	Thr	Glu	Ala	Val
465					470					475					480
Gly	His	Pro	Leu	Glu	Asp	Leu	Thr	Ile	Glu	Ala	Gly	Gly	Thr	Ile	Thr
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Val	Pro	Ala	Arg	Ser	Thr	Met	Leu	Leu	Arg	Gln	Val	Glu	Ala	Pro	Asp
			500					505					510		

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Met	His	Val	Asp	Gly	Phe	Arg	Phe	Asp	Leu	Ala	Ser	Thr	Leu	Ala	Arg	
1				5				10				15				
gaa	ttt	gat	gat	gtt	gac	cgc	ctg	gca	acc	ttc	ttc	gac	ctg	gtc	caa	96
Glu	Phe	Asp	Asp	Val	Asp	Arg	Leu	Ala	Thr	Phe	Phe	Asp	Leu	Val	Gln	
20				25				30								
caa	gac	ccg	gtg	gtc	tcc	cag	gtc	aag	ctc	att	gct	gag	ccg	tgg	gat	144
Gln	Asp	Pro	Val	Val	Ser	Gln	Val	Lys	Leu	Ile	Ala	Glu	Pro	Trp	Asp	
35				40				45								
gtt	ggc	gaa	ggc	gga	tac	caa	gtg	ggc	aac	ttc	cca	cca	ctg	tgg	act	192
Val	Gly	Glu	Gly	Gly	Tyr	Gln	Val	Gly	Asn	Phe	Pro	Pro	Leu	Trp	Thr	
50				55				60								
gag	tgg	aac	ggc	aaa	tac	cgc	gac	act	gtc	cgt	gat	ttc	tgg	cgt	ggc	240
Glu	Trp	Asn	Gly	Lys	Tyr	Arg	Asp	Thr	Val	Arg	Asp	Phe	Trp	Arg	Gly	
65				70				75				80				
gag	cca	gca	acc	ttg	ggc	gaa	ttc	gct	tcc	cga	cta	act	ggc	tcc	tct	288
Glu	Pro	Ala	Thr	Leu	Gly	Glu	Phe	Ala	Ser	Arg	Leu	Thr	Gly	Ser	Ser	
85				90				95								

gat	ttg	tat	gca	aac	aac	ggc	cgt	cgc	ccc	act	gca	tcg	atc	aac	ttt	336
Asp	Leu	Tyr	Ala	Asn	Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe	
			100					105					110			
gtg	act	gct	cac	gac	ggc	ttc	acc	ctc	aat	gac	ttg	gtc	agt	tac	aac	384
Val	Thr	Ala	His	Asp	Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn	
		115					120					125				
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Glu	Lys	His	Asn	Met	Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser	
	130					135					140					
cac	aac	cgt	tcc	tgg	aac	tgt	ggc	gtc	gaa	gga	cca	act	gac	gat	cct	480
His	Asn	Arg	Ser	Trp	Asn	Cys	Gly	Val	Glu	Gly	Pro	Thr	Asp	Asp	Pro	
145					150					155					160	
gag	att	atg	cag	ctg	cgt	gct	cag	caa	cga	cgc	aac	ttc	ctc	acc	acc	528
Glu	Ile	Met	Gln	Leu	Arg	Ala	Gln	Gln	Arg	Arg	Asn	Phe	Leu	Thr	Thr	
			165						170					175		
ttg	ttg	ctg	tcc	cag	ggc	acc	cct	atg	ttg	tcc	cac	ggg	gat	gaa	atg	576
Leu	Leu	Leu	Ser	Gln	Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met	
			180				185						190			
gcc	cgt	acc	caa	aac	ggc	aac	aac	aac	gtc	tac	tgc	caa	gac	aat	gaa	624
Ala	Arg	Thr	Gln	Asn	Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu	
		195					200					205				
ctg	gcg	tgg	gtg	aat	tgg	gat	cag	gct	gaa	gaa	aac	gct	gac	ttg	gtg	672
Leu	Ala	Trp	Val	Asn	Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val	
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agc	ttc	acc	agg	cgt	ttg	ctg	cgt	atc	cga	gca	aac	cac	cca	gta	ttt	720
Ser	Phe	Thr	Arg	Arg	Leu	Leu	Arg	Ile	Arg	Ala	Asn	His	Pro	Val	Phe	
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Arg	Arg	Arg	Gln	Phe	Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg	
			245					250						255		
gac	cgc	gat	atc	gca	tgg	ctg	gta	cca	aat	gga	acc	ttg	atg	act	caa	816
Asp	Arg	Asp	Ile	Ala	Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln	
			260				265						270			
gat	gac	tgg	gac	ttc	gct	ttc	ggg	aaa	tca	ctg	cag	gtg	ttc	ttc	aac	864
Asp	Asp	Trp	Asp	Phe	Ala	Phe	Gly	Lys	Ser	Leu	Gln	Val	Phe	Phe	Asn	
		275					280					285				
ggc	gat	gcc	atc	gaa	gag	cct	gat	tat	cga	gga	cag	aaa	atc	cac	gat	912
Gly	Asp	Ala	Ile	Glu	Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp	
	290					295					300					
gac	tcc	ttc	atc	ttg	atg	ttc	aac	gct	cac	ttc	gaa	cct	atc	gat	ttc	960
Asp	Ser	Phe	Ile	Leu	Met	Phe	Asn	Ala	His	Phe	Glu	Pro	Ile	Asp	Phe	
305					310					315					320	
aat	ctc	cct	cct	gag	cat	ttc	ggg	atg	aag	tgg	aag	ctt	ttg	gtc	gat	1008
Asn	Leu	Pro	Pro	Glu	His	Phe	Gly	Met	Lys	Trp	Lys	Leu	Leu	Val	Asp	
				325				330						335		
acc	acc	gaa	gcg	gtg	ggc	cac	ccg	ctg	gag	gat	ctc	acc	atc	gaa	gct	1056

Thr Thr Glu Ala Val Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala  
 340 345 350  
 ggc gga acc atc act gtt cct gcc cgt tcc acg atg ctg ctg cgc cag 1104  
 Gly Gly Thr Ile Thr Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln  
 355 360 365  
 gtg gag gct ccg gac tac acc aag ctt gag gaa aag atc gct gct gaa 1152  
 Val Glu Ala Pro Asp Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu  
 370 375 380  
 aag cgt gag caa gaa ctt gcg gca gag aag gaa gct gct gag aag cgc 1200  
 Lys Arg Glu Gln Glu Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg  
 385 390 395 400  
 gaa ttg gaa ctg gcg gca gca aag gaa gct gaa gat gct gct gag gct 1248  
 Glu Leu Glu Leu Ala Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala  
 405 410 415  
 ctc cac ctt gcg gca gaa cgt gct tcc act cag gaa gct gaa ttg gcc 1296  
 Leu His Leu Ala Ala Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala  
 420 425 430  
 cat caa cac ggt gct gat gcg att gcc gat gag gta gcg gaa gaa cca 1344  
 His Gln His Gly Ala Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro  
 435 440 445  
 caa gag ctg cca caa gat gaa gta gcg gca gag gtc gag act gag ccc 1392  
 Gln Glu Leu Pro Gln Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro  
 450 455 460  
 gac acc gag cct gac act gaa tct gac tcc gag cag gct gag gta gct 1440  
 Asp Thr Glu Pro Asp Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala  
 465 470 475 480  
 tca gag gag cct gaa gcg gac gaa gaa gag aag tagtacaccg aaagtggcgt 1493  
 Ser Glu Glu Pro Glu Ala Asp Glu Glu Glu Lys  
 485 490  
 cgc 1496

&lt;210&gt; 366

&lt;211&gt; 491

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 366

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Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln  
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Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp  
 35 40 45

Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr  
 50 55 60

Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly



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Glu	Pro	Ala	Thr	Leu	Gly	Glu	Phe	Ala	Ser	Arg	Leu	Thr	Gly	Ser	Ser
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Asp	Leu	Tyr	Ala	Asn	Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe
			100					105					110		
Val	Thr	Ala	His	Asp	Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn
		115					120					125			
Glu	Lys	His	Asn	Met	Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser
	130					135					140				
His	Asn	Arg	Ser	Trp	Asn	Cys	Gly	Val	Glu	Gly	Pro	Thr	Asp	Asp	Pro
145					150					155					160
Glu	Ile	Met	Gln	Leu	Arg	Ala	Gln	Gln	Arg	Arg	Asn	Phe	Leu	Thr	Thr
				165					170					175	
Leu	Leu	Leu	Ser	Gln	Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met
			180					185					190		
Ala	Arg	Thr	Gln	Asn	Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu
		195					200					205			
Leu	Ala	Trp	Val	Asn	Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val
	210					215					220				
Ser	Phe	Thr	Arg	Arg	Leu	Leu	Arg	Ile	Arg	Ala	Asn	His	Pro	Val	Phe
225					230				235						240
Arg	Arg	Arg	Gln	Phe	Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg
				245					250					255	
Asp	Arg	Asp	Ile	Ala	Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln
			260					265					270		
Asp	Asp	Trp	Asp	Phe	Ala	Phe	Gly	Lys	Ser	Leu	Gln	Val	Phe	Phe	Asn
		275					280					285			
Gly	Asp	Ala	Ile	Glu	Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp
	290					295					300				
Asp	Ser	Phe	Ile	Leu	Met	Phe	Asn	Ala	His	Phe	Glu	Pro	Ile	Asp	Phe
305					310					315					320
Asn	Leu	Pro	Pro	Glu	His	Phe	Gly	Met	Lys	Trp	Lys	Leu	Leu	Val	Asp
				325					330					335	
Thr	Thr	Glu	Ala	Val	Gly	His	Pro	Leu	Glu	Asp	Leu	Thr	Ile	Glu	Ala
			340					345					350		
Gly	Gly	Thr	Ile	Thr	Val	Pro	Ala	Arg	Ser	Thr	Met	Leu	Leu	Arg	Gln
		355					360					365			
Val	Glu	Ala	Pro	Asp	Tyr	Thr	Lys	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Glu
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Lys	Arg	Glu	Gln	Glu	Leu	Ala	Ala	Glu	Lys	Glu	Ala	Ala	Glu	Lys	Arg
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Met Thr Ser Thr Ile															115
1 5															
gag cac tcg tac caa gtt tgg cct gga cat gct tat cct ctg ggt tca															163
Glu His Ser Tyr Gln Val Trp Pro Gly His Ala Tyr Pro Leu Gly Ser															
10 15 20															
acc tat gac ggt gct gga acg aac ttc gca ctc ttc tcc gac gtt gca															211
Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu Phe Ser Asp Val Ala															
25 30 35															
gag cgt gtt gag ctg tgt cta tta gat gca gat aac aac gag act cga															259
Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp Asn Asn Glu Thr Arg															
40 45 50															
att cca ctc gaa gag cgc gat gcc cac att tgg cat tgc tac ctt cct															307
Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp His Cys Tyr Leu Pro															
55 60 65															
ggc gtt caa cct gga cag cgc tac gga ttc cga gtt cat ggc ccg tgg															355
Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg Val His Gly Pro Trp															
70 75 80 85															
aac cca gat gag ggt aag cgg tgc gac gcg aac aaa ctt cta gtt gat															403
Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn Lys Leu Leu Val Asp															
90 95 100															

ccc tat gct cgt gct ttc gat gga gat ttt gat gga cat ccg tca cta 451  
 Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp Gly His Pro Ser Leu  
                   105                  110                  115

ttt tct tac gac atc acc aat cca aat gac ccc aac ggt cgc aat acc 499  
 Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro Asn Gly Arg Asn Thr  
                   120                  125                  130

gaa gac agc att gat cac aca atg aag tct gtc gtg gtg aac cca ttc 547  
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<210> 368

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

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                   20                  25                  30

Phe Ser Asp Val Ala Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp  
                   35                  40                  45

Asn Asn Glu Thr Arg Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp  
                   50                  55                  60

His Cys Tyr Leu Pro Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg  
                   65                  70                  75                  80

Val His Gly Pro Trp Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn  
                   85                  90                  95

Lys Leu Leu Val Asp Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp  
                   100                  105                  110

Gly His Pro Ser Leu Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro  
                   115                  120                  125

Asn Gly Arg Asn Thr Glu Asp Ser Ile Asp His Thr Met Lys Ser Val  
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Val Val Asn Pro Phe  
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<210> 369

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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                               Val Gln Leu Asn Asp
                               1 5
act cac cca gtg ttg gct atc cct gag ctt atg cgt ctg ctc atg gac 163
Thr His Pro Val Leu Ala Ile Pro Glu Leu Met Arg Leu Leu Met Asp
                               10 15 20
gag cat gac atg ggc tgg gaa gaa tcc tgg gca atc gtg ttc aag acc 211
Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala Ile Val Phe Lys Thr
                               25 30 35
ttc gca tac acc aac cac acc gtg ctc acc gaa gct ctt gag cag tgg 259
Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu Ala Leu Glu Gln Trp
                               40 45 50
gat cag cag atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc 307
Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile
                               55 60 65
aca gag atc gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg 355
Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu
                               70 75 80 85
gat gaa gag acc atc gac cgc atg gct cca atc cag cac ggc act gtt 403
Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile Gln His Gly Thr Val
                               90 95 100
cat atg gca tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg 451
His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val
                               105 110 115
gca gcg ctg cac acc gag atc atc aag gcc gag acc ttg gct gac tgg 499
Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp
                               120 125 130
tac gca ctg tgg cca gag aag ttc aac aac aag act aac ggt gtt acc 547
Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr
                               135 140 145
cca cgc cgt tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc 595
Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu
                               150 155 160 165
act cga ctt tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg 643
Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu
                               170 175 180
aag aag ctg cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc 691
Lys Lys Leu Arg Ser Tyr Ala Asp Lys Ser Val Leu Glu Glu Leu
                               185 190 195
cgc gct atc aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc 739
Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu
                               200 205 210
gag cgc cag ggc att gag att gat cca gaa tcc atc ttt gac gtg cag 787
Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln
                               215 220 225

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att aag cgc ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr 230 235 240 245	835
gta cta gac ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile 250 255 260	883
cca gca cgc act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val 265 270 275	931
cgc gcc aag gcg att atc aag ctc atc aac tct att gct gac ttg gta Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val 280 285 290	979
aac aac gat cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu 295 300 305	1027
aac tac aac gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val 310 315 320 325	1075
tcc gaa cag att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn 330 335 340	1123
atg aag ttc atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly 345 350 355	1171
gcc aac gta gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile 360 365 370	1219
ttc ggt gct cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu 375 380 385	1267
cca tat gag ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp 390 395 400 405	1315
gcc ctg gat aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr 410 415 420	1363
gac ctc aag cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp 425 430 435	1411
acc tac tac gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp 440 445 450	1459
cgt atg gcc gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met 455 460 465	1507

gcc tgg atc aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc 1555  
 Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr  
 470 475 480 485

atc cgc gat tat gcc acc gag atc tgg aag ctc gag cca act cct gct 1603  
 Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala  
 490 495 500

gtt aag aag taggttttaa cctccgcttc taa 1635  
 Val Lys Lys

<210> 370

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

Val Gln Leu Asn Asp Thr His Pro Val Leu Ala Ile Pro Glu Leu Met  
 1 5 10 15

Arg Leu Leu Met Asp Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala  
 20 25 30

Ile Val Phe Lys Thr Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu  
 35 40 45

Ala Leu Glu Gln Trp Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg  
 50 55 60

Val Trp Glu Ile Ile Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg  
 65 70 75 80

Ala Ala Asp Gly Leu Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile  
 85 90 95

Gln His Gly Thr Val His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr  
 100 105 110

Ser Ile Asn Gly Val Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu  
 115 120 125

Thr Leu Ala Asp Trp Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys  
 130 135 140

Thr Asn Gly Val Thr Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly  
 145 150 155 160

Leu Ser Asp Leu Leu Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr  
 165 170 175

Asp Leu Asp Glu Leu Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser  
 180 185 190

Val Leu Glu Glu Leu Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe  
 195 200 205

Ala Glu Trp Ile Leu Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser  
 210 215 220

Ile Phe Asp Val Gln Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu  
 225 230 235 240  
 Met Asn Ala Leu Tyr Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp  
 245 250 255  
 Gly Leu Thr Asp Ile Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala  
 260 265 270  
 Ala Pro Gly Tyr Val Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser  
 275 280 285  
 Ile Ala Asp Leu Val Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys  
 290 295 300  
 Val Val Phe Val Glu Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu  
 305 310 315 320  
 Pro Ala Ser Asp Val Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala  
 325 330 335  
 Ser Gly Thr Ser Asn Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu  
 340 345 350  
 Gly Thr Met Asp Gly Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu  
 355 360 365  
 Glu Asn Ala Tyr Ile Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu  
 370 375 380  
 Arg Glu Ser Tyr Glu Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu  
 385 390 395 400  
 Lys Arg Ala Leu Asp Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn  
 405 410 415  
 Ser Gly Leu Phe Tyr Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly  
 420 425 430  
 Lys Asp Ala Ser Asp Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr  
 435 440 445  
 Arg Glu Thr Arg Asp Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu  
 450 455 460  
 Gly Trp Ala Arg Met Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe  
 465 470 475 480  
 Ser Ser Asp Arg Thr Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu  
 485 490 495  
 Glu Pro Thr Pro Ala Val Lys Lys  
 500

&lt;210&gt; 371

&lt;211&gt; 1367

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

<221> CDS  
 <222> (1)..(1344)  
 <223> FRXA01550

<400> 371

atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc aca gag atc	48
Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile Thr Glu Ile	
1 5 10 15	
gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg gat gaa gag	96
Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu	
20 25 30	
acc atc gac cgc atg gct cca atc cag cgc ggc act gtt cat atg gca	144
Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala	
35 40 45	
tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg gca gcg ctg	192
Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu	
50 55 60	
cac acc gag atc atc aag gcc gag acc ttg gct gac tgg tac gca ctg	240
His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu	
65 70 75 80	
tgg cca gag aag ttc aac aac aag act aac ggt gtt acc cca cgc cgt	288
Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg	
85 90 95	
tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc act cga ctt	336
Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu	
100 105 110	
tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg aag aag ctg	384
Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu	
115 120 125	
cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc cgc gct atc	432
Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile	
130 135 140	
aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc gag cgc cag	480
Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln	
145 150 155 160	
ggc att gag att gat cca gaa tcc atc ttt gac gtg cag att aag cgc	528
Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg	
165 170 175	
ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac gta cta gac	576
Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp	
180 185 190	
ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc cca gca cgc	624
Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg	
195 200 205	
act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc cgc gcc aag	672
Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys	
210 215 220	



gcg att atc aag ctc atc aac tct att gct gac ttg gta aac aac gat 720  
 Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp  
 225 230 235 240

cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag aac tac aac 768  
 Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn  
 245 250 255

gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc tcc gaa cag 816  
 Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln  
 260 265 270

att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac atg aag ttc 864  
 Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe  
 275 280 285

atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc gcc aac gta 912  
 Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val  
 290 295 300

gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc ttc ggt gct 960  
 Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala  
 305 310 315 320

cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag cca tat gag 1008  
 Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu  
 325 330 335

ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac gcc ctg gat 1056  
 Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp  
 340 345 350

aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac gac ctc aag 1104  
 Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys  
 355 360 365

cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac acc tac tac 1152  
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr  
 370 375 380

gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac cgt atg gcc 1200  
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala  
 385 390 395 400

gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg gcc tgg atc 1248  
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile  
 405 410 415

aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc atc cgc gat 1296  
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp  
 420 425 430

tat gcc acc gag atc tgg aag ctc gag cca act cct gct gtt aag aag 1344  
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys  
 435 440 445

taggttttaa cctccgcttc taa 1367

&lt;210&gt; 372

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 372

Ile	Phe	Gln	Gln	Leu	Phe	Trp	Arg	Val	Trp	Glu	Ile	Ile	Thr	Glu	Ile	1	5	10	15
Asp	Arg	Arg	Phe	Arg	Leu	Glu	Arg	Ala	Ala	Asp	Gly	Leu	Asp	Glu	Glu	20	25	30	
Thr	Ile	Asp	Arg	Met	Ala	Pro	Ile	Gln	Arg	Gly	Thr	Val	His	Met	Ala	35	40	45	
Trp	Ile	Ala	Cys	Tyr	Ala	Ala	Tyr	Ser	Ile	Asn	Gly	Val	Ala	Ala	Leu	50	55	60	
His	Thr	Glu	Ile	Ile	Lys	Ala	Glu	Thr	Leu	Ala	Asp	Trp	Tyr	Ala	Leu	65	70	75	80
Trp	Pro	Glu	Lys	Phe	Asn	Asn	Lys	Thr	Asn	Gly	Val	Thr	Pro	Arg	Arg	85	90	95	
Trp	Leu	Arg	Met	Ile	Asn	Pro	Gly	Leu	Ser	Asp	Leu	Leu	Thr	Arg	Leu	100	105	110	
Ser	Gly	Ser	Asp	Asp	Trp	Val	Thr	Asp	Leu	Asp	Glu	Leu	Lys	Lys	Leu	115	120	125	
Arg	Ser	Tyr	Ala	Asp	Asp	Lys	Ser	Val	Leu	Glu	Glu	Leu	Arg	Ala	Ile	130	135	140	
Lys	Ala	Ala	Asn	Lys	Gln	Asp	Phe	Ala	Glu	Trp	Ile	Leu	Glu	Arg	Gln	145	150	155	160
Gly	Ile	Glu	Ile	Asp	Pro	Glu	Ser	Ile	Phe	Asp	Val	Gln	Ile	Lys	Arg	165	170	175	
Leu	His	Glu	Tyr	Lys	Arg	Gln	Leu	Met	Asn	Ala	Leu	Tyr	Val	Leu	Asp	180	185	190	
Leu	Tyr	Phe	Arg	Ile	Lys	Glu	Asp	Gly	Leu	Thr	Asp	Ile	Pro	Ala	Arg	195	200	205	
Thr	Val	Ile	Phe	Gly	Ala	Lys	Ala	Ala	Pro	Gly	Tyr	Val	Arg	Ala	Lys	210	215	220	
Ala	Ile	Ile	Lys	Leu	Ile	Asn	Ser	Ile	Ala	Asp	Leu	Val	Asn	Asn	Asp	225	230	235	240
Pro	Glu	Val	Ser	Pro	Leu	Leu	Lys	Val	Val	Phe	Val	Glu	Asn	Tyr	Asn	245	250	255	
Val	Ser	Pro	Ala	Glu	His	Ile	Leu	Pro	Ala	Ser	Asp	Val	Ser	Glu	Gln	260	265	270	
Ile	Ser	Thr	Ala	Gly	Lys	Glu	Ala	Ser	Gly	Thr	Ser	Asn	Met	Lys	Phe	275	280	285	
Met	Met	Asn	Gly	Ala	Leu	Thr	Leu	Gly	Thr	Met	Asp	Gly	Ala	Asn	Val	290	295	300	

Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala  
305 310 315 320

Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu  
325 330 335

Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp  
340 345 350

Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys  
355 360 365

His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr  
370 375 380

Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala  
385 390 395 400

Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile  
405 410 415

Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp  
420 425 430

Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys  
435 440 445

<210> 373

<211> 2348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2325)

<223> RXN02100

<400> 373

cta ggt cga atc aac gcc gag gag caa aac ctc agc gaa tac ctc agc 48  
Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser  
1 5 10 15

gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga 96  
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly  
20 25 30

gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc 144  
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser  
35 40 45

ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg 192  
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met  
50 55 60

aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc 240  
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu  
65 70 75 80

tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln 85 90 95	288
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala 100 105 110	336
gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro 115 120 125	384
ggc gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg 130 135 140	432
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu 145 150 155 160	480
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg 165 170 175	528
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac Ile Lys Gln Glu Leu Val Leu Gly Val Gly Val Arg Ala Val Asn 180 185 190	576
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu 195 200 205	624
aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg 210 215 220	672
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala 225 230 235 240	720
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg 245 250 255	768
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu 260 265 270	816
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu 275 280 285	864
ggc caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu 290 295 300	912
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val 305 310 315 320	960

agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa	1008
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu	
325 330 335	
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc	1056
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val	
340 345 350	
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat	1104
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp	
355 360 365	
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag	1152
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu	
370 375 380	
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt	1200
Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val	
385 390 395 400	
gct cgc gct gca act gca aag tcc tgg tct cac cgt gga cac acc gaa	1248
Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu	
405 410 415	
gca gaa ctt gcg tgg acc tcc cgc gtt ctg gat cca aac gtg ctg acc	1296
Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr	
420 425 430	
att ggt ttc gca cgt cgc gta tcc acc tac aag cgc ttg acc ttg atg	1344
Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met	
435 440 445	
ctg cgc aac cct gaa cgc ctg cgt tcc atc ttg ctt aat gag gaa cgc	1392
Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg	
450 455 460	
cca gtt cag ttc gtt att gct ggt aag gca cac cca cat gac atg ggt	1440
Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly	
465 470 475 480	
ggc aag aag ctc atg cag gaa atc gtc cac ttc gct gat caa gct ggt	1488
Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly	
485 490 495	
gtc cgt gac cgt ttc ctc ttc ctg cct gat tac gac atc aac ctg gcc	1536
Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala	
500 505 510	
agc tac ctg atc tct ggt gct gac gtg tgg ctg aac aac cca gtg cgc	1584
Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg	
515 520 525	
cct cag gaa gca tcg gga acc tcc ggt atg aag gcc gtc atg aat ggt	1632
Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly	
530 535 540	
ggc ctg acc ctg tcc atc tct gat ggt tgg tgg gat gaa atg cct aag	1680
Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys	
545 550 555 560	
gag acc acc ggc tgg acc atc cca acc gtt gag tcc cag gac ttg gaa	1728

Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu	
565 570 575	
tgc cgc gac cac ctg gaa tcc cag gcg ctg tac gac ctg ctg gaa aac	1776
Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn	
580 585 590	
gaa gtt gca ccg ctg ttt tac aag cgc gac aag aac ggc atc cca cag	1824
Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln	
595 600 605	
gac tgg ctg gac ctg gtt cgc gaa tcc tgg acc acc ctg tca cca atg	1872
Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met	
610 615 620	
gtc acc tcc acc cgc atg gtg cgc gac tac acc acc cag tac tac cgc	1920
Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg	
625 630 635 640	
cca acc aaa cac cag gca gag ctc att gcg cag cct gca gaa gca gcg	1968
Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala	
645 650 655	
gat tac gcg gca tgg ctt gag cac atc aaa gca gag tgg gct ggc gtc	2016
Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val	
660 665 670	
aag gtc tca gac ctg aag atc agc gag agc gcc atc acg gcg cag gag	2064
Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu	
675 680 685	
ctt gaa gtc agc gtt cgc gtt gat tcc ggt tgc ctt aac gac gac gag	2112
Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu	
690 695 700	
ttc caa gct cag gca ctc ttt ggt gcg ctc gga cac aac ggt gac atc	2160
Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile	
705 710 715 720	
gaa gat cca gaa atc acc gtt ttg acc cca cgc ggc gat ggc gcc tac	2208
Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr	
725 730 735	
gcg gca aag gtc agc act gac ctg cca ggc aac tac ggc atc act gcc	2256
Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala	
740 745 750	
cgc gtt gtt cca aac aac agg atg ctg gtc agc cca gcg gaa acc cgc	2304
Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg	
755 760 765	
ctg atc acc tac ttg gag aac tagggcgaaa ctagctttac caa	2348
Leu Ile Thr Tyr Leu Glu Asn	
770 775	

&lt;210&gt; 374

&lt;211&gt; 775

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 374

Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser  
 1 5 10 15  
 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly  
 20 25 30  
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser  
 35 40 45  
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met  
 50 55 60  
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu  
 65 70 75 80  
 Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln  
 85 90 95  
 Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala  
 100 105 110  
 Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro  
 115 120 125  
 Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg  
 130 135 140  
 Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu  
 145 150 155 160  
 Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg  
 165 170 175  
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn  
 180 185 190  
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu  
 195 200 205  
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg  
 210 215 220  
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala  
 225 230 235 240  
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg  
 245 250 255  
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu  
 260 265 270  
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu  
 275 280 285  
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu  
 290 295 300  
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val  
 305 310 315 320

Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu  
 325 330 335  
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val  
 340 345 350  
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp  
 355 360 365  
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu  
 370 375 380  
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val  
 385 390 395 400  
 Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu  
 405 410 415  
 Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr  
 420 425 430  
 Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met  
 435 440 445  
 Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg  
 450 455 460  
 Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly  
 465 470 475 480  
 Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly  
 485 490 495  
 Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala  
 500 505 510  
 Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg  
 515 520 525  
 Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly  
 530 535 540  
 Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys  
 545 550 555 560  
 Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu  
 565 570 575  
 Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn  
 580 585 590  
 Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln  
 595 600 605  
 Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met  
 610 615 620  
 Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg  
 625 630 635 640  
 Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala



645										650					655				
Asp	Tyr	Ala	Ala	Trp	Leu	Glu	His	Ile	Lys	Ala	Glu	Trp	Ala	Gly	Val				
		660						665					670						
Lys	Val	Ser	Asp	Leu	Lys	Ile	Ser	Glu	Ser	Ala	Ile	Thr	Ala	Gln	Glu				
		675					680					685							
Leu	Glu	Val	Ser	Val	Arg	Val	Asp	Ser	Gly	Ser	Leu	Asn	Asp	Asp	Glu				
	690					695					700								
Phe	Gln	Ala	Gln	Ala	Leu	Phe	Gly	Ala	Leu	Gly	His	Asn	Gly	Asp	Ile				
705					710				715						720				
Glu	Asp	Pro	Glu	Ile	Thr	Val	Leu	Thr	Pro	Arg	Gly	Asp	Gly	Ala	Tyr				
				725				730						735					
Ala	Ala	Lys	Val	Ser	Thr	Asp	Leu	Pro	Gly	Asn	Tyr	Gly	Ile	Thr	Ala				
			740					745					750						
Arg	Val	Val	Pro	Asn	Asn	Arg	Met	Leu	Val	Ser	Pro	Ala	Glu	Thr	Arg				
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Leu	Ile	Thr	Tyr	Leu	Glu	Asn													
	770					775													

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (1)..(918)  
 <223> FRXA02100

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cag gaa atc gtc cac ttc gct gat caa gct ggt gtc cgt gac cgt ttc	96
Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe	
20 25 30	
ctc ttc ctg cct gat tac gac atc aac ctg gcc agc tac ctg atc tct	144
Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser	
35 40 45	
ggt gct gac gtg tgg ctg aac aac cca gtg cgc cct cag gaa gca tcg	192
Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser	
50 55 60	
gga acc tcc ggt atg aag gcc gtc atg aat ggt ggc ctg acc ctg tcc	240
Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser	
65 70 75 80	
atc tct gat ggt tgg tgg gat gaa atg cct aag gag acc acc ggc tgg	288
Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp	
85 90 95	

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acc atc cca acc gtt gag tcc cag gac ttg gaa tgc cgc gac cac ctg 336
Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu
100 105 110

gaa tcc cag gcg ctg tac gac ctg ctg gaa aac gaa gtt gca ccg ctg 384
Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu
115 120 125

ttt tac aag cgc gac aag aac ggc atc cca cag gac tgg ctg gac ctg 432
Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu
130 135 140

gtt cgc gaa tcc tgg acc acc ctg tca cca atg gtc acc tcc acc cgc 480
Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg
145 150 155 160

atg gtg cgc gac tac acc acc cag tac tac cgc cca acc aaa cac cag 528
Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln
165 170 175

gca gag ctc att gcg cag cct gca gaa gca gcg gat tac gcg gca tgg 576
Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp
180 185 190

ctt gag cac atc aaa gca gag tgg gct ggc gtc aag gtc tca gac ctg 624
Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu
195 200 205

aag atc agc gag agc gcc atc acg gcg cag gag ctt gaa gtc agc gtt 672
Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val
210 215 220

cgc gtt gat tcc ggt tcg ctt aac gac gac gag ttc caa gct cag gca 720
Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
225 230 235 240

ctc ttt ggt gcg ctc gga cac aac ggt gac atc gaa gat cca gaa atc 768
Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
245 250 255

acc gtt ttg acc cca cgc ggc gat ggc gcc tac gcg gca aag gtc agc 816
Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
260 265 270

act gac ctg cca ggc aac tac ggc atc act gcc cgc gtt gtt cca aac 864
Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
275 280 285

aac agg atg ctg gtc agc cca gcg gaa acc cgc ctg atc acc tac ttg 912
Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
290 295 300

gag aac tagggcgaaa ctagctttac caa 941
Glu Asn
305

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&lt;210&gt; 376

&lt;211&gt; 306

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 376

Ile Ala Gly Lys Ala His Pro His Asp Met Gly Gly Lys Lys Leu Met  
 1 5 10 15

Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe  
 20 25 30

Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser  
 35 40 45

Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser  
 50 55 60

Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser  
 65 70 75 80

Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp  
 85 90 95

Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu  
 100 105 110

Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu  
 115 120 125

Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu  
 130 135 140

Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg  
 145 150 155 160

Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln  
 165 170 175

Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp  
 180 185 190

Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu  
 195 200 205

Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val  
 210 215 220

Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala  
 225 230 235 240

Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile  
 245 250 255

Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser  
 260 265 270

Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn  
 275 280 285

Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu  
 290 295 300

Glu Asn

305

<210> 377  
 <211> 1206  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(1206)  
 <223> FRXA02113

<400> 377  
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 Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser  
   1                  5                  10                  15  
  
 gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga 96  
 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly  
                   20                  25                  30  
  
 gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc 144  
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser  
           35                  40                  45  
  
 ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg 192  
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met  
   50                  55                  60  
  
 aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc 240  
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu  
   65                  70                  75                  80  
  
 tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag 288  
 Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln  
                   85                  90                  95  
  
 cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca 336  
 Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala  
           100                  105                  110  
  
 gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca 384  
 Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro  
   115                  120                  125  
  
 ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc 432  
 Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg  
   130                  135                  140  
  
 atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag 480  
 Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu  
   145                  150                  155                  160  
  
 ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc 528  
 Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg  
           165                  170                  175  
  
 atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac 576  
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn  
           180                  185                  190

gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu 195 200 205	624
aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg 210 215 220	672
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala 225 230 235 240	720
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg 245 250 255	768
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu 260 265 270	816
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu 275 280 285	864
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu 290 295 300	912
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val 305 310 315 320	960
agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu 325 330 335	1008
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val 340 345 350	1056
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp 355 360 365	1104
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu 370 375 380	1152
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val 385 390 395 400	1200
gct cgc Ala Arg	1206

&lt;210&gt; 378

&lt;211&gt; 402

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 378

Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser  
 1 5 10 15  
 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly  
 20 25 30  
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser  
 35 40 45  
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met  
 50 55 60  
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu  
 65 70 75 80  
 Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln  
 85 90 95  
 Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala  
 100 105 110  
 Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro  
 115 120 125  
 Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg  
 130 135 140  
 Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu  
 145 150 155 160  
 Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg  
 165 170 175  
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn  
 180 185 190  
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu  
 195 200 205  
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg  
 210 215 220  
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala  
 225 230 235 240  
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg  
 245 250 255  
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu  
 260 265 270  
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu  
 275 280 285  
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu  
 290 295 300  
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val

305		310		315		320
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu						
		325		330		335
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val						
		340		345		350
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp						
		355		360		365
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu						
		370		375		380
Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val						
		385		390		395
						400

Ala Arg

<210> 379  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA02147

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 Met Phe Gly Arg Arg  
 1 5  
 tgg gtg agc gtt gtg gcg tca tgt gtt atc gca agc acg ctg att ctg 163  
 Trp Val Ser Val Val Ala Ser Cys Val Ile Ala Ser Thr Leu Ile Leu  
 10 15 20  
 gtg cct tcg cat tcc ggt gcg gag gaa gtc gat caa ctg att gct gat 211  
 Val Pro Ser His Ser Gly Ala Glu Glu Val Asp Gln Leu Ile Ala Asp  
 25 30 35  
 atc gag cat gtc tct cag gaa acg tct gcc cag aat gag gaa gtc aaa 259  
 Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln Asn Glu Glu Val Lys  
 40 45 50  
 cag ctt gag att gat att gag gct cgt gag gtc acg atc aag gaa gtt 307  
 Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val Thr Ile Lys Glu Val  
 55 60 65  
 cag gag cag tcg gta agc tac cgt gag gcg gct gat caa gca tcg gag 355  
 Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala Asp Gln Ala Ser Glu  
 70 75 80 85  
 aat gtc gaa gct tat cgt tcg gag atc aat cgg atc gct cag gcg aag 403  
 Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg Ile Ala Gln Ala Lys  
 90 95 100

tat	cgt	ggc	aca	gtc	acg	gat	cct	ttg	agc	att	gcg	gtg	tct	gca	gaa	451
Tyr	Arg	Gly	Thr	Val	Thr	Asp	Pro	Leu	Ser	Ile	Ala	Val	Ser	Ala	Glu	
			105							110				115		
gat	cca	caa	aac	gtg	att	gat	cgg	atg	agc	tac	ctt	tca	acg	ttg	act	499
Asp	Pro	Gln	Asn	Val	Ile	Asp	Arg	Met	Ser	Tyr	Leu	Ser	Thr	Leu	Thr	
			120							125				130		
aag	tcc	act	agt	gat	gtg	gtt	gaa	tcc	ctc	aac	gcg	gag	act	gag	aag	547
Lys	Ser	Thr	Ser	Asp	Val	Val	Glu	Ser	Leu	Asn	Ala	Glu	Thr	Glu	Lys	
			135							140				145		
tcc	gca	gaa	gct	gtg	tat	caa	gca	aac	cgt	act	aag	gcg	gaa	gcg	gag	595
Ser	Ala	Glu	Ala	Val	Tyr	Gln	Ala	Asn	Arg	Thr	Lys	Ala	Glu	Ala	Glu	
			150							155				160		
ttc	cag	ttg	ggg	cag	ctg	aag	gta	cgc	cag	gcg	gag	ctt	gaa	tct	gaa	643
Phe	Gln	Leu	Gly	Gln	Leu	Lys	Val	Arg	Gln	Ala	Glu	Leu	Glu	Ser	Glu	
			170							175				180		
aag	gaa	gca	ttg	gat	ggg	cga	aaa	tcg	gag	atc	cga	gac	cgg	gtg	gat	691
Lys	Glu	Ala	Leu	Asp	Gly	Arg	Lys	Ser	Glu	Ile	Arg	Asp	Arg	Val	Asp	
			185							190				195		
gcc	ctg	acg	cca	cag	gag	cgg	gaa	atg	tgg	gtt	gct	aag	aat	ggg	cca	739
Ala	Leu	Thr	Pro	Gln	Glu	Arg	Glu	Met	Trp	Val	Ala	Lys	Asn	Gly	Pro	
			200							205				210		
ttg	gac	att	gat	ctg	act	gat	ttg	ctt	ggg	ctt	tcc	gct	gcg	act	tcg	787
Leu	Asp	Ile	Asp	Leu	Thr	Asp	Leu	Leu	Gly	Leu	Ser	Ala	Ala	Thr	Ser	
			215							220				225		
ggg	gcg	gtg	gat	gct	gcc	ttg	tct	aag	ttg	gga	agc	cct	tat	ggg	tgg	835
Gly	Ala	Val	Asp	Ala	Ala	Leu	Ser	Lys	Leu	Gly	Ser	Pro	Tyr	Gly	Trp	
			230							235				240		
ggg	ggc	att	ggc	cca	aat	gag	ttt	gat	tgc	tca	ggg	ttg	atc	tat	tgg	883
Gly	Gly	Ile	Gly	Pro	Asn	Glu	Phe	Asp	Cys	Ser	Gly	Leu	Ile	Tyr	Trp	
			250							255				260		
gcg	tat	cag	cag	atg	ggg	aag	act	ttg	cca	cgt	acg	tct	caa	gct	cag	931
Ala	Tyr	Gln	Gln	Met	Gly	Lys	Thr	Leu	Pro	Arg	Thr	Ser	Gln	Ala	Gln	
			265							270				275		
atg	gct	ggc	gga	acg	ccg	gtg	agc	aga	gat	gag	ctg	cag	cct	ggc	gat	979
Met	Ala	Gly	Gly	Thr	Pro	Val	Ser	Arg	Asp	Glu	Leu	Gln	Pro	Gly	Asp	
			280							285				290		
gtc	att	gga	tat	tac	cca	ggg	gct	act	cac	gtg	gga	ctg	tat	att	ggg	1027
Val	Ile	Gly	Tyr	Tyr	Pro	Gly	Ala	Thr	His	Val	Gly	Leu	Tyr	Ile	Gly	
			295							300				305		
gac	gga	aag	att	gtg	cac	gcc	tca	gac	tac	gga	atc	cct	gtg	cag	gtg	1075
Asp	Gly	Lys	Ile	Val	His	Ala	Ser	Asp	Tyr	Gly	Ile	Pro	Val	Gln	Val	
			310							315				320		
gta	tct	gtt	gat	tca	gca	ccg	ttt	tat	ggg	gc						



taagaaatag ttcgtcagga gaa

1140

&lt;210&gt; 380

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 380

Met Phe Gly Arg Arg Trp Val Ser Val Val Ala Ser Cys Val Ile Ala  
 1 5 10 15

Ser Thr Leu Ile Leu Val Pro Ser His Ser Gly Ala Glu Glu Val Asp  
 20 25 30

Gln Leu Ile Ala Asp Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln  
 35 40 45

Asn Glu Glu Val Lys Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val  
 50 55 60

Thr Ile Lys Glu Val Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala  
 65 70 75 80

Asp Gln Ala Ser Glu Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg  
 85 90 95

Ile Ala Gln Ala Lys Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile  
 100 105 110

Ala Val Ser Ala Glu Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr  
 115 120 125

Leu Ser Thr Leu Thr Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn  
 130 135 140

Ala Glu Thr Glu Lys Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr  
 145 150 155 160

Lys Ala Glu Ala Glu Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala  
 165 170 175

Glu Leu Glu Ser Glu Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile  
 180 185 190

Arg Asp Arg Val Asp Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val  
 195 200 205

Ala Lys Asn Gly Pro Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu  
 210 215 220

Ser Ala Ala Thr Ser Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly  
 225 230 235 240

Ser Pro Tyr Gly Trp Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser  
 245 250 255

Gly Leu Ile Tyr Trp Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg  
 260 265 270

Thr Ser Gln Ala Gln Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu

275	280	285
Leu Gln Pro Gly Asp Val	Ile Gly Tyr Tyr Pro Gly	Ala Thr His Val
290	295	300
Gly Leu Tyr Ile Gly Asp	Gly Lys Ile Val His	Ala Ser Asp Tyr Gly
305	310	315
Ile Pro Val Gln Val Val	Ser Val Asp Ser Ala	Pro Phe Tyr Gly Ala
325	330	335

Arg Arg Tyr

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 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA01478

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 Met Thr Ile Pro Gly  
 1 5  
 gct tcc aca cag act gat atc cct ctg gac aca ctt ctt gag gat tac 163  
 Ala Ser Thr Gln Thr Asp Ile Pro Leu Asp Thr Leu Leu Glu Asp Tyr  
 10 15 20  
 gcg cta ctg tca gac act cac acc ggc gct ctg ctg tcc aac atg ggc 211  
 Ala Leu Leu Ser Asp Thr His Thr Gly Ala Leu Leu Ser Asn Met Gly  
 25 30 35  
 agt ttg gac tgg ttg tgc ctg cct cgt ttt gat tcc caa gcc atg ttc 259  
 Ser Leu Asp Trp Leu Cys Leu Pro Arg Phe Asp Ser Gln Ala Met Phe  
 40 45 50  
 acc agg ctg ctt ggt gat cgc gag cac gga cac tgg agt ttg cgt gtc 307  
 Thr Arg Leu Leu Gly Asp Arg Glu His Gly His Trp Ser Leu Arg Val  
 55 60 65  
 cca ggt ggt gag gtg atc agc caa aac tac ctc ggc gat tcc ttc gtg 355  
 Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu Gly Asp Ser Phe Val  
 70 75 80 85  
 gtg cag acc gtg tgg cgt tca gag acc ggt act gcc cgg gtt gtt gat 403  
 Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr Ala Arg Val Val Asp  
 90 95 100  
 ttc atg cca att cac ggt caa gaa caa ccc gat atc acc gac ctg gtg 451  
 Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp Ile Thr Asp Leu Val  
 105 110 115  
 cgc tct gtg cac tgc gtg gaa ggc gaa gtg gat gtg gaa tcg atc ctg 499

Arg	Ser	Val	His	Cys	Val	Glu	Gly	Glu	Val	Asp	Val	Glu	Ser	Ile	Leu		
		120					125					130					
cgc	ctg	cgt	ttt	gat	tat	ggc	gag	tcc	act	ccg	tat	ttc	cgc	acc	agc	547	
Arg	Leu	Arg	Phe	Asp	Tyr	Gly	Glu	Ser	Thr	Pro	Tyr	Phe	Arg	Thr	Ser		
		135					140					145					
act	gtc	gac	ggc	atc	agc	atc	gtg	cag	gct	gtc	gcc	ggc	ccc	aat	gcg	595	
Thr	Val	Asp	Gly	Ile	Ser	Ile	Val	Gln	Ala	Val	Ala	Gly	Pro	Asn	Ala		
		150				155				160					165		
gta	tat	gtt	cgt	gga	cct	gag	atg	cca	cac	cgc	cct	gca	aag	gat	tgt	643	
Val	Tyr	Val	Arg	Gly	Pro	Glu	Met	Pro	His	Arg	Pro	Ala	Lys	Asp	Cys		
				170				175						180			
cac	agt	ggc	acc	ttc	cac	ctg	acg	gcc	ggc	gaa	tcc	gtg	gaa	tgg	gtt	691	
His	Ser	Gly	Thr	Phe	His	Leu	Thr	Ala	Gly	Glu	Ser	Val	Glu	Trp	Val		
			185					190					195				
ctc	acc	tgg	gca	ccg	tcg	ttc	gaa	ccg	cat	ccc	ccc	atg	ccg	gat	tac	739	
Leu	Thr	Trp	Ala	Pro	Ser	Phe	Glu	Pro	His	Pro	Pro	Met	Pro	Asp	Tyr		
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acc	cgc	tct	ttg	gag	agc	acc	ttg	agc	ttc	tgg	gca	tca	tgg	gtt	gaa	787	
Thr	Arg	Ser	Leu	Glu	Ser	Thr	Leu	Ser	Phe	Trp	Ala	Ser	Trp	Val	Glu		
		215				220					225						
gag	ctc	ccc	cac	cag	cgc	ctc	tac	gac	gct	gaa	gtc	cgc	cgc	tcc	atg	835	
Glu	Leu	Pro	His	Gln	Arg	Leu	Tyr	Asp	Ala	Glu	Val	Arg	Arg	Ser	Met		
		230			235					240					245		
ctc	gta	ctg	cgc	gcc	ttg	acc	gat	cta	caa	acc	ggt	ggc	atc	gtg	gcc	883	
Leu	Val	Leu	Arg	Ala	Leu	Thr	Asp	Leu	Gln	Thr	Gly	Gly	Ile	Val	Ala		
				250					255					260			
gca	ccg	acc	acc	tca	cta	cca	gag	gat	ttc	gga	ggc	atc	cgt	aac	tgg	931	
Ala	Pro	Thr	Thr	Ser	Leu	Pro	Glu	Asp	Phe	Gly	Gly	Ile	Arg	Asn	Trp		
			265					270					275				
gac	tac	cgc	tac	gtg	tgg	ctg	cgc	gac	tcc	gca	ctc	acc	att	gaa	gcc	979	
Asp	Tyr	Arg	Tyr	Val	Trp	Leu	Arg	Asp	Ser	Ala	Leu	Thr	Ile	Glu	Ala		
		280					285					290					
ctc	gtg	gaa	tac	gga	ttc	tcc	caa	gca	gcc	ctc	caa	tgg	cgc	acc	tgg	1027	
Leu	Val	Glu	Tyr	Gly	Phe	Ser	Gln	Ala	Ala	Leu	Gln	Trp	Arg	Thr	Trp		
		295				300					305						
ctg	ctg	cgc	gcc	atc	gca	ggc	gac	ccg	gaa	aac	ctc	cgc	atc	atg	tat	1075	
Leu	Leu	Arg	Ala	Ile	Ala	Gly	Asp	Pro	Glu	Asn	Leu	Arg	Ile	Met	Tyr		
					315					320				325			
ggc	ctc	ggc	ggc	gaa	cga	cac	ctc	cct	gaa	cgc	gaa	ctc	caa	cac	ctg	1123	
Gly	Leu	Gly	Gly	Glu	Arg	His	Leu	Pro	Glu	Arg	Glu	Leu	Gln	His	Leu		
				330					335					340			
cgc	gga	tac	gaa	aac	tcc	gtg	cct	gtt	cgc	gtt	ggc	aat	gga	gcc	gcc	1171	
Arg	Gly	Tyr	Glu	Asn	Ser	Val	Pro	Val	Arg	Val	Gly	Asn	Gly	Ala	Ala		
			345					350				355					
gaa	caa	tac	caa	gca	gat	gtc	gtc	ggc	gaa	gta	atg	gtc	gcg	ctt	gaa	1219	
Glu	Gln	Tyr	Gln	Ala	Asp	Val	Val	Gly	Glu	Val	Met	Val	Ala	Leu	Glu		

360	365	370	
acc atc cgc cgc gcc ggg tgc ctc gag gac gaa ttc tcc tgg ggc atg Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu Phe Ser Trp Gly Met 375 380 385			1267
caa aaa gcc atc ctc gat ttc caa gaa gcc aac ttc gac cgc aag gat Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn Phe Asp Arg Lys Asp 390 395 400 405			1315
caa ggc atc tgg gaa atg cgc tcc gaa ccg caa tat ttc acc cac ggc Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln Tyr Phe Thr His Gly 410 415 420			1363
cgc gcc atg atg tgg gcc ggc ttc gac cgc ggc atc aaa gcc atc gaa Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly Ile Lys Ala Ile Glu 425 430 435			1411
gaa ttc aac ctc gac ggc ccc atc gag cgc tgg cgt gaa ctc cgc gcc Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp Arg Glu Leu Arg Ala 440 445 450			1459
aaa ctc cgc gaa gaa atc atg acc aac ggc ttc aac gaa gag atc caa Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe Asn Glu Glu Ile Gln 455 460 465			1507
tcc ttc acc cag tgc tac gac aac acc caa gtc gac gcc tcg ctg ctt Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val Asp Ala Ser Leu Leu 470 475 480 485			1555
cag ctc gcc caa ata ggc ttc atc ggc ttc gac gat cca aaa atg ctc Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp Asp Pro Lys Met Leu 490 495 500			1603
agc acc gta gcg cgc att gag caa gag ctt ctc gac gcc cac ggc ttt Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu Asp Ala His Gly Phe 505 510 515			1651
ctt cac agg tac cac acc gac ggg tct gac ggc ctt gcc ggc gac gaa Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly Leu Ala Gly Asp Glu 520 525 530			1699
tac ccc ttc ctc atc tgt tca ttc tgg ctg gta gaa caa tac gca agc Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val Glu Gln Tyr Ala Ser 535 540 545			1747
tcc aac cgc ctc gac gag gcc aaa gaa aag atg aac cgc atc ctt gcc Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met Asn Arg Ile Leu Ala 550 555 560 565			1795
gtc caa agc cca ctt ggc cta ctg gct gag gaa tac tcc acc cac cat Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu Tyr Ser Thr His His 570 575 580			1843
ggc agg ctc gct gga aac tac cct cag gcc ttt tcc cac att ggt ctg Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe Ser His Ile Gly Leu 585 590 595			1891
atc agc gct gcc cgt gcc ata aat ttc gaa gaa gcg cga aac agg Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu Ala Arg Asn Arg 600 605 610			1936

tagagtctaa ggtgtcattc ttg

1959

&lt;210&gt; 382

&lt;211&gt; 612

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 382

Met Thr Ile Pro Gly Ala Ser Thr Gln Thr Asp Ile Pro Leu Asp Thr  
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Leu Leu Glu Asp Tyr Ala Leu Leu Ser Asp Thr His Thr Gly Ala Leu  
 20 25 30

Leu Ser Asn Met Gly Ser Leu Asp Trp Leu Cys Leu Pro Arg Phe Asp  
 35 40 45

Ser Gln Ala Met Phe Thr Arg Leu Leu Gly Asp Arg Glu His Gly His  
 50 55 60

Trp Ser Leu Arg Val Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu  
 65 70 75 80

Gly Asp Ser Phe Val Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr  
 85 90 95

Ala Arg Val Val Asp Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp  
 100 105 110

Ile Thr Asp Leu Val Arg Ser Val His Cys Val Glu Gly Glu Val Asp  
 115 120 125

Val Glu Ser Ile Leu Arg Leu Arg Phe Asp Tyr Gly Glu Ser Thr Pro  
 130 135 140

Tyr Phe Arg Thr Ser Thr Val Asp Gly Ile Ser Ile Val Gln Ala Val  
 145 150 155 160

Ala Gly Pro Asn Ala Val Tyr Val Arg Gly Pro Glu Met Pro His Arg  
 165 170 175

Pro Ala Lys Asp Cys His Ser Gly Thr Phe His Leu Thr Ala Gly Glu  
 180 185 190

Ser Val Glu Trp Val Leu Thr Trp Ala Pro Ser Phe Glu Pro His Pro  
 195 200 205

Pro Met Pro Asp Tyr Thr Arg Ser Leu Glu Ser Thr Leu Ser Phe Trp  
 210 215 220

Ala Ser Trp Val Glu Glu Leu Pro His Gln Arg Leu Tyr Asp Ala Glu  
 225 230 235 240

Val Arg Arg Ser Met Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr  
 245 250 255

Gly Gly Ile Val Ala Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly  
 260 265 270

Gly Ile Arg Asn Trp Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala  
 275 280 285  
 Leu Thr Ile Glu Ala Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu  
 290 295 300  
 Gln Trp Arg Thr Trp Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn  
 305 310 315 320  
 Leu Arg Ile Met Tyr Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg  
 325 330 335  
 Glu Leu Gln His Leu Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val  
 340 345 350  
 Gly Asn Gly Ala Ala Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val  
 355 360 365  
 Met Val Ala Leu Glu Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu  
 370 375 380  
 Phe Ser Trp Gly Met Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn  
 385 390 395 400  
 Phe Asp Arg Lys Asp Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln  
 405 410 415  
 Tyr Phe Thr His Gly Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly  
 420 425 430  
 Ile Lys Ala Ile Glu Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp  
 435 440 445  
 Arg Glu Leu Arg Ala Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe  
 450 455 460  
 Asn Glu Glu Ile Gln Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val  
 465 470 475 480  
 Asp Ala Ser Leu Leu Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp  
 485 490 495  
 Asp Pro Lys Met Leu Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu  
 500 505 510  
 Asp Ala His Gly Phe Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly  
 515 520 525  
 Leu Ala Gly Asp Glu Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val  
 530 535 540  
 Glu Gln Tyr Ala Ser Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met  
 545 550 555 560  
 Asn Arg Ile Leu Ala Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu  
 565 570 575  
 Tyr Ser Thr His His Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe  
 580 585 590  
 Ser His Ile Gly Leu Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu

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595                               600                               605

Ala Arg Asn Arg
610

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<211> 658
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<213> Corynebacterium glutamicum

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<222> (101)..(658)
<223> RXA01888

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attaagaaaa gaggtagata tggcgtcaaa gcgaccgaca atg gct gat gtg gca 115
                                         Met Ala Asp Val Ala
                                         1      5

aaa gct gct gga gta tcc act gcg ctg gtc tcc atc gtg ttt cgc gat 163
Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser Ile Val Phe Arg Asp
              10              15              20

gcc ccc gga gca agt gaa tcc acc cgc aac cat gtg aaa gaa aaa gcc 211
Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His Val Lys Glu Lys Ala
              25              30              35

gcc gaa ctc gga tac att cct gat cga cga gcc caa aaa ctt cgc caa 259
Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala Gln Lys Leu Arg Gln
              40              45              50

aac cgc tcc gga ctc atc ggt gtg gca ttc gaa atg cac caa gca ttc 307
Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu Met His Gln Ala Phe
              55              60              65

cac ggc gat atc gtc gaa cac ctc tat ccc acc gcc cga aaa cat ggc 355
His Gly Asp Ile Val Glu His Leu Tyr Pro Thr Ala Arg Lys His Gly
              70              75              80              85

ttc gac ctg tac ctt agc gcg atc aca ccg act cgc act gaa aaa gat 403
Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr Arg Thr Glu Lys Asp
              90              95              100

gcc gtc aac gcc ctg atc agg gaa cga tgc gaa gca gta att ctt cta 451
Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu Ala Val Ile Leu Leu
              105              110              115

gga tct cgc atg tca cct agt gat ttg gaa aca atc gca cag caa ctt 499
Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr Ile Ala Gln Gln Leu
              120              125              130

ccc gtc caa gta att gcc cgc ggt tcc gga acc ccc aaa gtc agt tcc 547
Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser
              135              140              145

gtc cat gtc gac gac gca gtt ggc gcc caa tta gcc ctc aac cac ctc 595
Val His Val Asp Asp Ala Val Gly Ala Gln Leu Ala Leu Asn His Leu

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cct ggc acc cag gaa 658  
Pro Gly Thr Gln Glu  
185

<400> 384															
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Ile	Val	Phe	Arg	Asp	Ala	Pro	Gly	Ala	Ser	Glu	Ser	Thr	Arg	Asn	His
			20					25					30		
Val	Lys	Glu	Lys	Ala	Ala	Glu	Leu	Gly	Tyr	Ile	Pro	Asp	Arg	Arg	Ala
		35					40					45			
Gln	Lys	Leu	Arg	Gln	Asn	Arg	Ser	Gly	Leu	Ile	Gly	Val	Ala	Phe	Glu
	50					55					60				
Met	His	Gln	Ala	Phe	His	Gly	Asp	Ile	Val	Glu	His	Leu	Tyr	Pro	Thr
65					70					75					80
Ala	Arg	Lys	His	Gly	Phe	Asp	Leu	Tyr	Leu	Ser	Ala	Ile	Thr	Pro	Thr
				85					90					95	
Arg	Thr	Glu	Lys	Asp	Ala	Val	Asn	Ala	Leu	Ile	Arg	Glu	Arg	Cys	Glu
			100					105					110		
Ala	Val	Ile	Leu	Leu	Gly	Ser	Arg	Met	Ser	Pro	Ser	Asp	Leu	Glu	Thr
		115					120					125			
Ile	Ala	Gln	Gln	Leu	Pro	Val	Gln	Val	Ile	Ala	Arg	Gly	Ser	Gly	Thr
	130					135					140				
Pro	Lys	Val	Ser	Ser	Val	His	Val	Asp	Asp	Ala	Val	Gly	Ala	Gln	Leu
145					150					155					160
Ala	Leu	Asn	His	Leu	Ile	Glu	Leu	Gly	His	Glu	His	Ile	Ile	Tyr	Ile
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Asp	Gly	Gly	Asp	Ala	Pro	Gly	Thr	Gln	Glu						
			180					185							

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<223> RXN01927

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Met Ala Leu Val Leu  
1 5

gga atc gat agt tcc acc caa tcc tgc aag gct ttg ctt gtc gac gcc 163  
Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala Leu Leu Val Asp Ala  
10 15 20

gcc acc ggc cag gtt atc gac gaa ggc cgc gcg agt cac ccg agc ggg 211  
Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala Ser His Pro Ser Gly  
25 30 35

tcg	gag	gta	gat	cca	cgt	gcg	tgg	atc	gct	gcg	ctg	gat	caa	gct	acc	259
Ser	Glu	Val	Asp	Pro	Arg	Ala	Trp	Ile	Ala	Ala	Leu	Asp	Gln	Ala	Thr	
		40					45					50				

gag ggg ttg tta gaa cgc gcg gac gct gta tct att gca ggc cag cag 307  
Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser Ile Ala Gly Gln Gln  
55 60 65

cac ggc atg gtg gcg ttg gat gaa aac gat gaa atc gtt cgc ccg gcg 355  
 His Gly Met Val Ala Leu Asp Glu Asn Asp Glu Ile Val Arg Pro Ala  
 70 75 80 85

ttg	tta	tgg	aat	gac	act	cgt	tct	gcc	cag	gct	gcg	ttg	gat	ctc	aat	403
Leu	Leu	Trp	Asn	Asp	Thr	Arg	Ser	Ala	Gln	Ala	Ala	Leu	Asp	Leu	Asn	
				90					95					100		

gag gag atc ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg 451  
Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val  
105 110 115

tat	gtt	gct	tct	tta	act	gcc	acc	aaa	atg	cgg	tgg	atg	cgt	gat	cat	499
Tyr	Val	Ala	Ser	Leu	Thr	Ala	Thr	Lys	Met	Arg	Trp	Met	Arg	Asp	His	
		120					125					130				

gaa cca gaa aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat 547  
Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp  
135 140 145

ttc	ctc	acc	tgg	cat	ttg	atg	gga	cgc	gga	cgc	aaa	gtc	acc	gac	cat	595
Phe	Leu	Thr	Trp	His	Leu	Met	Gly	Arg	Gly	Arg	Lys	Val	Thr	Asp	His	
150					155					160					165	

ggt gat gct tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg 643  
Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp  
170 175 180

cgc acc gat cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct 691  
Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro  
185 190 195

gaa ctc ctg gcc cca aat gcg att gcg gga aca act cca ggt gga gtg 739  
Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val  
200 205 210

aaa gtt gct gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt	787
Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu	
215 220 225	
gat ttg cag cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt	835
Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val	
230 235 240 245	
gcc ggc atg acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc	883
Ala Gly Met Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val	
250 255 260	
act ggt ttc gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg	931
Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr	
265 270 275	
ctt aat ggc gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg	979
Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val	
280 285 290	
gaa tgg gaa gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca	1027
Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser	
295 300 305	
ggt ggc gtg acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat	1075
Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn	
310 315 320 325	
cgt ccc gca gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc	1123
Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr	
330 335 340	
cgc gag gac ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg	1171
Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Ala Leu	
345 350 355	
gat gat gct gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag	1219
Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln	
360 365 370	
cgc atc cag ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag	1267
Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu	
375 380 385	
att gcc cct gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct	1315
Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala	
390 395 400 405	
gaa tat gtg gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg	1363
Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser	
410 415 420	
ggt gag gcc acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac	1411
Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His	
425 430 435	
cgc gca cct aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt	1459
Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg	
440 445 450	

gct gca acg cag ggt tgg tac tagagctcga tattgtcgat caa  
 Ala Ala Thr Gln Gly Trp Tyr  
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1503

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 386  
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 Leu Leu Val Asp Ala Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala  
           20                  25                  30  
 Ser His Pro Ser Gly Ser Glu Val Asp Pro Arg Ala Trp Ile Ala Ala  
           35                  40                  45  
 Leu Asp Gln Ala Thr Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser  
   50                  55                  60  
 Ile Ala Gly Gln Gln His Gly Met Val Ala Leu Asp Glu Asn Asp Glu  
   65                  70                  75                  80  
 Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala  
           85                  90                  95  
 Ala Leu Asp Leu Asn Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp  
          100                 105                 110  
 Ala Thr Gly Ser Val Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg  
          115                 120                 125  
 Trp Met Arg Asp His Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val  
   130                 135                 140  
 Met Leu Pro His Asp Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg  
 145                 150                 155                 160  
 Lys Val Thr Asp His Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr  
          165                 170                 175  
 Arg Asp Arg Ala Trp Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His  
          180                 185                 190  
 Glu Val Glu Leu Pro Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr  
          195                 200                 205  
 Thr Pro Gly Gly Val Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala  
   210                 215                 220  
 Ala Ala Leu Gly Leu Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile  
 225                 230                 235                 240  
 Gly Thr Ser Gly Val Ala Gly Met Thr Val Gln His Ser Val His Asp  
          245                 250                 255  
 Pro Ser Gly Leu Val Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe  
          260                 265                 270

Pro Leu Ala Cys Thr Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg  
 275 280 285  
 Arg Ile Leu Gly Val Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala  
 290 295 300  
 Ala Gln Pro Gly Ser Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly  
 305 310 315 320  
 Glu Arg Thr Pro Asn Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu  
 325 330 335  
 Asn Cys Ala Thr Thr Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly  
 340 345 350  
 Leu Leu Leu Ala Leu Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr  
 355 360 365  
 Gly Val Pro Val Gln Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser  
 370 375 380  
 Gln Ala Val Arg Glu Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val  
 385 390 395 400  
 Val Pro Glu Pro Ala Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala  
 405 410 415  
 Ala Trp Ala Leu Ser Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro  
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 Gly Ser Asp Pro His Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg  
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 Tyr Ala Lys Leu Arg Ala Ala Thr Gln Gly Trp Tyr  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(1116)  
 <223> FRXA01927

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 ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg tat gtt gct 96  
 Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala  
 20 25 30  
 tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat gaa cca gaa 144  
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu  
 35 40 45

aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat ttc ctc acc	192
Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr	
50 55 60	
tggt cat ttg atg gga cgc gga cgc aaa gtc acc gac cat ggt gat gct	240
Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala	
65 70 75 80	
tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg cgc acc gat	288
Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp	
85 90 95	
cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct gaa ctc ctg	336
Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu	
100 105 110	
gcc cca aat gcg att gcg gga aca act cca ggt gga gtg aaa gtt gct	384
Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala	
115 120 125	
gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt gat ttg cag	432
Ala Gly Thr Gly Asp Asn Ala Ala Ala Leu Gly Leu Asp Leu Gln	
130 135 140	
cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt gcc ggc atg	480
Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met	
145 150 155 160	
acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc act ggt ttc	528
Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe	
165 170 175	
gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg ctt aat ggc	576
Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly	
180 185 190	
gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg gaa tgg gaa	624
Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu	
195 200 205	
gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca ggt ggc gtg	672
Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val	
210 215 220	
acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat cgt ccc gca	720
Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala	
225 230 235 240	
gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc cgc gag gac	768
Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp	
245 250 255	
ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg gat gat gct	816
Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala	
260 265 270	
gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag cgc atc cag	864
Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln	
275 280 285	
ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag att gcc cct	912

Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro  
 290 295 300  
 gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct gaa tat gtg 960  
 Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val  
 305 310 315 320  
 gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg ggt gag gcc 1008  
 Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala  
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 acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac cgc gca cct 1056  
 Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro  
 340 345 350  
 aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt gct gca acg 1104  
 Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr  
 355 360 365  
 cag ggt tgg tac tagagctcga.tattgtcgat caa 1139  
 Gln Gly Trp Tyr  
 370

&lt;210&gt; 388

&lt;211&gt; 372

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 388

Asn Asp Thr Arg Ser Ala Gln Ala Ala Leu Asp Leu Asn Glu Glu Ile  
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Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala  
 20 25 30

Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu  
 35 40 45

Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr  
 50 55 60

Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala  
 65 70 75 80

Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp  
 85 90 95

Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu  
 100 105 110

Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala  
 115 120 125

Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln  
 130 135 140

Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met  
 145 150 155 160

Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe

165										170					175				
Ala	Asp	Ala	Thr	Gly	Ala	Tyr	Phe	Pro	Leu	Ala	Cys	Thr	Leu	Asn	Gly				
			180					185					190						
Ala	Pro	Val	Leu	Glu	Phe	Gly	Arg	Arg	Ile	Leu	Gly	Val	Glu	Trp	Glu				
		195					200					205							
Glu	Phe	Asp	Ala	Leu	Ala	Leu	Ala	Ala	Gln	Pro	Gly	Ser	Gly	Gly	Val				
		210				215					220								
Thr	Leu	Gln	Pro	Tyr	Leu	Glu	Gly	Glu	Arg	Thr	Pro	Asn	Arg	Pro	Ala				
225					230					235					240				
Ala	Arg	Gly	Val	Leu	Ala	Gly	Leu	Asn	Cys	Ala	Thr	Thr	Arg	Glu	Asp				
				245				250						255					
Phe	Ala	Arg	Ala	Thr	Val	Glu	Gly	Leu	Leu	Leu	Ala	Leu	Asp	Asp	Ala				
			260					265					270						
Val	Thr	Ala	Leu	Val	Glu	Ala	Thr	Gly	Val	Pro	Val	Gln	Arg	Ile	Gln				
		275					280					285							
Leu	Ile	Gly	Gly	Gly	Ala	Arg	Ser	Gln	Ala	Val	Arg	Glu	Ile	Ala	Pro				
		290				295					300								
Glu	Ile	Phe	Gly	His	Glu	Ile	Val	Val	Pro	Glu	Pro	Ala	Glu	Tyr	Val				
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Ala	Leu	Gly	Ala	Ala	Arg	Gln	Ala	Ala	Trp	Ala	Leu	Ser	Gly	Glu	Ala				
			325						330					335					
Thr	Pro	Pro	Gln	Trp	Pro	Thr	Pro	Gly	Ser	Asp	Pro	His	Arg	Ala	Pro				
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Lys	Asn	Thr	Glu	Leu	Ser	Thr	Arg	Tyr	Ala	Lys	Leu	Arg	Ala	Ala	Thr				
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Gln	Gly	Trp	Tyr																
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA02729

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 Met Asp Ser Pro Met  
 1 5  
 agt aac tca acc ggt acc gac att gtc gtt gtc gga tcc atc aat gcc 163  
 Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val Gly Ser Ile Asn Ala

10										15										20									
gat	ctc	acc	gca	aaa	gtt	caa	cgc	cac	cct	gaa	cct	gga	gaa	acc	ctc														
Asp	Leu	Thr	Ala	Lys	Val	Gln	Arg	His	Pro	Glu	Pro	Gly	Glu	Thr	Leu														
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ctg	ggt	agc	ggc	ggc	aca	gtg	agt	gct	ggt	ggc	aaa	ggc	gcc	aac	caa														
Leu	Gly	Ser	Gly	Gly	Thr	Val	Ser	Ala	Gly	Gly	Lys	Gly	Ala	Asn	Gln														
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gct	gtg	gcg	gca	gcg	caa	tta	ggt	gcc	aaa	gtc	acc	atg	atc	ggt	gcg														
Ala	Val	Ala	Ala	Ala	Gln	Leu	Gly	Ala	Lys	Val	Thr	Met	Ile	Gly	Ala														
		55				60					65																		
gtc	gga	acc	gat	caa	atg	gct	ggc	gag	gcg	ctg	aca	cat	ttg	cgt	caa														
Val	Gly	Thr	Asp	Gln	Met	Ala	Gly	Glu	Ala	Leu	Thr	His	Leu	Arg	Gln														
	70				75					80					85														
tca	gga	gca	gat	atg	tcc	gcg	att	gcc	act	gtg	gac	ggt	ccc	act	ggt														
Ser	Gly	Ala	Asp	Met	Ser	Ala	Ile	Ala	Thr	Val	Asp	Gly	Pro	Thr	Gly														
				90					95					100															
ctt	gcc	atc	atc	act	gtg	tct	gac	gat	ggg	gaa	aac	acc	atc	atc	gtt														
Leu	Ala	Ile	Ile	Thr	Val	Ser	Asp	Asp	Gly	Glu	Asn	Thr	Ile	Ile	Val														
			105				110						115																
atc	cct	ggc	gct	aac	gct	tct	gtc	acc	gcg	gaa	ttt	gtt	gat	aaa	cac														
Ile	Pro	Gly	Ala	Asn	Ala	Ser	Val	Thr	Ala	Glu	Phe	Val	Asp	Lys	His														
		120					125					130																	
tcc	caa	ctc	att	gag	aac	gcc	ggc	att	gtg	ttg	ctt	cag	ggt	gag	atc														
Ser	Gln	Leu	Ile	Glu	Asn	Ala	Gly	Ile	Val	Leu	Leu	Gln	Gly	Glu	Ile														
		135				140					145																		
cct	gcc	gat	ggt	ttc	gag	cgt	gcc	gtt	gat	ctt	tca	caa	gga	cgt	gtg														
Pro	Ala	Asp	Gly	Phe	Glu	Arg	Ala	Val	Asp	Leu	Ser	Gln	Gly	Arg	Val														
	150				155					160				165															
gtg	atc	aat	ctg	gct	cca	gtt	gtg	ccc	gtg	gga	cat	gat	cag	ctg	cgt														
Val	Ile	Asn	Leu	Ala	Pro	Val	Val	Pro	Val	Gly	His	Asp	Gln	Leu	Arg														
				170				175					180																
cgt	gcc	gat	cca	ttg	ctg	gtc	aac	gaa	cac	gaa	ggc	gct	ctg	gtg	ctg														
Arg	Ala	Asp	Pro	Leu	Leu	Val	Asn	Glu	His	Glu	Gly	Ala	Leu	Val	Leu														
			185				190						195																
gac	atg	ctt	gga	act	cca	gcg	acc	acg	tct	gat	ccc	caa	agt	ttg	gtc														
Asp	Met	Leu	Gly	Thr	Pro	Ala	Thr	Thr	Ser	Asp	Pro	Gln	Ser	Leu	Val														
		200					205					210																	
act	gaa	ttg	ctg	gag	cag	ggt	ttt	act	tcc	gtg	gtg	atg	aca	ctt	ggt														
Thr	Glu	Leu	Leu	Glu	Gln	Gly	Phe	Thr	Ser	Val	Val	Met	Thr	Leu	Gly														
		215				220					225																		
gcc	gaa	ggt	gct	ctg	gtt	ggc	acg	ccg	ggc	caa	ctc	acg	gca	att	cct														
Ala	Glu	Gly	Ala	Leu	Val	Gly	Thr	Pro	Gly	Gln	Leu	Thr	Ala	Ile	Pro														
	230				235					240					245														
acc	cca	aag																											
Thr	Pro	Lys																											



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 <211> 248  
 <212> PRT  
 <213> Corynebacterium glutamicum

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                   20                  25                  30  
 Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly  
           35                  40                  45  
 Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val  
       50                  55                  60  
 Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu  
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 Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val  
                   85                  90                  95  
 Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu  
                   100                  105                  110  
 Asn Thr Ile Ile Val Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu  
           115                  120                  125  
 Phe Val Asp Lys His Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu  
   130                  135                  140  
 Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu  
 145                  150                  155                  160  
 Ser Gln Gly Arg Val Val Ile Asn Leu Ala Pro Val Val Pro Val Gly  
                   165                  170                  175  
 His Asp Gln Leu Arg Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu  
                   180                  185                  190  
 Gly Ala Leu Val Leu Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp  
           195                  200                  205  
 Pro Gln Ser Leu Val Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val  
   210                  215                  220  
 Val Met Thr Leu Gly Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln  
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 Leu Thr Ala Ile Pro Thr Pro Lys  
                   245

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 <213> Corynebacterium glutamicum

<223> RXA02797

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Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn Val Leu Val Asp Arg  
10 15 20

cac cca gca cct ggc gaa aca ctg ttg ggc agt ggt gga cac atc act      211  
His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly His Ile Thr

                25                         30                         35

gca gga ggc aaa ggc gcc aac cag gca gta gct gcc gct ctt caa ggt 259  
Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Leu Gln Gly  
40 45 50

gca gac gtc gcc ttt gtc ggc gct gtg ggc aag gat cct tac gct gcc 307  
Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys Asp Pro Tyr Ala Ala  
55 60 65

cca gcc tta gaa ttc ctt cgt tcg tca ggc gtc gac ctt acg gca gta 355  
Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val Asp Leu Thr Ala Val  
70 75 80 85

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tcc gaa gta gat gac acc acc ggg ctt gca gtt atc acc gtt gcc aaa    403
Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val Ile Thr Val Ala Lys
          90                      95                      100
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Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly Ala Asn Ser Leu Val  
105 110 115

aat tgt gat tat gta agc agc caa tcc gct ctt tta gct gaa gct gga 499  
Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu Leu Ala Glu Ala Gly  
120 125 130

atc ctg ttg ctg caa ggt gag atc cct gcg gat ggc ttc aaa gag gcc 547  
Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Lys Glu Ala  
135 140 145

att cac cac acc atg ggt cgc gtc gtg gtg aat cta gcg ccc gtc atc 595  
Ile His His Thr Met Gly Arg Val Val Val Asn Leu Ala Pro Val Ile  
150 155 160 165

gag gta gag aag tcc gcg tta ctt gag gct gat ccg atc atc gcc aat 643  
Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp Pro Ile Ile Ala Asn  
170 175 180

gag cac gag gcc ggc ctg att ctg gat caa ttc ggg gca ggc atc gat 691  
Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe Gly Ala Gly Ile Asp  
185 190 195

tcc atg gat ccc cac gag ctc gcg caa gct ctc ctc gac gcc ggt ttc 739  
 Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu Leu Asp Ala Gly Phe  
 200 205 210  
 gcc tct gtt gtt tta acg ctt gga tcc gca ggc gcg ttg gtc gcc gat 787  
 Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly Ala Leu Val Ala Asp  
 215 220 225  
 gcc acc ggt atc acg gac atc gcc aca cca acg gtg cag gca gtt gac 835  
 Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr Val Gln Ala Val Asp  
 230 235 240 245  
 acc acg gga gcc ggt gac gct ttt gcc gga gcc ttc tgc gca cga cta 883  
 Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala Phe Cys Ala Arg Leu  
 250 255 260  
 att aaa ggc gat tcg ctt atc gac gcc gcc acc cac gca gca cgc gtc 931  
 Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr His Ala Ala Arg Val  
 265 270 275  
 ggc gct tac tcg gtg caa acc gcc gga gcg caa gcg tcc tat ccg gac 979  
 Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln Ala Ser Tyr Pro Asp  
 280 285 290  
 gcg agc gtt tca ctt ccc tct gtt taaaaaaaaact atttaagaag agg 1026  
 Ala Ser Val Ser Leu Pro Ser Val  
 295 300

<210> 392  
 <211> 301  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 392  
 Met Asn Asn Arg Ile Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn  
 1 5 10 15  
 Val Leu Val Asp Arg His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser  
 20 25 30  
 Gly Gly His Ile Thr Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala  
 35 40 45  
 Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys  
 50 55 60  
 Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val  
 65 70 75 80  
 Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val  
 85 90 95  
 Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly  
 100 105 110  
 Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu  
 115 120 125  
 Leu Ala Glu Ala Gly Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp  
 130 135 140

Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn  
 145 150 155 160  
 Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp  
 165 170 175  
 Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe  
 180 185 190  
 Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu  
 195 200 205  
 Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly  
 210 215 220  
 Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr  
 225 230 235 240  
 Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala  
 245 250 255  
 Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr  
 260 265 270  
 His Ala Ala Arg Val Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln  
 275 280 285  
 Ala Ser Tyr Pro Asp Ala Ser Val Ser Leu Pro Ser Val  
 290 295 300

<210> 393  
 <211> 1161  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1138)  
 <223> RXA02730

<400> 393  
 ccaacatcgc cttgcacgta ataggttaaa acacaagtga atgtaatcgt ttgcagcaat 60  
 cgattacata aaggtagata atgagataaa gcgaggcgct atg gcg acg gaa aaa 115  
 Met Ala Thr Glu Lys  
 1 5  
 ttc cga ccg act ctt aaa gat gtc gct cgt caa gca ggt gtc tcc atc 163  
 Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln Ala Gly Val Ser Ile  
 10 15 20  
 gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg 211  
 Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser  
 25 30 35  
 act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc 259  
 Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala  
 40 45 50

aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt	307
Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly	
55 60 65	
gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act	355
Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr	
70 75 80 85	
gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc	403
Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr	
90 95 100	
aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc	451
Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu	
105 110 115	
acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc	499
Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys	
120 125 130	
gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg	547
Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu	
135 140 145	
gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct	595
Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser	
150 155 160 165	
aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac	643
Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn	
170 175 180	
aac gcg ttg ccg att ggt tac ctc tca ggt ccc atg gac acc tca aca	691
Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro Met Asp Thr Ser Thr	
185 190 195	
ggt aga gag cga tta gag gat ttc aaa gca gcc tgc gcc aac tcc aaa	739
Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala Cys Ala Asn Ser Lys	
200 205 210	
att ggc gaa cag ctc gtt ttt ctg ggt ggg tac gaa caa agc gtt gga	787
Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr Glu Gln Ser Val Gly	
215 220 225	
ttt gaa ggc gct acg aaa ttg ctc gat caa gga gct aaa act ctt ttt	835
Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly Ala Lys Thr Leu Phe	
230 235 240 245	
gcc ggc gat tct atg atg acg atc ggt gtc att gaa gcc tgc cat aag	883
Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile Glu Ala Cys His Lys	
250 255 260	
gct ggt ttg gtt atc ggc aag gat gtc agc gtg att ggt ttt gat aca	931
Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val Ile Gly Phe Asp Thr	
265 270 275	
cat ccg ctt ttt gcc ctg caa cct cat ccg ttg aca gtg att gat caa	979
His Pro Leu Phe Ala Leu Gln Pro His Pro Leu Thr Val Ile Asp Gln	
280 285 290	
aat gta gaa caa cta gcc caa cga gca gtg tct atc ctc acc gaa tta	1027

Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser Ile Leu Thr Glu Leu  
 295 300 305  
 att gca ggc acg gta cct agc gtg acg aaa act acg atc ccc act gcc 1075  
 Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr Thr Ile Pro Thr Ala  
 310 315 320 325  
 ctt att cat cgt gaa tca atc atc aac tcc act tta agg aag aag gat 1123  
 Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr Leu Arg Lys Lys Asp  
 330 335 340  
 gga ctc ccc aat gag taactcaacc ggtaccgaca ttg 1161  
 Gly Leu Pro Asn Glu  
 345

<210> 394  
 <211> 346  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 394  
 Met Ala Thr Glu Lys Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln  
 1 5 10 15  
 Ala Gly Val Ser Ile Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro  
 20 25 30  
 Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp  
 35 40 45  
 Leu Gly Tyr Arg Ala Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg  
 50 55 60  
 Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe  
 65 70 75 80  
 Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu  
 85 90 95  
 Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly  
 100 105 110  
 Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val  
 115 120 125  
 Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly  
 130 135 140  
 Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile  
 145 150 155 160  
 Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu  
 165 170 175  
 Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro  
 180 185 190  
 Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala  
 195 200 205

Cys Ala Asn Ser Lys Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr  
 210 215 220  
 Glu Gln Ser Val Gly Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly  
 225 230 235 240  
 Ala Lys Thr Leu Phe Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile  
 245 250 255  
 Glu Ala Cys His Lys Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val  
 260 265 270  
 Ile Gly Phe Asp Thr His Pro Leu Phe Ala Leu Gln Pro His Pro Leu  
 275 280 285  
 Thr Val Ile Asp Gln Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser  
 290 295 300  
 Ile Leu Thr Glu Leu Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr  
 305 310 315 320  
 Thr Ile Pro Thr Ala Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr  
 325 330 335  
 Leu Arg Lys Lys Asp Gly Leu Pro Asn Glu  
 340 345

<210> 395  
 <211> 483  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(460)  
 <223> RXA02551

<400> 395  
 gctgcacaaa ttccgcgaaa gggatcacc atcgacatca cagatgaaga ccgtgagatc 60  
 ttaaaaaaac accgtcgatt tcatttcctt ctctatttac atg tcc gta tgt gaa 115  
 Met Ser Val Cys Glu  
 1 5  
 gcc cac aac ccc gaa aac tac tca acc ggt ggc ggt aac atc atc ggc 163  
 Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly Gly Asn Ile Ile Gly  
 10 15 20  
 gga gtg gtc agc ccc act ctc gcg gct tcc gaa tgg ggt tgg caa gtt 211  
 Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu Trp Gly Trp Gln Val  
 25 30 35  
 gat ccc ctc ggt ttg cgc atc gtc ctg aac aac tac tgg gag cgc tgg 259  
 Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn Tyr Trp Glu Arg Trp  
 40 45 50  
 cag aag cca ctg ttc atc gtc gaa aac gga cta gga gca aag gac gtg 307  
 Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val  
 55 60 65

ctt atc gac gga ccc tcc ggc cca aca gta aac gat gac tac cgc atc 355  
 Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn Asp Asp Tyr Arg Ile  
 70 75 80 85

aaa tac ctc gac gac ggc ggc tca gga atc ttg aag cgc tac aag aag 403  
 Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu Lys Arg Tyr Lys Lys  
 90 95 100

aag tcc ttt gat tgg tgc cgc gac atc atc gcc acc aat ggc gaa agc 451  
 Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala Thr Asn Gly Glu Ser  
 105 110 115

ctg gaa tcc taagaaataa aggtaggtgt cac 483  
 Leu Glu Ser  
 120

<210> 396

<211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

Met Ser Val Cys Glu Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly  
 1 5 10 15

Gly Asn Ile Ile Gly Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu  
 20 25 30

Trp Gly Trp Gln Val Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn  
 35 40 45

Tyr Trp Glu Arg Trp Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu  
 50 55 60

Gly Ala Lys Asp Val Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn  
 65 70 75 80

Asp Asp Tyr Arg Ile Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu  
 85 90 95

Lys Arg Tyr Lys Lys Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala  
 100 105 110

Thr Asn Gly Glu Ser Leu Glu Ser  
 115 120

<210> 397

<211> 795

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(772)

<223> RXA01325

<400> 397

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cctgggaaatt ttcccacact aagtcagggtc taagtaggggt											atg Met	gat Asp	atg Met	acg Thr	att Ile	115
											1				5	
tcc Ser	cgc Arg	tcc Ser	acc Thr	atg Met	gcc Ala	caa Gln	atc Ile	ctt Leu	gac Asp	tac Tyr	acc Thr	ctc Leu	ctc Leu	gga Gly	cca Pro	163
											15				20	
gaa Glu	gta Val	acc Thr	aac Asn	tcc Ser	gaa Glu	ctg Leu	gcc Ala	gca Ala	ttt Phe	ata Ile	gat Asp	tcc Ser	gca Ala	att Ile	gag Glu	211
											30				35	
ctg Leu	gga Gly	gtc Val	ggc Gly	acg Thr	atc Ile	tgt Cys	gtc Val	ccc Pro	aac Asn	agc Ser	atg Met	gtc Val	aac Asn	cta Leu	act Thr	259
											45				50	
gca Ala	aaa Lys	gcc Ala	caa Gln	gaa Glu	gct Ala	gga Gly	att Ile	cga Arg	gtg Val	gcc Ala	acc Thr	gtc Val	gca Ala	gga Gly	ttc Phe	307
											60				65	
ccg Pro	cac His	ggc Gly	aaa Lys	acc Thr	ccc Pro	gcg Ala	ttg Leu	gtg Val	aaa Lys	gcc Ala	gcc Ala	gaa Glu	gcg Ala	cgc Arg	ctt Leu	355
											75				80	
gcc Ala	gta Val	cag Gln	tcc Ser	gga Gly	gct Ala	tcc Ser	gaa Glu	gta Val	gat Asp	gtt Val	gtt Val	ttg Leu	gat Asp	att Ile	gcg Ala	403
											95				100	
gta Val	gtg Val	aaa Lys	gag Glu	gga Gly	gat Asp	gcc Ala	aat Asn	agg Arg	ttg Leu	ctg Leu	cag Gln	gaa Glu	att Ile	gtg Val	gca Ala	451
											110				115	
atc Ile	agg Arg	gag Glu	gct Ala	gtt Val	cca Pro	tct Ser	cct Pro	gtg Val	gtg Val	ctg Leu	aaa Lys	ttc Phe	atc Ile	ctc Leu	gaa Glu	499
											125				130	
aca Thr	gct Ala	gtt Val	gtg Val	agt Ser	gat Asp	gaa Glu	gca Ala	att Ile	gtg Val	act Thr	gca Ala	gtg Val	aat Asn	gcg Ala	ttg Leu	547
											140				145	
att Ile	gct Ala	gct Ala	ggt Gly	gct Ala	gac Asp	ttc Phe	gct Ala	aaa Lys	act Thr	tcc Ser	acg Thr	gga Gly	ttc Phe	cac His	cca Pro	595
											155				160	
gcg Ala	gga Gly	ggg Gly	gca Ala	act Thr	gtt Val	gag Glu	gct Ala	gtt Val	cgg Arg	gtg Val	atg Met	gct Ala	tcg Ser	gct Ala	tct Ser	643
											175				180	
cgg Arg	gga Gly	agg Arg	gtt Val	gga Gly	att Ile	aag Lys	gct Ala	gcc Ala	ggt Gly	ggg Gly	gtg Val	aaa Lys	act Thr	tgg Trp	gaa Glu	691
											190				195	
gat Asp	gcg Ala	gtg Val	gcg Ala	ttt Phe	gtt Val	gaa Glu	gca Ala	ggg Gly	gct Ala	act Thr	cgc Arg	att Ile	gga Gly	act Thr	tct Ser	739
											205				210	
aat Asn	gcg Ala	gga Gly	gcc Ala	att Ile	ttg Leu	gag Glu	ggt Gly	gcg Ala	ccg Pro	gag Glu	tagttttggcg	ttctaatcgg				792
											220					
gac																795

&lt;210&gt; 398

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 398

Met Asp Met Thr Ile Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr  
1 5 10 15

Thr Leu Leu Gly Pro Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile  
20 25 30

Asp Ser Ala Ile Glu Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser  
35 40 45

Met Val Asn Leu Thr Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala  
50 55 60

Thr Val Ala Gly Phe Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala  
65 70 75 80

Ala Glu Ala Arg Leu Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val  
85 90 95

Val Leu Asp Ile Ala Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu  
100 105 110

Gln Glu Ile Val Ala Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu  
115 120 125

Lys Phe Ile Leu Glu Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr  
130 135 140

Ala Val Asn Ala Leu Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser  
145 150 155 160

Thr Gly Phe His Pro Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val  
165 170 175

Met Ala Ser Ala Ser Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly  
180 185 190

Val Lys Thr Trp Glu Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr  
195 200 205

Arg Ile Gly Thr Ser Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu  
210 215 220

&lt;210&gt; 399

&lt;211&gt; 684

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(661)

&lt;223&gt; RXA00195

&lt;400&gt; 399

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tcgcagtcacat catgcaggca taacctgaaa cccatccggtt tggattgccc caaatgggtg 60

tagtgggtgc gtttacccaa caagtgaag aatgggagtc gtg act aaa aag atc 115
                               Val Thr Lys Lys Ile
                               1                               5

ctt att ttg gga agc act ggt tcg att gga act cag gcg ctg gac gtt 163
Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr Gln Ala Leu Asp Val
                               10                               15                               20

att gct gat aat tca gac aag ttt gag gtg gtg ggt atc gct gcg ggc 211
Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val Gly Ile Ala Ala Gly
                               25                               30                               35

ggg tct cag cca gac ctc gtt att tcg cag gcg cag cag ttg ggg ctg 259
Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala Gln Gln Leu Gly Leu
                               40                               45                               50

gct gca gac aag gtt gcg gtt gct gat gca cag gct gcc gca gta att 307
Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln Ala Ala Ala Val Ile
                               55                               60                               65

tcg aag gct ctc ggc ggc gag atc atc tct gga acc gat gct gcg aag 355
Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly Thr Asp Ala Ala Lys
                               70                               75                               80                               85

att ctg gtg gaa acc aca aag gcc gac act gtg ctt aat gct ctg gtt 403
Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val Leu Asn Ala Leu Val
                               90                               95                               100

ggg tct ttg ggg ctt gcg gca acg ctg gcc act ctg gaa tct ggt gcg 451
Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr Leu Glu Ser Gly Ala
                               105                               110                               115

cat ctt gcc ttg gct aac aaa gaa tcg ctg gtt gcc ggt ggt gag ttt 499
His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val Ala Gly Gly Glu Phe
                               120                               125                               130

gtt acc tca aag gca aag ctg ggg cag atc att ccg gtc gat tcg gag 547
Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile Pro Val Asp Ser Glu
                               135                               140                               145

cac tct gcc atg gcg cag tgt ttg cgt tcg ggt act cgt gat gag gtt 595
His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly Thr Arg Asp Glu Val
                               150                               155                               160                               165

gcg cgg att gtg ctg aca gct tcg ggc gga cct ttc agg gct gga cca 643
Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro Phe Arg Ala Gly Pro
                               170                               175                               180

ggg aga aga tgt ggg agg tgactcccga gcaggcagca gcg 684
Gly Arg Arg Cys Gly Arg
                               185

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&lt;210&gt; 400

&lt;211&gt; 187

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 400

Val Thr Lys Lys Ile Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr  
 1 5 10 15

Gln Ala Leu Asp Val Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val  
 20 25 30

Gly Ile Ala Ala Gly Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala  
 35 40 45

Gln Gln Leu Gly Leu Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln  
 50 55 60

Ala Ala Ala Val Ile Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly  
 65 70 75 80

Thr Asp Ala Ala Lys Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val  
 85 90 95

Leu Asn Ala Leu Val Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr  
 100 105 110

Leu Glu Ser Gly Ala His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val  
 115 120 125

Ala Gly Gly Glu Phe Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile  
 130 135 140

Pro Val Asp Ser Glu His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly  
 145 150 155 160

Thr Arg Asp Glu Val Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro  
 165 170 175

Phe Arg Ala Gly Pro Gly Arg Arg Cys Gly Arg  
 180 185

&lt;210&gt; 401

&lt;211&gt; 738

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(715)

&lt;223&gt; RXA00196

&lt;400&gt; 401

ctgccatggc gcagtggttg cggtcgggta ctcgtgatga ggttgcgcg g attgtgctga 60

cagcttcggg cggacctttc agggctggac cagggagaag atg tgg gag gtg act 115  
 Met Trp Glu Val Thr  
 1 5

ccc gag cag gca gca gcg cac cca acg tgg gcg atg ggg cag atg aac 163  
 Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala Met Gly Gln Met Asn  
 10 15 20

acg ttg aac tcc gcc acc ctt att aat aaa ggc ctc gaa ctc atc gag 211  
 Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly Leu Glu Leu Ile Glu  
 25 30 35  
 gcg acc ctg ctg ttt gaa acg gat gcg gat ctc att gat gtg acg gtg 259  
 Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu Ile Asp Val Thr Val  
 40 45 50  
 cat ccg cag tcg atc atc cac tcc atg atc acg ttt acg gat ggt gcg 307  
 His Pro Gln Ser Ile Ile His Ser Met Ile Thr Phe Thr Asp Gly Ala  
 55 60 65  
 acc atc gcg cag gcg tcg cca cca tcg atg aaa ctg ccg atc gcg ttg 355  
 Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys Leu Pro Ile Ala Leu  
 70 75 80 85  
 gcg ctt gat tgg cca cat ccg gtg ccg aag gct cag ccg gcg ctg gat 403  
 Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala Gln Pro Ala Leu Asp  
 90 95 100  
 ttc acc gct gct cat acc tgg gct ttt gag ccg gtg gat gat gcc gca 451  
 Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro Val Asp Asp Ala Ala  
 105 110 115  
 ttc cct gcg gtg cag ctg gct agg cac gtc gca aag caa aaa ggc acg 499  
 Phe Pro Ala Val Gln Leu Ala Arg His Val Ala Lys Gln Lys Gly Thr  
 120 125 130  
 tac ccc gcg gtg tat aac gcc gcc aac gag gag gcg gct gag gcg ttt 547  
 Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu Ala Ala Glu Ala Phe  
 135 140 145  
 ttg cgc ggg cga atc aag ttt ccg cag atc gtg gac gtg gtg gac gag 595  
 Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val Asp Val Val Asp Glu  
 150 155 160 165  
 gtc ctc caa gga gct tct cag ttt gct ggt gta gca tca cac gtc gat 643  
 Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val Ala Ser His Val Asp  
 170 175 180  
 gat att ttg gca acc gaa tct gag gca cgc gcg cgt gcg aat gct ttg 691  
 Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala Arg Ala Asn Ala Leu  
 185 190 195  
 atc aac cgg ttg gca acc aac ttg taagctaagg agcttccgcc tcg 738  
 Ile Asn Arg Leu Ala Thr Asn Leu  
 200 205

&lt;210&gt; 402

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 402

Met Trp Glu Val Thr Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala  
 1 5 10 15

Met Gly Gln Met Asn Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly  
 20 25 30

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<210> 403
<211> 2031
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(2008)
<223> RXN01562
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<400> 403
gcaggtgcac atttgttttg tcacctgcac aaaagtgtcg ccagcccgat acttgtacaa 60

ccgtccgcat ccgagaagca aaggtgtctg actcgcgcc  atg gga att ctg aac    115
                                     Met Gly Ile Leu Asn
                                     1                               5

agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg    163
Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu
                10                                15                                20

gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca    211
Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala
                25                                30                                35

gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc    259

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Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr	
40 45 50	
atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt	307
Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe	
55 60 65	
gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct	355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala	
70 75 80 85	
aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc	403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr	
90 95 100	
tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg	451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser	
105 110 115	
gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat	499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp	
120 125 130	
ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta	547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu	
135 140 145	
act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa	595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys	
150 155 160 165	
gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct	643
Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser	
170 175 180	
cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag	691
Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln	
185 190 195	
cct ttc tat gat cgc ttc atg gaa aag ggc aag acg tcc ctg aaa tcc	739
Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys Thr Ser Leu Lys Ser	
200 205 210	
atg ggg tgg gta ggg gag cgt act ttt gaa gcg ctc cat gca ttt aaa	787
Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala Leu His Ala Phe Lys	
215 220 225	
gaa ggt gtg aag agc acc gtc att ccc acc gaa atg ttc cct gaa ctg	835
Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu Met Phe Pro Glu Leu	
230 235 240 245	
ggc atg aaa tac gtg ggt ccg gtt gat gga cat aac caa aaa gct gtc	883
Gly Met Lys Tyr Val Gly Pro Val Asp Gly His Asn Gln Lys Ala Val	
250 255 260	
gac aat gcg ctg aaa tac gct cat gat tat gat ggc ccc atc atc gtg	931
Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp Gly Pro Ile Ile Val	
265 270 275	
cac atg gtc acc gaa aag ggt cgt ggt tac gcg cct gct gag cag gat	979
His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala Pro Ala Glu Gln Asp	

280	285	290	
ttg gac gaa ttg atg cac tcc acg ggc gtc atc gat ccg ctc aca gga Leu Asp Glu Leu Met His Ser Thr Gly Val Ile Asp Pro Leu Thr Gly 295 300 305			1027
gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg ttc agc gat Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val Phe Ser Asp 310 315 320 325			1075
gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt gcc atc acc Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val Ala Ile Thr 330 335 340			1123
gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa gcc aat ttc Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu Ala Asn Phe 345 350 355			1171
ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac gcg gta act Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His Ala Val Thr 360 365 370			1219
tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg gtg gct att Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val Val Ala Ile 375 380 385			1267
tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc atg gat gtg Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu Met Asp Val 390 395 400 405			1315
ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc tca ggt gtc Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg Ser Gly Val 410 415 420			1363
acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat atg gcg ctg Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp Met Ala Leu 425 430 435			1411
acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt gat gag gat Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg Asp Glu Asp 440 445 450			1459
tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat gat ggc ccc Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp Asp Gly Pro 455 460 465			1507
aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca att gtt gct Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro Ile Val Ala 470 475 480 485			1555
atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat gaa gac gcc Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr Glu Asp Ala 490 495 500			1603
act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc atc att gcg Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu Ile Ile Ala 505 510 515			1651
gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc agg att aaa Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser Arg Ile Lys 520 525 530			1699



cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg att gtc ccc 1747  
 Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp Ile Val Pro  
 535 540 545  
 atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac ctc gtg atc 1795  
 Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp Leu Val Ile  
 550 555 560 565  
 acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc ttg ctc tct 1843  
 Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser Leu Leu Ser  
 570 575 580  
 gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga caa atc gcc 1891  
 Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg Gln Ile Ala  
 585 590 595  
 gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa gtg ctc gcc 1939  
 Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu Val Leu Ala  
 600 605 610  
 gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt gtt gga tgg 1987  
 Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val Val Gly Trp  
 615 620 625  
 ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg ccg 2031  
 Leu Asp Ser Leu Phe Gly Glu  
 630 635

&lt;210&gt; 404

&lt;211&gt; 636

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 404

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Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu  
 20 25 30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly  
 35 40 45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln  
 50 55 60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile  
 65 70 75 80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly  
 85 90 95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu  
 100 105 110

Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys  
 115 120 125

Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val

130					135					140						
Gly	Asp	Gly	Ala	Leu	Thr	Gly	Gly	Met	Cys	Trp	Glu	Ala	Leu	Asn	Asn	
145					150					155					160	
Ile	Ala	Ala	Gly	Lys	Asp	Arg	Lys	Val	Val	Val	Val	Val	Val	Asn	Asp	Asn
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Gly	Arg	Ser	Tyr	Ser	Pro	Thr	Ile	Gly	Gly	Phe	Ala	Glu	Asn	Leu	Ala	
			180					185					190			
Gly	Leu	Arg	Met	Gln	Pro	Phe	Tyr	Asp	Arg	Phe	Met	Glu	Lys	Gly	Lys	
			195				200					205				
Thr	Ser	Leu	Lys	Ser	Met	Gly	Trp	Val	Gly	Glu	Arg	Thr	Phe	Glu	Ala	
						215					220					
Leu	His	Ala	Phe	Lys	Glu	Gly	Val	Lys	Ser	Thr	Val	Ile	Pro	Thr	Glu	
225					230					235					240	
Met	Phe	Pro	Glu	Leu	Gly	Met	Lys	Tyr	Val	Gly	Pro	Val	Asp	Gly	His	
				245					250					255		
Asn	Gln	Lys	Ala	Val	Asp	Asn	Ala	Leu	Lys	Tyr	Ala	His	Asp	Tyr	Asp	
			260					265					270			
Gly	Pro	Ile	Ile	Val	His	Met	Val	Thr	Glu	Lys	Gly	Arg	Gly	Tyr	Ala	
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Pro	Ala	Glu	Gln	Asp	Leu	Asp	Glu	Leu	Met	His	Ser	Thr	Gly	Val	Ile	
						295					300					
Asp	Pro	Leu	Thr	Gly	Ala	Pro	Lys	Ser	Ala	Ser	Lys	Pro	Gly	Trp	Thr	
305					310					315					320	
Ser	Val	Phe	Ser	Asp	Glu	Leu	Val	Lys	Ile	Gly	Ala	Gln	Asn	Glu	Asn	
				325					330					335		
Val	Val	Ala	Ile	Thr	Ala	Ala	Met	Ala	Gly	Pro	Thr	Gly	Leu	Ser	Lys	
			340					345					350			
Phe	Glu	Ala	Asn	Phe	Pro	Asn	Arg	Phe	Phe	Asp	Val	Gly	Ile	Ala	Glu	
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Gln	His	Ala	Val	Thr	Ser	Ala	Ala	Gly	Leu	Ala	Leu	Gly	Gly	Lys	His	
			370			375					380					
Pro	Val	Val	Ala	Ile	Tyr	Ser	Thr	Phe	Leu	Asn	Arg	Ala	Phe	Asp	Gln	
385					390					395					400	
Leu	Leu	Met	Asp	Val	Gly	Met	Leu	Asn	Gln	Pro	Val	Thr	Leu	Val	Leu	
				405					410					415		
Asp	Arg	Ser	Gly	Val	Thr	Gly	Ser	Asp	Gly	Ala	Ser	His	Asn	Gly	Val	
			420					425					430			
Trp	Asp	Met	Ala	Leu	Thr	Ser	Ile	Val	Pro	Gly	Val	Gln	Val	Ala	Ala	
			435				440					445				
Pro	Arg	Asp	Glu	Asp	Ser	Leu	Arg	Glu	Leu	Leu	Asn	Glu	Ala	Ile	Ser	
			450			455					460					

Ile Asp Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro  
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 Thr Pro Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu  
 485 490 495  
 Ala Tyr Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser  
 500 505 510  
 Val Leu Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val  
 515 520 525  
 Ala Ser Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro  
 530 535 540  
 Arg Trp Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp  
 545 550 555 560  
 His Asp Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val  
 565 570 575  
 Gly Ser Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro  
 580 585 590  
 Arg Arg Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg  
 595 600 605  
 Asn Glu Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr  
 610 615 620  
 Thr Val Val Gly Trp Leu Asp Ser Leu Phe Gly Glu  
 625 630 635

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> FRXA01562

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 ctc aca gga gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg 96  
 Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val  
 20 25 30  
 ttc agc gat gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt 144  
 Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val  
 35 40 45  
 gcc atc acc gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa 192  
 Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu  
 50 55 60

gcc aat ttc ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac	240
Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His	
65 70 75 80	
gcg gta act tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg	288
Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val	
85 90 95	
gtg gct att tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc	336
Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu	
100 105 110	
atg gat gtg ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc	384
Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg	
115 120 125	
tca ggt gtc acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat	432
Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp	
130 135 140	
atg gcg ctg acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt	480
Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg	
145 150 155 160	
gat gag gat tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat	528
Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp	
165 170 175	
gat ggc ccc aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca	576
Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro	
180 185 190	
att gtt gct atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat	624
Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr	
195 200 205	
gaa gac gcc act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc	672
Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu	
210 215 220	
atc att gcg gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc	720
Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser	
225 230 235 240	
agg att aaa cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg	768
Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp	
245 250 255	
att gtc ccc atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac	816
Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp	
260 265 270	
ctc gtg atc acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc	864
Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser	
275 280 285	
ttg ctc tct gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga	912
Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg	
290 295 300	

caa atc gcc gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa 960  
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu  
 305 310 315 320  
 gtg ctc gcc gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt 1008  
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val  
 325 330 335  
 gtt gga tgg ctg gat tcc ctg ttc ggg gaa taaaaccctg cttatcgacg 1058  
 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu  
 340 345  
 ccg 1061

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 <211> 346  
 <212> PRT  
 <213> Corynebacterium glutamicum

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 Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val  
 35 40 45  
 Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu  
 50 55 60  
 Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His  
 65 70 75 80  
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val  
 85 90 95  
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu  
 100 105 110  
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg  
 115 120 125  
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp  
 130 135 140  
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg  
 145 150 155 160  
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp  
 165 170 175  
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro  
 180 185 190  
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr  
 195 200 205  
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu

210	215	220
Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser		
225	230	235 240
Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp		
	245	250 255
Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp		
	260	265 270
Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser		
	275	280 285
Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg		
	290	295 300
Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu		
305	310	315 320
Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val		
	325	330 335
Val Gly Trp Leu Asp Ser Leu Phe Gly Glu		
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 <212> DNA  
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<220>  
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 <222> (101)..(703)  
 <223> FRXA01705

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 ccgtccgcat ccgagaagca aaggtgtctg actcgcgcca atg gga att ctg aac 115  
 Met Gly Ile Leu Asn  
 1 5  
 agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163  
 Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu  
 10 15 20  
 gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211  
 Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala  
 25 30 35  
 gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259  
 Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr  
 40 45 50  
 atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt 307  
 Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe  
 55 60 65  
 gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355

Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala  
 70 75 80 85  
 aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc 403  
 Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr  
 90 95 100  
 tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg 451  
 Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser  
 105 110 115  
 gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499  
 Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp  
 120 125 130  
 ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547  
 Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu  
 135 140 145  
 act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa 595  
 Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys  
 150 155 160 165  
 gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643  
 Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser  
 170 175 180  
 cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag 691  
 Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln  
 185 190 195  
 cct ttc tat gat 703  
 Pro Phe Tyr Asp  
 200

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly  
 35 40 45  
 Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln  
 50 55 60  
 Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile  
 65 70 75 80  
 Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly  
 85 90 95  
 Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu

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Ser	Ser	His	Ala	Ser	Ala	Ala	Leu	Ser	Tyr	Ala	Asp	Gly	Leu	Ser	Lys
		115					120					125			
Ala	Lys	Gln	Leu	Asp	Gly	Asp	Thr	Thr	His	Ser	Val	Val	Ala	Val	Val
	130					135					140				
Gly	Asp	Gly	Ala	Leu	Thr	Gly	Gly	Met	Cys	Trp	Glu	Ala	Leu	Asn	Asn
145					150				155					160	
Ile	Ala	Ala	Gly	Lys	Asp	Arg	Lys	Val	Val	Val	Val	Val	Asn	Asp	Asn
				165				170					175		
Gly	Arg	Ser	Tyr	Ser	Pro	Thr	Ile	Gly	Gly	Phe	Ala	Glu	Asn	Leu	Ala
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Gly	Leu	Arg	Met	Gln	Pro	Phe	Tyr	Asp							
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 <223> RXN00879

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 Val Thr Ala Arg 5  
 1  
 ttt ttg aat gaa ctc gcc gat ctc tac ggc gta gca act tcc tac act 163  
 Phe Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr 20  
 10 15  
 gat tac aaa ggt gcc cat att gag gtc agc gat gac aca tta gtg aaa 211  
 Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys 35  
 25 30  
 atc ctg cgt gct ctg ggt gtg aat tta gat aca agc aac ctc ccc aac 259  
 Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn 50  
 40 45  
 gat gac gct atc caa cgc caa att gcc ctc ttc cat gat cga gag ttc 307  
 Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe 65  
 55 60  
 act cgc cca ctg cct cca tcg gtg gtt gca gtt gaa ggt gat gaa cta 355  
 Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu 85  
 70 75 80  
 gtt ttc ccg gtg cat gtg cac gac ggt tcc cct gca gat gtc cac atc 403  
 Val Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile 100  
 90 95 100



gaa ttg gaa gac ggc acg cag cgg gat gtt tct cag gtg gaa aac tgg	451
Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp	
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Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe	
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Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys	
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tcc aat gaa cgc tca gct gag tgc ggt ttg atc atc acc ccg gct cgt	595
Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg	
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ctg tct act gct gat aag tat ctt gat tcc cct cgc agt ggt gtc atg	643
Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met	
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gcg cag atc tac tct gtg cgt tcc acg ttg tgc tgg ggc atg ggt gat	691
Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp	
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Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala	
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Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro	
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act gag gac tct cct tat ctg ccc aca acc agg cgc ttt atc aac ccg	835
Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro	
230 235 240 245	
atc tac att cgg gta gaa gat att ccg gag ttt aat cag ctt gag att	883
Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile	
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Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg	
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Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys	
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Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile	
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Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser	
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Val	His	Gly	Thr	Glu	Pro	Asp	Arg	Asp	Glu	Leu	Thr	Met	Phe	Tyr	Met	
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Trp	Leu	Gln	Trp	Leu	Cys	Asp	Glu	Gln	Leu	Ala	Ala	Ala	Gln	Lys	Arg	
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gct	gtc	gat	gcc	gga	atg	tcg	atc	ggc	atc	atg	gca	gac	ctg	gca	gtt	1267
Ala	Val	Asp	Ala	Gly	Met	Ser	Ile	Gly	Ile	Met	Ala	Asp	Leu	Ala	Val	
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ggc	gtg	cat	cca	ggc	ggc	gct	gat	gcc	cag	aac	ctc	agc	cac	gta	ctt	1315
Gly	Val	His	Pro	Gly	Gly	Ala	Asp	Ala	Gln	Asn	Leu	Ser	His	Val	Leu	
390					395					400					405	
gct	ccg	gat	gcg	tca	gtg	ggc	gcc	cca	cca	gat	gga	tac	aac	cag	cag	1363
Ala	Pro	Asp	Ala	Ser	Val	Gly	Ala	Pro	Pro	Asp	Gly	Tyr	Asn	Gln	Gln	
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ggc	caa	gac	tgg	tcc	cag	cca	cca	tgg	cat	cca	gtg	cgt	ctt	gca	gag	1411
Gly	Gln	Asp	Trp	Ser	Gln	Pro	Pro	Trp	His	Pro	Val	Arg	Leu	Ala	Glu	
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Glu	Gly	Tyr	Ile	Pro	Trp	Arg	Asn	Leu	Leu	Arg	Thr	Val	Leu	Arg	His	
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Ser	Gly	Gly	Ile	Arg	Val	Asp	His	Val	Leu	Gly	Leu	Phe	Arg	Leu	Phe	
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gtc	atg	cca	cgc	atg	caa	tcc	cct	gct	acg	ggc	acc	tat	atc	cgc	ttc	1555
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Gly	Ala	Val	Val	Ile	Gly	Glu	Asp	Leu	Gly	Thr	Phe	Glu	Pro	Trp	Val	
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Gln	Asp	Ala	Leu	Ala	Gln	Arg	Gly	Ile	Met	Gly	Thr	Ser	Ile	Leu	Trp	
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Phe	Glu	His	Ser	Pro	Ser	Gln	Pro	Gly	Pro	Arg	Arg	Gln	Glu	Glu	Tyr	
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cgt	ccg	ctg	gcc	ttg	acc	act	gtg	acc	act	cat	gat	ctc	cct	ccg	act	1795
Arg	Pro	Leu	Ala	Leu	Thr	Thr	Val	Thr	Thr	His	Asp	Leu	Pro	Pro	Thr	
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gct	ggt	tat	ttg	gag	ggc	gag	cac	att	gct	ctt	cgt	gag	cga	ttg	ggg	1843
Ala	Gly	Tyr	Leu	Glu	Gly	Glu	His	Ile	Ala	Leu	Arg	Glu	Arg	Leu	Gly	
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gtg	ctc	aac	act	gat	cct	gct	gca	gaa	ctc	gct	gag	gat	ctg	cag	tgg	1891

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Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala  
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cgg gaa tac gtg gga ctc gaa cgc gat cag cgc ggt gag ttg gct gag 1987  
Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu  
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ctg ttg gaa ggc ctg cac act ttc gtt gcg aaa acc cct tca gca ctg 2035  
Leu Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu  
630 635 640 645

acc tgt gtc tgc ttg gta gac atg gtc ggt gaa aag cgg gca cag aat 2083  
Thr Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn  
650 655 660

cag ccg ggc aca acg agg gat atg tat ccc aac tgg tgt atc cca ctg 2131  
Gln Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu  
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Cys Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn  
680 685 690

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Glu Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp  
695 700 705

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&lt;211&gt; 706

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 410

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Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe  
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His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val  
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Glu Gly Asp Glu Leu Val Phe Pro Val His Val His Asp Gly Ser Pro  
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Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser  
100 105 110

Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp  
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 Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His  
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 Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile  
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 Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro  
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 Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser  
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 Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val  
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 Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg  
 225 230 235 240  
 Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe  
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 Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro  
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 Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr  
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 Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu  
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 Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala  
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 Ala Asp Leu Ala Val Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn  
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 Leu Ser His Val Leu Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp  
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 Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro  
 420 425 430  
 Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg

435		440		445
Thr Val Leu Arg His Ser Gly	Gly Ile Arg Val Asp His Val Leu Gly			
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Leu Phe Arg Leu Phe Val Met Pro Arg Met Gln Ser Pro Ala Thr Gly				
465	470	475		480
Thr Tyr Ile Arg Phe Asp His Asn Ala Leu Val Gly Ile Leu Ala Leu				
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Glu Ala Glu Leu Ala Gly Ala Val Val Ile Gly Glu Asp Leu Gly Thr				
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Phe Glu Pro Trp Val Gln Asp Ala Leu Ala Gln Arg Gly Ile Met Gly				
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Thr Ser Ile Leu Trp Phe Glu His Ser Pro Ser Gln Pro Gly Pro Arg				
	530	535		540
Arg Gln Glu Glu Tyr Arg Pro Leu Ala Leu Thr Thr Val Thr Thr His				
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Asp Leu Pro Pro Thr Ala Gly Tyr Leu Glu Gly Glu His Ile Ala Leu				
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Arg Glu Arg Leu Gly Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala				
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Glu Asp Leu Gln Trp Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala				
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Asn Ala Leu Pro Ala Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg				
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Gly Glu Leu Ala Glu Leu Leu Glu Gly Leu His Thr Phe Val Ala Lys				
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Thr Pro Ser Ala Leu Thr Cys Val Cys Leu Val Asp Met Val Gly Glu				
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Lys Arg Ala Gln Asn Gln Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn				
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Trp Cys Ile Pro Leu Cys Asp Ser Glu Gly Asn Ser Val Leu Ile Glu				
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Ser Leu Arg Glu Asn Glu Leu Tyr His Arg Val Ala Lys Ala Ser Lys				
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Arg Asp				
705				

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&lt;222&gt; (101)..(2200)

&lt;223&gt; FRXA00879

&lt;400&gt; 411

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gat ctc tac ggc gta gca act tcc tac act gat tac aaa ggt gcc cat 163
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Ile Glu Val Ser Asp Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly
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gtg aat tta gat aca agc aac ctc ccc aac gat gac gct atc caa cgc 259
Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg
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caa att gcc ctc ttc cat gat cga gag ttc act cgc cca ctg cct cca 307
Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro
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tcg gtg gtt gca gtt gaa ggt gat gaa cta gtt ttc ccg gtg cat gtg 355
Ser Val Val Ala Val Glu Gly Asp Glu Leu Val Phe Pro Val His Val
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cac gac ggt tcc cct gca gat gtc cac atc gaa ttg gaa gac ggc acg 403
His Asp Gly Ser Pro Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr
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cag cgg gat gtt tct cag gtg gaa aac tgg aca gcg cca cgg gaa att 451
Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile
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gat ggg att agg tgg ggc gag gca tcg ttt aag att cct ggt gat ctc 499
Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu
                                   120                               125                               130

ccc ttg ggt tgg cac aag ctt cac ctt aaa tcc aat gaa cgc tca gct 547
Pro Leu Gly Trp His Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala
                                   135                               140                               145

gag tgc ggt ttg atc atc acc ccg gct cgt ctg tct act gct gat aag 595
Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys
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tat ctt gat tcc cct cgc agt ggt gtc atg gcg cag atc tac tct gtg 643
Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val
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cgt tcc acg ttg tcg tgg ggc atg ggt gat ttc aat gat tta gga aac 691
Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn
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ttg gca agt gtg gtt gcc cag gat gga gca gac ttc ctg ctc atc aac 739
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Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr	
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Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser	
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Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met	
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Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly Val His Pro Gly Gly	
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ggc gcc cca cca gat gga tac aac cag cag ggc caa gac tgg tcc cag	1363
Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln	
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Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser Gly Gly Ile Arg Val	
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gaa	gat	ctg	gga	acg	ttt	gag	cct	tgg	gta	caa	gat	gca	ttg	gct	cag	1651
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Val	Ala	Ala	Ser	Ala	Asn	Ala	Leu	Pro	Ala	Arg	Glu	Tyr	Val	Gly	Leu	
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Glu	Arg	Asp	Gln	Arg	Gly	Glu	Leu	Ala	Glu	Leu	Leu	Glu	Gly	Leu	His	
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Thr	Phe	Val	Ala	Lys	Thr	Pro	Ser	Ala	Leu	Thr	Cys	Val	Cys	Leu	Val	
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gac	atg	gtc	ggt	gaa	aag	cgg	gca	cag	aat	cag	ccg	ggc	aca	acg	agg	2083
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gat	atg	tat	ccc	aac	tgg	tgt	atc	cca	ctg	tgt	gac	agc	gaa	ggc	aac	2131
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Ser	Val	Leu	Ile	Glu	Ser	Leu	Arg	Glu	Asn	Glu	Leu	Tyr	His	Arg	Val	
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Ala Lys Ala Ser Lys Arg Asp  
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Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp  
35 40 45  
Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr  
50 55 60  
Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu Val  
65 70 75 80  
Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile Glu  
85 90 95  
Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr  
100 105 110  
Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys  
115 120 125  
Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys Ser  
130 135 140  
Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu  
145 150 155 160  
Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala  
165 170 175  
Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe  
180 185 190  
Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp  
195 200 205  
Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr  
210 215 220  
Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile  
225 230 235 240  
Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp  
245 250 255  
Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn  
260 265 270

Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu  
 275 280 285  
 Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu  
 290 295 300  
 Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp  
 305 310 315 320  
 Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val  
 325 330 335  
 His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp  
 340 345 350  
 Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala  
 355 360 365  
 Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly  
 370 375 380  
 Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala  
 385 390 395 400  
 Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly  
 405 410 415  
 Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu  
 420 425 430  
 Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser  
 435 440 445  
 Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val  
 450 455 460  
 Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp  
 465 470 475 480  
 His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly  
 485 490 495  
 Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln  
 500 505 510  
 Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe  
 515 520 525  
 Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg  
 530 535 540  
 Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala  
 545 550 555 560  
 Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val  
 565 570 575  
 Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln  
 580 585 590  
 Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg

595	600	605
Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu		
610	615	620
Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr		
625	630	635
Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln		
645	650	655
Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys		
660	665	670
Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu		
675	680	685
Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp		
690	695	700

<210> 413  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1264)  
 <223> RXN00043

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 Met Ala Glu Val Val  
 1 5  
 cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga 163  
 His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg  
 10 15 20  
 att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac 211  
 Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn  
 25 30 35  
 ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga 259  
 Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly  
 40 45 50  
 ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat 307  
 Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His  
 55 60 65  
 aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag 355  
 Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln  
 70 75 80 85  
 gcg agg aat gcc gcg cag tat cac gcg gaa cat ggc acg acc gtg atg 403  
 Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met  
 90 95 100

ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg	451
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val	
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gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac	499
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His	
120 125 130	
ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg	547
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro	
135 140 145	
gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat	595
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His	
150 155 160 165	
gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac	643
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp	
170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala	
185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile	
200 205 210	
gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe	
215 220 225	
aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct	835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala	
230 235 240 245	
ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc	883
Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala	
250 255 260	
gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac	931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn	
265 270 275	
aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac	979
Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp	
280 285 290	
ggg gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc	1027
Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val	
295 300 305	
gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta	1075
Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu	
310 315 320 325	
gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac	1123
Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp	
330 335 340	

gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc 1171  
 Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser  
                   345                  350                  355

gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac 1219  
 Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp  
                   360                  365                  370

tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att 1264  
 Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile  
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taaatacgag caaaacttttc ctg 1287

<210> 414  
 <211> 388  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 414  
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Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe  
                   20                  25                  30

Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala  
                   35                  40                  45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser  
                   50                  55                  60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr  
   65                  70                  75                  80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His  
                   85                  90                  95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala  
                   100                  105                  110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu  
                   115                  120                  125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys  
                   130                  135                  140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu  
   145                  150                  155                  160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val  
                   165                  170                  175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala  
                   180                  185                  190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr  
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Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr

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<210> 415
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1264)
<223> FRXA00043
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gtcctatgct tgctggaagg aagcaaataa cctcagaaa atg gca gaa gtg gtg      115
                               Met Ala Glu Val Val
                               1                      5

cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga      163
His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg
                        10                      15                      20

att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac      211
Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn
                25                      30                      35
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ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga	259
Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly	
40 45 50	
ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat	307
Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His	
55 60 65	
aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag	355
Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln	
70 75 80 85	
gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg	403
Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met	
90 95 100	
ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg	451
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val	
105 110 115	
gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac	499
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His	
120 125 130	
ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg	547
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro	
135 140 145	
gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat	595
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His	
150 155 160 165	
gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac	643
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp	
170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala	
185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile	
200 205 210	
gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe	
215 220 225	
aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct	835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala	
230 235 240 245	
ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc	883
Leu Leu Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala	
250 255 260	
gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac	931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn	
265 270 275	
aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac	979

Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp  
 280 285 290  
 ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc 1027  
 Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val  
 295 300 305  
 gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta 1075  
 Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu  
 310 315 320 325  
 gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac 1123  
 Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp  
 330 335 340  
 gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc 1171  
 Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser  
 345 350 355  
 gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac 1219  
 Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp  
 360 365 370  
 tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att 1264  
 Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile  
 375 380 385  
 taaatacgag caaaacttttc ctg 1287

&lt;210&gt; 416

&lt;211&gt; 388

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 416

Met Ala Glu Val Val His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys  
 1 5 10 15

Lys Ile Glu Gly Arg Ile Val Thr Pro His Gly Val Ile Asp Gly Phe  
 20 25 30

Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala  
 35 40 45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser  
 50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr  
 65 70 75 80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His  
 85 90 95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala  
 100 105 110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu  
 115 120 125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys



130	135	140
Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu 145 150 155 160		
Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val 165 170 175		
Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala 180 185 190		
His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr 195 200 205		
Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr 210 215 220		
Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro 225 230 235 240		
Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr 245 250 255		
Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp 260 265 270		
Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala 275 280 285		
Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr 290 295 300		
Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly 305 310 315 320		
Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly 325 330 335		
Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys 340 345 350		
Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn 355 360 365		
Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp 370 375 380		
His Gln Val Ile 385		

<210> 417  
 <211> 1584  
 <212> DNA  
 <213> Corynebacterium glutamicum  
  
 <220>  
 <221> CDS  
 <222> (101)..(1561)  
 <223> RXN01752

&lt;400&gt; 417

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ttggccgtca gatcgtggca gaacaacagg tggggagggtc atg atg gaa caa gat 115
                                         Met Met Glu Gln Asp
                                         1 5

ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa 163
Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys
                        10 15 20

aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg 211
Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro
                        25 30 35

cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc 259
Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe
                        40 45 50

att gct gtg gtg gtg ggc ttt atc ttg atg ctc att ttt gct cgg caa 307
Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln
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gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att 355
Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile
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aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa 403
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu
                        90 95 100

tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac 451
Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp
                        105 110 115

aag ctg aaa acc tac acg gtg ttg gtg ccc gcc tat ggc gaa cct gag 499
Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala Tyr Gly Glu Pro Glu
                        120 125 130

gtg att gcg cag ctg ctg gca tcc atg cac gct ttt gat tac ccc aag 547
Val Ile Ala Gln Leu Leu Ala Ser Met His Ala Phe Asp Tyr Pro Lys
                        135 140 145

cat ctt ctg cag gta ttg ctc atg ttg gag gaa gat gat ctg ccc acg 595
His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp Asp Leu Pro Thr
                        150 155 160 165

atc gcc gcg gca gag gca gcg gga gtg gat cag gtg gca acg atc att 643
Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln Val Ala Thr Ile Ile
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aag gtg ccg cca gcg cag ccc cgc acc aag ccg aag gcc tgt aac tat 691
Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro Lys Ala Cys Asn Tyr
                        185 190 195

gga ttg cac ttt gcc acg ggg gaa att gtc acg atc ttt gac gcg gaa 739
Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr Ile Phe Asp Ala Glu
                        200 205 210

gac atg cca gat ccc ctc caa ctg cgt cgc gtg gtg gtg gca ttt gaa 787
Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val Val Val Ala Phe Glu

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215	220	225	
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aac gcc agg cag aat ctg cta act gcg tgg ttc acc att gaa tat gac Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe Thr Ile Glu Tyr Asp 250 255 260			883
gtg tgg ttt aac ttc ctg ctg cca ggc gtc atg cgc atg aac gca cct Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met Arg Met Asn Ala Pro 265 270 275			931
gtc cca ttg ggc ggt acc tcc aac cat ctg ctc acg ggt gtc ctg aaa Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys 280 285 290			979
gat ctc ggc gcg tgg gat cct ttc aat gtc aca gaa aat gcc gac ctc Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr Glu Asn Ala Asp Leu 295 300 305			1027
ggc gta ccc atc gcg gca aaa gga tat tcc acc gcg gtg ttg gat tcg Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser 310 315 320 325			1075
gtg acg tgg gag gaa gca aac tcc gac acc atc aac tgg ttg cgc cag Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln 330 335 340			1123
cgt tct cgc tgg tac aag ggc tat ctg caa aca tgg ctt gtg tat atg Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met 345 350 355			1171
cgc agg cca aag tgg tta gtc caa gag ctt ggc atc att cct gct gtg Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val 360 365 370			1219
cgt ttt acc ttc ctc atg gca ggc acc ccg atc att gcg gtg ctc aat Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn 375 380 385			1267
ctg ctc ttt tgg tac ttg tcg ctc acg tgg att ctg ggc cag ccc ggc Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly 390 395 400 405			1315
acc att gag cag atg ttc cca cct gcg gtg tac tac cca gcg ttg gtg Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val 410 415 420			1363
tgt ttg gtg gtg gcc aat gct gcg acc atc ttt atg aat ctc att ggc Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly 425 430 435			1411
tgc cgg gaa ggc cgc gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe 440 445 450			1459
ccg ctg tat tgg ctg ctc atg agc att gca gcg ttg aaa ggc acg tgg Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp 455 460 465			1507

caa ttg atc acg cga cca tcc tat tgg gag aaa act gcc cac gga ttg 1555  
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gag gcg taagcgggtgc ccatcgtaa acc 1584  
 Glu Ala

<210> 418

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

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Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu  
 20 25 30

Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly  
 35 40 45

Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu  
 50 55 60

Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr  
 65 70 75 80

Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg  
 85 90 95

Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu  
 100 105 110

Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala  
 115 120 125

Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala  
 130 135 140

Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu  
 145 150 155 160

Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln  
 165 170 175

Val Ala Thr Ile Ile Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro  
 180 185 190

Lys Ala Cys Asn Tyr Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr  
 195 200 205

Ile Phe Asp Ala Glu Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val  
 210 215 220

Val Val Ala Phe Glu Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser  
 225 230 235 240

Arg Leu Ser Tyr Arg Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe  
 245 250 255  
 Thr Ile Glu Tyr Asp Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met  
 260 265 270  
 Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu  
 275 280 285  
 Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr  
 290 295 300  
 Glu Asn Ala Asp Leu Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr  
 305 310 315 320  
 Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile  
 325 330 335  
 Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr  
 340 345 350  
 Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly  
 355 360 365  
 Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile  
 370 375 380  
 Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile  
 385 390 395 400  
 Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr  
 405 410 415  
 Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe  
 420 425 430  
 Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile  
 435 440 445  
 Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala  
 450 455 460  
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 465 470 475 480  
 Thr Ala His Gly Leu Glu Ala  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> FRXA01839

<400> 419  
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acc tcc aac cat ctg ctc acg ggt gtc ctg aaa gat ctc ggc gcg tgg 99												
Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp												
	15				20					25		
gat cct ttc aat gtc aca gaa gat gcg gac ctc ggc gta cgc atc gcg 147												
Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala												
	30				35				40			
gca aag gga tat tcc acc gcg gtg ttg gat tcg gtg acg tgg gag gaa 195												
Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu												
	45				50				55			
gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac 243												
Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr												
	60				65			70				75
aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg 291												
Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp												
			80					85				90
tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc 339												
Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu												
			95					100				105
atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac 387												
Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr												
	110						115			120		
ttg tcg ctc acg tgg att ctg ggc cag ccc ggc acc att gag cag atg 435												
Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met												
	125					130			135			
ttc cca cct gcg gtg tac tac cca gcg ttg gtg tgt ttg gtg gtg gcc 483												
Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala												
	140				145			150				155
aat gct gcg acc atc ttt atg aat ctc att ggc tgc cgg gaa ggc cgc 531												
Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg												
			160				165			170		
gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc ccg ctg tat tgg ctg 579												
Asp Pro Leu Leu Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu												
			175				180			185		
ctc atg agc att gca gcg ttg aaa ggc acg tgg caa ttg atc acg cga 627												
Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg												
	190					195			200			
cca tcc tat tgg gag aaa act gcc cac gga ttg gag gcg taagcgggtgc 676												
Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu Glu Ala												
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ccatcgtcaa acc 689												

&lt;210&gt; 420

&lt;211&gt; 216

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 420

Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu  
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Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val  
20 25 30

Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala Ala Lys Gly Tyr Ser  
35 40 45

Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr  
50 55 60

Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln  
65 70 75 80

Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu  
85 90 95

Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro  
100 105 110

Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp  
115 120 125

Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val  
130 135 140

Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile  
145 150 155 160

Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu  
165 170 175

Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala  
180 185 190

Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu  
195 200 205

Lys Thr Ala His Gly Leu Glu Ala  
210 215

<210> 421

<211> 1050

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1027)

<223> RXA01859

<400> 421

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ctcgagacga accaaaccgc tacctggggg taggaagaat atg aaa aag aag agc 115  
Met Lys Lys Lys Ser

															1	5	
ttt	cca	atc	gca	aga	gtc	atc	ggc	atc	ggc	gtc	ctt	ggc	atc	gcc	ggg	163	
Phe	Pro	Ile	Ala	Arg	Val	Ile	Gly	Ile	Gly	Val	Leu	Gly	Ile	Ala	Gly		
				10					15					20			
atg	gga	ata	ttg	ttg	cta	tgg	ctt	gca	gtt	acc	ctg	tct	gat	cca	gca	211	
Met	Gly	Ile	Leu	Leu	Leu	Trp	Leu	Ala	Val	Thr	Leu	Ser	Asp	Pro	Ala		
				25					30					35			
tca	ccg	ggc	gcc	aaa	gaa	acc	gaa	gtc	ttt	gat	agg	tgg	aaa	gtg	ctc	259	
Ser	Pro	Gly	Ala	Lys	Glu	Thr	Glu	Val	Phe	Asp	Arg	Trp	Lys	Val	Leu		
				40					45					50			
ttt	gat	gac	tat	att	cca	cca	gtc	agg	gta	ttg	gtt	gct	gcg	att	atc	307	
Phe	Asp	Asp	Tyr	Ile	Pro	Pro	Val	Arg	Val	Leu	Val	Ala	Ala	Ile	Ile		
				55					60					65			
gtt	gca	tta	att	ttc	gtc	ttt	atc	gct	gcc	aca	gtg	gaa	cga	acc	gta	355	
Val	Ala	Leu	Ile	Phe	Val	Phe	Ile	Ala	Ala	Thr	Val	Glu	Arg	Thr	Val		
				70					75					80			
acc	aac	cgc	tac	cga	agc	tcc	gta	gac	ggc	gaa	aga	gtg	cca	tta	gcg	403	
Thr	Asn	Arg	Tyr	Arg	Ser	Ser	Val	Asp	Gly	Glu	Arg	Val	Pro	Leu	Ala		
				90					95					100			
ccg	aag	att	gtg	atg	gca	gaa	acc	cga	ggg	gta	ttt	cat	gga	ccg	att	451	
Pro	Lys	Ile	Val	Met	Ala	Glu	Thr	Arg	Gly	Val	Phe	His	Gly	Pro	Ile		
				105					110					115			
acc	att	aac	gtg	ctc	gtg	cca	gca	cac	aat	gag	gcg	gaa	aga	att	act	499	
Thr	Ile	Asn	Val	Leu	Val	Pro	Ala	His	Asn	Glu	Ala	Glu	Arg	Ile	Thr		
				120					125					130			
gga	aca	att	cag	gca	ttg	aaa	tca	caa	cat	gag	cct	cca	gaa	cgc	atc	547	
Gly	Thr	Ile	Gln	Ala	Leu	Lys	Ser	Gln	His	Glu	Pro	Pro	Glu	Arg	Ile		
				135					140					145			
gtt	gta	gtt	gcc	gat	aat	tgc	act	gat	gaa	act	acg	gaa	tta	gcc	cgt	595	
Val	Val	Val	Ala	Asp	Asn	Cys	Thr	Asp	Glu	Thr	Thr	Glu	Leu	Ala	Arg		
				150					155					160			
gct	gag	gga	gtg	gag	gtc	ttg	gaa	aca	gtc	aat	aat	aag	ttt	aag	aag	643	
Ala	Glu	Gly	Val	Glu	Val	Leu	Glu	Thr	Val	Asn	Asn	Lys	Phe	Lys	Lys		
				170					175					180			
gcc	gga	gga	ctc	aat	cag	gct	ttg	agc	cgg	atg	ctt	ccc	aca	ttg	ggg	691	
Ala	Gly	Gly	Leu	Asn	Gln	Ala	Leu	Ser	Arg	Met	Leu	Pro	Thr	Leu	Gly		
				185					190					195			
gag	aat	gac	att	gtg	atg	atc	gtt	gac	gct	gat	aca	gca	ctt	gat	caa	739	
Glu	Asn	Asp	Ile	Val	Met	Ile	Val	Asp	Ala	Asp	Thr	Ala	Leu	Asp	Gln		
				200					205					210			
ggc	ttc	ctc	aag	gaa	gca	cgg	cgc	cgc	ttt	gag	tct	gat	cgc	gct	cta	787	
Gly	Phe	Leu	Lys	Glu	Ala	Arg	Arg	Arg	Phe	Glu	Ser	Asp	Arg	Ala	Leu		
				215					220					225			
atg	gcc	gtg	ggc	gga	ttg	ttc	tac	ggc	gag	tca	ggc	tcc	gga	tgg	ctt	835	
Met	Ala	Val	Gly	Gly	Leu	Phe	Tyr	Gly	Glu	Ser	Gly	Ser	Gly	Trp	Leu		
				230					235					240			



ggc caa tat cag cgc aac gaa tac acc cgt tat agc cgt gac atc tat 883  
 Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr Ser Arg Asp Ile Tyr  
                   250                  255                  260  
  
 cga cgc cgc gga cgt gtg ttt gtt ttg act gga aca gcg tcg gct ttt 931  
 Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly Thr Ala Ser Ala Phe  
                   265                  270                  275  
  
 cgg cca cgc ggc ctg cgg aca gta gcg gaa tca cgc ggg aca ttg atc 979  
 Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser Arg Gly Thr Leu Ile  
                   280                  285                  290  
  
 ccc gga cgt aaa gcc gat gtt tat gac acc gcg ggc gtt gac cga aga 1027  
 Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala Gly Val Asp Arg Arg  
                   295                  300                  305  
  
 taatgagttg accctggctt tga 1050

<210> 422  
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 422  
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 Leu Gly Ile Ala Gly Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr  
                   20                  25                  30  
  
 Leu Ser Asp Pro Ala Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp  
                   35                  40                  45  
  
 Arg Trp Lys Val Leu Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu  
                   50                  55                  60  
  
 Val Ala Ala Ile Ile Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr  
                   65                  70                  75                  80  
  
 Val Glu Arg Thr Val Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu  
                   85                  90                  95  
  
 Arg Val Pro Leu Ala Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val  
                   100                  105                  110  
  
 Phe His Gly Pro Ile Thr Ile Asn Val Leu Val Pro Ala His Asn Glu  
                   115                  120                  125  
  
 Ala Glu Arg Ile Thr Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu  
                   130                  135                  140  
  
 Pro Pro Glu Arg Ile Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr  
                   145                  150                  155                  160  
  
 Thr Glu Leu Ala Arg Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn  
                   165                  170                  175  
  
 Asn Lys Phe Lys Lys Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met  
                   180                  185                  190

Leu Pro Thr Leu Gly Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp  
 195 200 205  
 Thr Ala Leu Asp Gln Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu  
 210 215 220  
 Ser Asp Arg Ala Leu Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser  
 225 230 235 240  
 Gly Ser Gly Trp Leu Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr  
 245 250 255  
 Ser Arg Asp Ile Tyr Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly  
 260 265 270  
 Thr Ala Ser Ala Phe Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser  
 275 280 285  
 Arg Gly Thr Leu Ile Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala  
 290 295 300  
 Gly Val Asp Arg Arg  
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<210> 423  
 <211> 882  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA00042

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 atacgagcaa aactttcctg ataataaaaag gagtccgacc atg gac atc atc atc 115  
 Met Asp Ile Ile Ile  
 1 5  
 tgc aaa gac gag caa gaa gtc ggc aaa gca gcg gca gcc ctg atc gca 163  
 Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala Ala Leu Ile Ala  
 10 15 20  
 ccc ttc gca act aag ggc gga acc ttg ggg ctt gca act gga tcg tca 211  
 Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu Ala Thr Gly Ser Ser  
 25 30 35  
 cct ttg agc acc tac caa gag ctc att cgc atg tat gaa gct ggg gaa 259  
 Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met Tyr Glu Ala Gly Glu  
 40 45 50  
 gtg tca ttc aag aac tgc aag gca ttc ttg ttg gat gaa tac gtg gga 307  
 Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu Asp Glu Tyr Val Gly  
 55 60 65  
 tta acg cgc gac gat gaa aac agc tac ttc aaa acc att cgt aaa gag 355  
 Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys Thr Ile Arg Lys Glu

70	75	80	85	
ttc act gac cac atc gac atc gtt gat gaa gag gtc tac agc cca gat				403
Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu Val Tyr Ser Pro Asp	90	95	100	
ggt gca aac cct gat cca tac gaa gca gct gca gag tat gag gca aag				451
Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala Glu Tyr Glu Ala Lys	105	110	115	
atc gct gca gaa tcc gtt gat gtt caa atc ctt ggc atc ggc gga aac				499
Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu Gly Ile Gly Gly Asn	120	125	130	
ggc cac atc gct ttc aat gag cca tca tct tct ctg tca gga ctg aca				547
Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser Leu Ser Gly Leu Thr	135	140	145	
aag gtc cag gcg ctg cac cct aaa act gtg gag gac aac gct cga ttc				595
Lys Val Gln Ala Leu His Pro Lys Thr Val Glu Asp Asn Ala Arg Phe	150	155	160	165
ttc aac acc atc gaa gag gtc cca acc cac gcc ctc acc cag ggt ttg				643
Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala Leu Thr Gln Gly Leu	170	175	180	
ggc act ttg tcc cgc gcg caa aac atc gtg ttg gtg gca act ggt gaa				691
Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu Val Ala Thr Gly Glu	185	190	195	
gga aaa gcc gac gcc atc cgc gga act gtg gaa ggc cca ctg acc gcc				739
Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu Gly Pro Leu Thr Ala	200	205	210	
atg tgc cca ggt tcc atc ctg cag atg cac aac aat gcc acc atc atc				787
Met Cys Pro Gly Ser Ile Leu Gln Met His Asn Asn Ala Thr Ile Ile	215	220	225	
gtt gat gaa gca gca gca tcc aag ctg gaa aac gct gat cac tac cgt				835
Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn Ala Asp His Tyr Arg	230	235	240	245
ctc atg gag caa tta aag ctg cgc tagaaacaaa aaggaaagta gtg				882
Leu Met Glu Gln Leu Lys Leu Arg	250			

&lt;210&gt; 424

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 424

Met Asp Ile Ile Ile Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala	
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Ala Ala Leu Ile Ala Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu	
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Ala Thr Gly Ser Ser Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met	
35 40 45	

Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu  
 50 55 60  
 Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys  
 65 70 75 80  
 Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu  
 85 90 95  
 Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala  
 100 105 110  
 Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu  
 115 120 125  
 Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser  
 130 135 140  
 Leu Ser Gly Leu Thr Lys Val Gln Ala Leu His Pro Lys Thr Val Glu  
 145 150 155 160  
 Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala  
 165 170 175  
 Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu  
 180 185 190  
 Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu  
 195 200 205  
 Gly Pro Leu Thr Ala Met Cys Pro Gly Ser Ile Leu Gln Met His Asn  
 210 215 220  
 Asn Ala Thr Ile Ile Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn  
 225 230 235 240  
 Ala Asp His Tyr Arg Leu Met Glu Gln Leu Lys Leu Arg  
 245 250

<210> 425  
 <211> 1998  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1975)  
 <223> RXA01482

<400> 425  
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 Met Arg Met Cys Gly  
 1 5  
 att gtt gga tat att ggc caa gcg ggc gac tcc cgt gat tac ttt gct 163  
 Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser Arg Asp Tyr Phe Ala  
 10 15 20

cta gat gta gtt gtt gaa gga cta cgt cgc ctg gaa tac cgc gga tat	211
Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr	
25 30 35	
gac tcc gca ggt att gct att cac gcc aat ggt gag att agc tac cga	259
Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly Glu Ile Ser Tyr Arg	
40 45 50	
aag aag gcc gga aag gtt gct gca cta gat gca gaa atc gct aaa gca	307
Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala Glu Ile Ala Lys Ala	
55 60 65	
cct ctt cca gat tct att ttg gga att gga cac acc cgt tgg gca act	355
Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His Thr Arg Trp Ala Thr	
70 75 80 85	
cat ggt ggc cca acc gat gtc aac gct cac ccc cac gtt gtt tcc aat	403
His Gly Gly Pro Thr Asp Val Asn Ala His Pro His Val Val Ser Asn	
90 95 100	
ggc aag ctt gcc gta gta cac aac ggc atc atc gaa aac ttt gcg gaa	451
Gly Lys Leu Ala Val Val His Asn Gly Ile Ile Glu Asn Phe Ala Glu	
105 110 115	
ctg cgc tct gag ctt tcc gct aag ggc tac aac ttt gta tcc gat acc	499
Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn Phe Val Ser Asp Thr	
120 125 130	
gat acc gaa gtt gct gct tct ttg ctt gct gaa att tac aat act cag	547
Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu Ile Tyr Asn Thr Gln	
135 140 145	
gca aac ggt gac ctc acc ctt gct atg cag ctg acc ggt cag cgc ctt	595
Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu Thr Gly Gln Arg Leu	
150 155 160 165	
gag ggt gct ttc acc ctg cta gct att cat gct gat cac gat gac cgc	643
Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala Asp His Asp Asp Arg	
170 175 180	
atc gtt gca gct cgt cgt aac tct cct ttg gtt atc ggc gtc ggc gag	691
Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val Ile Gly Val Gly Glu	
185 190 195	
ggc gag aac ttc ctc gga tct gac gtt tct ggc ttt att gat tac acc	739
Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly Phe Ile Asp Tyr Thr	
200 205 210	
cgc aag gct gta gag ctg gct aat gac cag gtt gtt acc atc acc gct	787
Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val Val Thr Ile Thr Ala	
215 220 225	
gat gat tac gcc atc acc aac ttt gat gga tca gaa gca gtt ggc aag	835
Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser Glu Ala Val Gly Lys	
230 235 240 245	
cct ttc gac gtg gag tgg gac gct gca gct gct gaa aag ggt ggc ttc	883
Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Glu Lys Gly Gly Phe	
250 255 260	

ggt tcc ttc atg gag aag gaa atc cac gat cag cca gca gct gtt cgc	931
Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln Pro Ala Ala Val Arg	
265 270 275	
gat acc ctg atg ggc cgt ctt gat gaa gat ggc aag ctc gtt ctt gat	979
Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly Lys Leu Val Leu Asp	
280 285 290	
gag ctg cgc atc gat gaa gct att ctg cgt agt gtc gac aag atc gtc	1027
Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser Val Asp Lys Ile Val	
295 300 305	
att gtt gct tgt ggt act gca gct tat gca ggc cag gtt gct cgt tac	1075
Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly Gln Val Ala Arg Tyr	
310 315 320 325	
gcc att gag cac tgg tgc cgc atc cca acc gag gtg gag ctg gct cac	1123
Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu Val Glu Leu Ala His	
330 335 340	
gag ttc cgt tac cgc gac cca atc ctc aac gag aag acc ctt gtt gtg	1171
Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu Lys Thr Leu Val Val	
345 350 355	
gca ttg tcc cag tcc ggc gag acc atg gat acc ctc atg gct gtt cgc	1219
Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr Leu Met Ala Val Arg	
360 365 370	
cac gca cgt gag cag ggt gcc aag gtt gtt gct att tgt aac act gtt	1267
His Ala Arg Glu Gln Gly Ala Lys Val Val Ala Ile Cys Asn Thr Val	
375 380 385	
gga tcc act ctt cca cgt gaa gca gat gcg tcc ctg tac acc tac gct	1315
Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser Leu Tyr Thr Tyr Ala	
390 395 400 405	
ggc cct gag atc gct gtg gcg tcc acc aag gcg ttc ttg gct cag atc	1363
Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala Phe Leu Ala Gln Ile	
410 415 420	
act gct tct tac ttg ctt ggc ctg tac ttg gct cag ctg cgc ggc aac	1411
Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala Gln Leu Arg Gly Asn	
425 430 435	
aag ttc gct gat gag gtt tct tcc att ctg gac agc ctg cgt gag atg	1459
Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp Ser Leu Arg Glu Met	
440 445 450	
cct gag aag att cag cag gtc atc gat gca gaa gag cag atc aag aag	1507
Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu Glu Gln Ile Lys Lys	
455 460 465	
ctt ggc caa gat atg gca gat gct aag tct gtg ctg ttc ctg ggc cgc	1555
Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val Leu Phe Leu Gly Arg	
470 475 480 485	
cac gtt ggt ttc cca gtt gcg ctt gag ggt gcg ttg aag ctc aag gag	1603
His Val Gly Phe Pro Val Ala Leu Glu Gly Ala Leu Lys Leu Lys Glu	
490 495 500	
atc gca tac ctg cac gct gaa ggt ttc gct gca ggc gag ctc aag cac	1651

Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala Gly Glu Leu Lys His  
 505 510 515  
 ggc cca att gct ttg gtt gag gaa ggc cag ccg atc ttc gtt atc gtg 1699  
 Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro Ile Phe Val Ile Val  
 520 525 530  
 cct tca cct cgt ggt cgc gat tcc ctg cac tcc aag gtt gtc tcc aac 1747  
 Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser Lys Val Val Ser Asn  
 535 540 545  
 att cag gag atc cgt gca cgt ggc gct gtc acc atc gtg att gca gag 1795  
 Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr Ile Val Ile Ala Glu  
 550 555 560 565  
 gaa ggc gat gag gct gtc aac gat tac gcc aac ttc atc atc cgc att 1843  
 Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn Phe Ile Ile Arg Ile  
 570 575 580  
 cct cag gcc cca acc ctg atg cag cct ctg ctg tcc acc gtg cct ctg 1891  
 Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu Ser Thr Val Pro Leu  
 585 590 595  
 cag atc ttt gcg tgc gct gtg gca acc gca aag ggc tac aac gtg gat 1939  
 Gln Ile Phe Ala Cys Ala Val Ala Thr Ala Lys Gly Tyr Asn Val Asp  
 600 605 610  
 cag cct cgt aac ctg gca aag tct gtc acc gtc gaa taaaaagatt 1985  
 Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu  
 615 620 625  
 tcgcttctcg acg 1998

&lt;210&gt; 426

&lt;211&gt; 625

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 426

Met Arg Met Cys Gly Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser  
 1 5 10 15  
 Arg Asp Tyr Phe Ala Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu  
 20 25 30  
 Glu Tyr Arg Gly Tyr Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly  
 35 40 45  
 Glu Ile Ser Tyr Arg Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala  
 50 55 60  
 Glu Ile Ala Lys Ala Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His  
 65 70 75 80  
 Thr Arg Trp Ala Thr His Gly Gly Pro Thr Asp Val Asn Ala His Pro  
 85 90 95  
 His Val Val Ser Asn Gly Lys Leu Ala Val Val His Asn Gly Ile Ile  
 100 105 110

Glu Asn Phe Ala Glu Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn  
 115 120 125  
 Phe Val Ser Asp Thr Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu  
 130 135 140  
 Ile Tyr Asn Thr Gln Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu  
 145 150 155 160  
 Thr Gly Gln Arg Leu Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala  
 165 170 175  
 Asp His Asp Asp Arg Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val  
 180 185 190  
 Ile Gly Val Gly Glu Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly  
 195 200 205  
 Phe Ile Asp Tyr Thr Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val  
 210 215 220  
 Val Thr Ile Thr Ala Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser  
 225 230 235 240  
 Glu Ala Val Gly Lys Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala  
 245 250 255  
 Glu Lys Gly Gly Phe Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln  
 260 265 270  
 Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly  
 275 280 285  
 Lys Leu Val Leu Asp Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser  
 290 295 300  
 Val Asp Lys Ile Val Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly  
 305 310 315 320  
 Gln Val Ala Arg Tyr Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu  
 325 330 335  
 Val Glu Leu Ala His Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu  
 340 345 350  
 Lys Thr Leu Val Val Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr  
 355 360 365  
 Leu Met Ala Val Arg His Ala Arg Glu Gln Gly Ala Lys Val Val Ala  
 370 375 380  
 Ile Cys Asn Thr Val Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser  
 385 390 395 400  
 Leu Tyr Thr Tyr Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala  
 405 410 415  
 Phe Leu Ala Gln Ile Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala  
 420 425 430  
 Gln Leu Arg Gly Asn Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp



435	440	445
Ser Leu Arg Glu Met Pro	Glu Lys Ile Gln Gln Val	Ile Asp Ala Glu
450	455	460
Glu Gln Ile Lys Lys Leu	Gly Gln Asp Met Ala Asp	Ala Lys Ser Val
465	470	475
Leu Phe Leu Gly Arg His	Val Gly Phe Pro Val Ala	Leu Glu Gly Ala
485	490	495
Leu Lys Leu Lys Glu Ile	Ala Tyr Leu His Ala Glu	Gly Phe Ala Ala
500	505	510
Gly Glu Leu Lys His Gly	Pro Ile Ala Leu Val Glu	Glu Gly Gln Pro
515	520	525
Ile Phe Val Ile Val Pro	Ser Pro Arg Gly Arg Asp	Ser Leu His Ser
530	535	540
Lys Val Val Ser Asn Ile	Gln Glu Ile Arg Ala Arg	Gly Ala Val Thr
545	550	555
Ile Val Ile Ala Glu Glu	Gly Asp Glu Ala Val Asn	Asp Tyr Ala Asn
565	570	575
Phe Ile Ile Arg Ile Pro	Gln Ala Pro Thr Leu Met	Gln Pro Leu Leu
580	585	590
Ser Thr Val Pro Leu Gln	Ile Phe Ala Cys Ala Val	Ala Thr Ala Lys
595	600	605
Gly Tyr Asn Val Asp Gln	Pro Arg Asn Leu Ala Lys	Ser Val Thr Val
610	615	620
Glu		
625		

<210> 427  
 <211> 666  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(666)  
 <223> RXN03179

<400> 427	
gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca	48
Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala	
1 5 10 15	
gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc	96
Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe	
20 25 30	
ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac	144
Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp	
35 40 45	

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gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga 192
Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
    50                      55                      60

cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc 240
Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
    65                      70                      75                      80

gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat 288
Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
                      85                      90                      95

cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac 336
Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
                      100                      105                      110

acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc 384
Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
    115                      120                      125

gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca 432
Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
    130                      135                      140

atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg 480
Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
    145                      150                      155                      160

gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat 528
Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
                      165                      170                      175

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576
Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
    180                      185                      190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt tcg cgg aaa tgt 624
Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
    195                      200                      205

cca aga aga cgg ctg gtc atg acc atc cac cag gtg tgt acc 666
Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
    210                      215                      220

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&lt;210&gt; 428

&lt;211&gt; 222

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 428

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Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
  1                      5                      10                      15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
    20                      25                      30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
    35                      40                      45

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Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg  
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr  
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp  
 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr  
 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile  
 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala  
 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala  
 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp  
 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys  
 195 200 205

Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr  
 210 215 220

<210> 429  
 <211> 672  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(672)  
 <223> FRXA02872

<400> 429  
 gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca 48  
 Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala  
 1 5 10 15

gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc 96  
 Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe  
 20 25 30

ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac 144  
 Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp  
 35 40 45

gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga 192  
 Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg  
 50 55 60

cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc 240  
 Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr  
 65 70 75 80

gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat 288  
 Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp  
 85 90 95

cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac 336  
 Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr  
 100 105 110

acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc 384  
 Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile  
 115 120 125

gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca 432  
 Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala  
 130 135 140

atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg 480  
 Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala  
 145 150 155 160

gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat 528  
 Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp  
 165 170 175

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576  
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
 180 185 190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt ttc gcg gaa atg 624  
 Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met  
 195 200 205

tcc caa gaa gac ggc ctg gtc atg acc atc cac cca ggt gtg tac cgc 672  
 Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg  
 210 215 220

&lt;210&gt; 430

&lt;211&gt; 224

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 430

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala  
 1 5 10 15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe  
 20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp  
 35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg  
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr  
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp  
                     85                    90                    95  
 Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr  
                     100                    105                    110  
 Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile  
                     115                    120                    125  
 Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala  
                     130                    135                    140  
 Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala  
                     145                    150                    155                    160  
 Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp  
                     165                    170                    175  
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala  
                     180                    185                    190  
 Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met  
                     195                    200                    205  
 Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg  
                     210                    215                    220

<210> 431  
 <211> 533  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(510)  
 <223> RXN03180

<400> 431  
 ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48  
 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp  
   1                    5                    10                    15  
 ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96  
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala  
                     20                    25                    30  
 gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144  
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg  
                     35                    40                    45  
 gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192  
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn  
                     50                    55                    60  
 ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc 240  
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe

65	70	75	80	
att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga				288
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly	85	90	95	
ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc				336
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu	100	105	110	
cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat				384
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp	115	120	125	
gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa				432
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln	130	135	140	
atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac				480
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His	145	150	155	160
gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga				530
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln	165	170		
tgt				533

&lt;210&gt; 432

&lt;211&gt; 170

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 432

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp			
1	5	10	15

Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala			
20	25	30	

Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg			
35	40	45	

Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn			
50	55	60	

Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe			
65	70	75	80

Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly			
85	90	95	

Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu			
100	105	110	

Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp			
115	120	125	

Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln			
130	135	140	

Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His  
145 150 155 160

Val Arg Ile Ile Pro Asn Gly Lys Asp Gln  
165 170

<210> 433

<211> 533

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(510)

<223> FRXA02873

<400> 433

ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48  
Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp  
1 5 10 15

ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96  
Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala  
20 25 30

gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144  
Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg  
35 40 45

gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192  
Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn  
50 55 60

ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc 240  
Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe  
65 70 75 80

att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga 288  
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly  
85 90 95

ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc 336  
Leu Ser Glu Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu  
100 105 110

cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat 384  
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp  
115 120 125

gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa 432  
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln  
130 135 140

atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac 480  
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His  
145 150 155 160

gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga 530  
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln

170

533

<400> 434																
Phe	Gly	Glu	Asn	Lys	Asp	Leu	Ile	Ser	Asp	Ser	Ser	Phe	Asn	Arg	Trp	
1				5					10					15		
Leu	Arg	Thr	Val	Ser	Leu	Gly	Ser	Thr	Gln	Asp	Ala	Asp	Met	Ala	Ala	
			20					25					30			
Ala	Ser	Asn	Leu	Ala	Ala	Asn	Ser	Lys	Met	Ala	Arg	Gln	Asn	Thr	Arg	
		35					40					45				
Asp	Ile	Leu	Asp	Ala	Val	Ser	Asp	Gly	Gly	Val	Met	Leu	Gly	Arg	Asn	
	50					55					60					
Gly	Ala	Leu	Val	Leu	Gly	Pro	Val	Val	Gly	Thr	Leu	His	Ile	Lys	Phe	
65					70					75					80	
Ile	Ala	Pro	Leu	Asn	Lys	Arg	Val	Glu	Arg	Val	Met	Tyr	Lys	Thr	Gly	
				85					90					95		
Leu	Ser	Glu	Ala	Ala	Ala	Ala	Glu	Gln	Cys	Ala	Leu	Glu	Asp	Arg	Leu	
			100					105					110			
Arg	Glu	Glu	Met	Ala	His	Ala	Leu	Tyr	Gln	Trp	Asn	Pro	Gly	Arg	Asp	
		115					120					125				
Glu	Asn	Tyr	Asp	Leu	Val	Ile	Asn	Thr	Gly	Ser	Met	Thr	Tyr	Glu	Gln	
	130					135					140					
Ile	Val	Asp	Leu	Val	Val	Glu	Thr	Tyr	Ala	Arg	Lys	Tyr	Pro	Leu	His	
145					150					155					160	
Val	Arg	Ile	Ile	Pro	Asn	Gly	Lys	Asp	Gln							
				165					170							

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<400> 435
tgcaccacgc cagctgcaac cctgcgcggt ggtctgggaa gttggtggag gggatcgtcg 60
aaaagcgtag gcactaaagt tctcctgcac aatggaggat atg gac aat gac ttt 115
Met Asp Asn Asp Phe
1 5
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gaa tct atc gag aaa atg agc agc ggc gat tgg tac gtg gct acc ggc 163  
 Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp Tyr Val Ala Thr Gly  
 10 15 20

gcg gaa cgt gaa gaa gtg gca caa aaa aca gcg tta ctt ttc cac gaa 211  
 Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala Leu Leu Phe His Glu  
 25 30 35

tac aac caa att gga cct aca gac ccc gca cga act gcc gaa ata cta 259  
 Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg Thr Ala Glu Ile Leu  
 40 45 50

aga act gta cta aat cct gcc agc gga acc tgc acg atc aaa gcg cca 307  
 Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys Thr Ile Lys Ala Pro  
 55 60 65

gcc atc att gaa tac ggc ttc aac acc acg atc ggc gag cat gtg ttc 355  
 Ala Ile Ile Glu Tyr Phe Asn Thr Thr Ile Gly Glu His Val Phe  
 70 75 80 85

atc aac ttt ggc ctc acc att tta gat atc gca ccg gtt cgc atc ggg 403  
 Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala Pro Val Arg Ile Gly  
 90 95 100

gca cgc agc atg ctc ggg cca aac tgt cag ctc ttc acc gca ggt cac 451  
 Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu Phe Thr Ala Gly His  
 105 110 115

ccg gtc gat gac tgg gaa atg cgc tcc ggt ggg tgg gaa aat ggc gca 499  
 Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly Trp Glu Asn Gly Ala  
 120 125 130

ccc att tcc att ggc gag gat acg tgg ctg ggt gga aat gtc acc gtc 547  
 Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly Gly Asn Val Thr Val  
 135 140 145

gtt ggt ggc gtg agc att ggc gat agg tgt gtg att ggc gcg ggg ccc 595  
 Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val Ile Gly Ala Gly Pro  
 150 155 160 165

gtg gtg acc aag gat att ccg gat gat tct att gct gtg ggc aac cct 643  
 Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile Ala Val Gly Asn Pro  
 170 175 180

gcg cga gta gtg cgg aaa cgt gat gat agc cgg ctc gaa cgt tcg cag 691  
 Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg Leu Glu Arg Ser Gln  
 185 190 195

ctg cca gaa ggt gct tcc gtg gat gcg ttg ggg att ctt cct aca aaa 739  
 Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly Ile Leu Pro Thr Lys  
 200 205 210

tca cct agg ctg tca gaa aat att gcc gaa aaa tat taaatacgca 785  
 Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys Tyr  
 215 220 225

ggcaactaaga aga 798

&lt;211&gt; 225

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 436

Met Asp Asn Asp Phe Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp  
 1 5 10 15

Tyr Val Ala Thr Gly Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala  
 20 25 30

Leu Leu Phe His Glu Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg  
 35 40 45

Thr Ala Glu Ile Leu Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys  
 50 55 60

Thr Ile Lys Ala Pro Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile  
 65 70 75 80

Gly Glu His Val Phe Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala  
 85 90 95

Pro Val Arg Ile Gly Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu  
 100 105 110

Phe Thr Ala Gly His Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly  
 115 120 125

Trp Glu Asn Gly Ala Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly  
 130 135 140

Gly Asn Val Thr Val Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val  
 145 150 155 160

Ile Gly Ala Gly Pro Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile  
 165 170 175

Ala Val Gly Asn Pro Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg  
 180 185 190

Leu Glu Arg Ser Gln Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly  
 195 200 205

Ile Leu Pro Thr Lys Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys  
 210 215 220

Tyr

225

&lt;210&gt; 437

&lt;211&gt; 891

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(868)

&lt;223&gt; RXA02666

&lt;400&gt; 437

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gctcggcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga 60

tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga 115
                                         Met Ser Ser Thr Arg
                                         1 5

atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163
Ile Pro Val Ile Ala Leu Leu Ala Ala Gly Arg Gly Thr Arg Leu
                        10 15 20

ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211
Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu
                        25 30 35

tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259
Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu
                        40 45 50

atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307
Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu
                        55 60 65

ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg 355
Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg
                        70 75 80 85

ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt 403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu
                        90 95 100

cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc 451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile
                        105 110 115

cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg 499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val
                        120 125 130

gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca 547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro
                        135 140 145

gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc 595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val
                        150 155 160 165

gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc 643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly
                        170 175 180

ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac 691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp
                        185 190 195

ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg 739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp
                        200 205 210

tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa 787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys

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      215              220              225
gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa 835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu
230              235              240              245

gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg 888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
                250              255

tag 891

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<210> 438
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

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<400> 438
Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly
 1              5              10              15

Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu
                20              25              30

Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser
          35              40              45

Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr
 50              55              60

Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu
 65              70              75              80

Gly Val Arg Val Arg Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser
          85              90              95

Val Trp Ala Gly Leu Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp
          100              105              110

Ala Ile Val Leu Ile His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly
          115              120              125

Met Ile Ala Arg Val Val Arg Lys Val His Glu Gly Ala Thr Ala Val
 130              135              140

Ile Pro Val Leu Pro Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp
 145              150              155              160

Gly Gly Val Val Val Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val
          165              170              175

Gln Thr Pro Gln Gly Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu
          180              185              190

Lys Phe Phe Ala Asp Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala
          195              200              205

Ser Leu Met Glu Trp Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp
 210              215              220

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Pro Met Ala Phe Lys Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln  
 225 230 235 240  
 Arg Ile Thr Asp Glu Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp  
 245 250 255

<210> 439  
 <211> 1065  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1042)  
 <223> RXA00202

<400> 439  
 ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60  
 aaacaaaacc tctaagtaat tcctgaaagg aaattttcac atg tac gct cgt aaa 115  
 Met Tyr Ala Arg Lys  
 1 5  
 ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163  
 Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala  
 10 15 20  
 tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat 211  
 Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp  
 25 30 35  
 ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg 259  
 Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val  
 40 45 50  
 cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc 307  
 Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr  
 55 60 65  
 ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag 355  
 Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln  
 70 75 80 85  
 ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca 403  
 Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro  
 90 95 100  
 act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct 451  
 Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala  
 105 110 115  
 gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg 499  
 Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val  
 120 125 130  
 gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct 547  
 Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala

135	140	145	
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg			595
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu			
150	155	160	165
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt			643
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe			
	170	175	180
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag			691
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln			
	185	190	195
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg			739
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu			
	200	205	210
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag			787
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu			
	215	220	225
atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat			835
Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp			
230	235	240	245
gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt			883
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val			
	250	255	260
gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg			931
Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu			
	265	270	275
gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac			979
Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp			
	280	285	290
gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac			1027
Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn			
	295	300	305
gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt			1065
Val Ala Asp Phe Lys			
310			

&lt;210&gt; 440

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 440

Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala
1 5 10 15

Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
20 25 30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
35 40 45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp  
 50 55 60  
 Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala  
 65 70 75 80  
 Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val  
 85 90 95  
 Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu  
 100 105 110  
 Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser  
 115 120 125  
 Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly  
 130 135 140  
 Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly  
 145 150 155 160  
 Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp  
 165 170 175  
 Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser  
 180 185 190  
 Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp  
 195 200 205  
 Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe  
 210 215 220  
 Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala  
 225 230 235 240  
 Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp  
 245 250 255  
 Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln  
 260 265 270  
 Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu  
 275 280 285  
 Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr  
 290 295 300  
 Val Lys Leu Asp Asn Val Ala Asp Phe Lys  
 305 310

&lt;210&gt; 441

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(940)

<400> 441

aggcggagga accgtcgata cgcctcggtt ggttgtcgcg atg gtg agc cac ggc 115  
Met Val Ser His Gly  
1 5

gcg ccg ggc gat act ttt tgg gat ttg gtc cga aaa ggt gct gaa gac 163  
Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg Lys Gly Ala Glu Asp  
10 15 20

gcc gcc caa aaa gac aac gtt gaa ctc cgc tat tcc tct aat ccg gaa 211  
Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr Ser Ser Asn Pro Glu  
25 30 35

atc cct gaa caa tcc aac ctc gtg caa aat gcc atc gat tca cgc gtc 259  
Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala Ile Asp Ser Arg Val  
40 45 50

gac ggc atc gcc atg acc atg cct aat gct caa tca cta gga ccg gtc 307  
Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln Ser Leu Gly Pro Val  
55 60 65

gct caa aag gcc gtg gat gcg ggc att cct gtg gtt ggt ctc aac gct 355  
Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val Val Gly Leu Asn Ala  
70 75 80 85

gga atg aac gaa tac caa gat tat gga atg aca gga ttc ttt ggt caa 403  
Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr Gly Phe Phe Gly Gln  
90 95 100

gat gaa tcc gtc gca gga gca tcc gca gga gcg cgc ctt gcc gag gaa 451  
Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala Arg Leu Ala Glu Glu  
105 110 115

aac gca caa aaa gtt ttg tgt gtg atc cat gaa cag ggc aac tcc tcc 499  
Asn Ala Gln Lys Val Leu Cys Val Ile His Glu Gln Gly Asn Ser Ser  
120 125 130

cag gaa gct cgc tgt ggt ggc gtg tct gaa ggt ttg ggc aaa caa gta 547  
Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly Leu Gly Lys Gln Val  
135 140 145

gaa acc ctg tat gtc aac ggc atg gat ctc acc tca gtg aac tcc acc 595  
Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr Ser Val Asn Ser Thr  
150 155 160 165

ctg cag gca aaa ctt gct caa gac cgc agc att gat tgg gtt gtg gga 643  
Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile Asp Trp Val Val Gly  
170 175 180

ctc cag gct ggt gta tca atg gct att tct gat gcg gca gac gct gcg 691  
Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp Ala Ala Asp Ala Ala  
185 190 195

aac tca gaa gta aag atc gcc acc ttt gat aca aac gca cag ctc atg 739  
Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr Asn Ala Gln Leu Met  
200 205 210



acc gct att cgt gat ggc aag atc caa ttc gcc att gat cag caa cca 787  
 Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala Ile Asp Gln Gln Pro  
 215 220 225

tat ctg cag ggc tac atg gcc gtg gat tcg ctg tgg ttg gcg cac cga 835  
 Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu Trp Leu Ala His Arg  
 230 235 240 245

aac ggc acc act gtt ggt ggc gga cga ccc gtg tac aca gga cca gcc 883  
 Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val Tyr Thr Gly Pro Ala  
 250 255 260

att gtg gat gcc acc aac gtt gat gtc att gct gaa gcc gtt ggg gag 931  
 Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala Glu Ala Val Gly Glu  
 265 270 275

ggt ctg cga tgacaaaaat caagagtggg gag 963  
 Gly Leu Arg  
 280

<210> 442  
 <211> 280  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 442  
 Met Val Ser His Gly Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg  
 1 5 10 15

Lys Gly Ala Glu Asp Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr  
 20 25 30

Ser Ser Asn Pro Glu Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala  
 35 40 45

Ile Asp Ser Arg Val Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln  
 50 55 60

Ser Leu Gly Pro Val Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val  
 65 70 75 80

Val Gly Leu Asn Ala Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr  
 85 90 95

Gly Phe Phe Gly Gln Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala  
 100 105 110

Arg Leu Ala Glu Glu Asn Ala Gln Lys Val Leu Cys Val Ile His Glu  
 115 120 125

Gln Gly Asn Ser Ser Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly  
 130 135 140

Leu Gly Lys Gln Val Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr  
 145 150 155 160

Ser Val Asn Ser Thr Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile  
 165 170 175

Asp Trp Val Val Gly Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp

180	185	190
Ala Ala Asp Ala Ala Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr		
195	200	205
Asn Ala Gln Leu Met Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala		
210	215	220
Ile Asp Gln Gln Pro Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu		
225	230	235
Trp Leu Ala His Arg Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val		
245	250	255
Tyr Thr Gly Pro Ala Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala		
260	265	270
Glu Ala Val Gly Glu Gly Leu Arg		
275	280	

<210> 443  
 <211> 1482  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1459)  
 <223> RXN01569

<400> 443  
 aaggcctaga gcagaccatc gattggtacc gcgaaaacga ggccctggtgg cgccctgcca 60  
 agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115  
 Met Glu Tyr Gly Lys 5  
 1  
 caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163  
 Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp 20  
 10 15  
 ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211  
 Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln 35  
 25 30  
 cgc acc aag atg acc aac ctg ggc ctg ccc gat ttt ggc ccc gtc caa 259  
 Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln 50  
 40 45  
 aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307  
 Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His 65  
 55 60  
 gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355  
 Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe 85  
 70 75 80  
 gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc 403  
 Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val 100  
 90 95

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt	451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly	
105 110 115	
gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac	499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr	
120 125 130	
ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac	547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn	
135 140 145	
ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa	595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys	
150 155 160 165	
gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc	643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg	
170 175 180	
aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc	691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg	
185 190 195	
gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc	739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile	
200 205 210	
acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc	787
Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile	
215 220 225	
ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc	835
Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg	
230 235 240 245	
gca gca gcg tgg gac atc aac gca gcg gca gtg gct aac ctc gcg acc	883
Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Asn Leu Ala Thr	
250 255 260	
atc gcg cgc gac aac aac ctc acc ctc gtg cac gtg tcc tca gat tat	931
Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His Val Ser Ser Asp Tyr	
265 270 275	
gtc ttc gac ggt gcg gcc gaa tcc tac gat gaa aac gca ccg ttt tcc	979
Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu Asn Ala Pro Phe Ser	
280 285 290	
cca ctc ggc gtg tac ggc caa tcc aaa gca gcc ggc gac atc gga gac	1027
Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala Gly Asp Ile Gly Asp	
295 300 305	
acc acc gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc	1075
Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly	
310 315 320 325	
gat ggc aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc	1123
Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly	
330 335 340	

atc gca cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc 1171  
 Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr  
                   345                                  350                                  355

gaa gac atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca 1219  
 Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala  
                   360                                  365                                  370

tat ggc acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc 1267  
 Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala  
                   375                                  380                                  385

gat gtt gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg 1315  
 Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val  
                   390                                  395                                  400                                  405

agc acc gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg 1363  
 Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu  
                   410                                  415                                  420

aac tcc gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca 1411  
 Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala  
                   425                                  430                                  435

ccg acc tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 1459  
 Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys  
                   440                                  445                                  450

tgaaaggcat catcctcgca ggt 1482

<210> 444

<211> 453

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly  
   1                                  5                                  10                                  15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe  
                   20                                  25                                  30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp  
                   35                                  40                                  45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr  
                   50                                  55                                  60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala  
                   65                                  70                                  75                                  80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser  
                   85                                  90                                  95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val  
                   100                                  105                                  110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly  
                   115                                  120                                  125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His  
 130 135 140  
 Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr  
 145 150 155 160  
 Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr  
 165 170 175  
 Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu  
 180 185 190  
 Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg  
 195 200 205  
 Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys  
 210 215 220  
 Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln  
 225 230 235 240  
 Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val  
 245 250 255  
 Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His  
 260 265 270  
 Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu  
 275 280 285  
 Asn Ala Pro Phe Ser Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala  
 290 295 300  
 Gly Asp Ile Gly Asp Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr  
 305 310 315 320  
 Ser Trp Val Ile Gly Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser  
 325 330 335  
 Leu Asp Glu Arg Gly Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly  
 340 345 350  
 Arg Leu Ser Phe Thr Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu  
 355 360 365  
 Glu Val Gly Ala Ala Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu  
 370 375 380  
 Pro Ala Ser Trp Ala Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr  
 385 390 395 400  
 Lys Val Thr Gly Val Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala  
 405 410 415  
 Ala Pro Arg Pro Leu Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala  
 420 425 430  
 Thr Gly Phe Ser Ala Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu  
 435 440 445  
 Lys Glu Leu Ser Lys

450

<210> 445  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(426)  
 <223> FRXA01569

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 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly  
 1 5 10 15  
 aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc atc gca 96  
 Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala  
 20 25 30  
 cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc gaa gac 144  
 Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp  
 35 40 45  
 atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca tat ggc 192  
 Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly  
 50 55 60  
 acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc gat gtt 240  
 Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val  
 65 70 75 80  
 gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg agc acc 288  
 Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr  
 85 90 95  
 gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg aac tcc 336  
 Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser  
 100 105 110  
 gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca ccg acc 384  
 Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr  
 115 120 125  
 tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 426  
 Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys  
 130 135 140  
 tgaaaggcat catcctcgca ggt 449

<210> 446  
 <211> 142  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 446  
 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly  
 1 5 10 15

Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala  
                   20                                  25                                  30  
 Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp  
                   35                                  40                                  45  
 Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly  
                   50                                  55                                  60  
 Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val  
                   65                                  70                                  75                                  80  
 Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr  
                                   85                                  90                                  95  
 Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser  
                   100                                  105                                  110  
 Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr  
                   115                                  120                                  125  
 Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys  
                   130                                  135                                  140

<210> 447  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1021)  
 <223> FRXA02055

<400> 447  
 aaggcctaga gcagaccatc gattggtacc gcgaaaacga ggccctggtgg cgccctgccca 60  
 agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115  
   Met Glu Tyr Gly Lys  
   1  5  
 caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163  
 Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp  
                                   10                                  15                                  20  
 ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211  
 Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln  
                   25                                  30                                  35  
 cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259  
 Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln  
                   40                                  45                                  50  
 aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307  
 Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His  
                   55                                  60                                  65  
 gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355  
 Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe

70	75	80	85	
gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val 90 95 100				403
gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly 105 110 115				451
gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr 120 125 130				499
ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn 135 140 145				547
ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys 150 155 160 165				595
gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg 170 175 180				643
aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg 185 190 195				691
gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile 200 205 210				739
acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile 215 220 225				787
ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg 230 235 240 245				835
gca gca gcg tgg gac att aac gca gcg gca gtg gct acc tcg cga cca Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Thr Ser Arg Pro 250 255 260				883
tcg cgc gcg aca aca acc tca ccc tcg tgc acg tgt cct cag att atg Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr Cys Pro Gln Ile Met 265 270 275				931
tct tcg acg gtg cgg gcg aat cct acg atg aaa acg cac cgt ttt ccc Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys Thr His Arg Phe Pro 280 285 290				979
cac tcg gcg tgt acg gcc aat cca aag cag ccg gcg aca tcg His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro Ala Thr Ser 295 300 305				1021
taagcac				1028



&lt;210&gt; 448

&lt;211&gt; 307

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 448

Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly  
 1 5 10 15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe  
 20 25 30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp  
 35 40 45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr  
 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala  
 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser  
 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val  
 100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly  
 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His  
 130 135 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr  
 145 150 155 160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr  
 165 170 175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu  
 180 185 190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg  
 195 200 205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys  
 210 215 220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln  
 225 230 235 240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val  
 245 250 255

Ala Thr Ser Arg Pro Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr  
 260 265 270

Cys Pro Gln Ile Met Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys  
 275 280 285

Thr His Arg Phe Pro His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro

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290                               295                               300

Ala Thr Ser
305

<210> 449
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXA00825

<400> 449
cccgttcacg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60

tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt 115
Met Arg Thr Val Val
1 5

acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile
10 15 20

aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg
25 30 35

ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg 259
Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val
40 45 50

gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac 307
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His
55 60 65

aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac 355
Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His
70 75 80 85

tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc 403
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr
90 95 100

atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc 451
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val
105 110 115

ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca 499
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro
120 125 130

gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc 547
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser
135 140 145

aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc 595
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly

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150	155	160	165	
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa				643
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln				
	170	175	180	
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt				691
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu				
	185	190	195	
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc				739
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg				
	200	205	210	
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct				787
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser				
	215	220	225	
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa				835
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu				
	230	235	240	245
acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc				883
Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser				
	250	255	260	
aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc				931
Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg				
	265	270	275	
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct				979
Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro				
	280	285	290	
gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc				1027
Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg				
	295	300	305	
act cac taggggaaaaa tccaccacaa atc				1056
Thr His				
310				

&lt;210&gt; 450

&lt;211&gt; 311

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 450

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu
1 5 10 15

Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn
20 25 30

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
35 40 45

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
50 55 60

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln  
 65 70 75 80  
 Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr  
 85 90 95  
 Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly  
 100 105 110  
 Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu  
 115 120 125  
 Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser  
 130 135 140  
 Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe  
 145 150 155 160  
 Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val  
 165 170 175  
 Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile  
 180 185 190  
 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp  
 195 200 205  
 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala  
 210 215 220  
 Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile  
 225 230 235 240  
 Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala  
 245 250 255  
 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu  
 260 265 270  
 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val  
 275 280 285  
 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr  
 290 295 300  
 Val Glu Tyr Phe Arg Thr His  
 305 310

<210> 451  
 <211> 1140  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1117)  
 <223> RXA02054

<400> 451  
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taactctgcc agctcgcccg gacgaactaa ggtagacggc	atg act tct ttg ctt	115
	Met Thr Ser Leu Leu	
	1 5	
gtg acc gga ggt gcc gga ttt atc ggc gcc aac ttc gtc cgc caa acc	163	
Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn Phe Val Arg Gln Thr		
	10 15 20	
gta gag cag cac cct gaa tac acc cac atc acg gtg ctg gat aaa ctc	211	
Val Glu Gln His Pro Glu Tyr Thr His Ile Thr Val Leu Asp Lys Leu		
	25 30 35	
acc tac gca gga aac gcc gac aat ctc aaa ggc ctc ccc gac agc aaa	259	
Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly Leu Pro Asp Ser Lys		
	40 45 50	
gta acc ctc atc gaa ggc gat atc tgc gat gct gaa tta gtc gac tcc	307	
Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala Glu Leu Val Asp Ser		
	55 60 65	
ctg gtc aaa gac cac gac atc aca gtc cac ttc gca gca gaa tcc cac	355	
Leu Val Lys Asp His Asp Ile Thr Val His Phe Ala Ala Glu Ser His		
	70 75 80 85	
aac gac aac tcc ctc aac gac ccc tcc ccg ttt gtt cac act aac ctc	403	
Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe Val His Thr Asn Leu		
	90 95 100	
atc ggc acc ttt gtc ctg cta gaa gca gtc cgc aag cac aac aaa cgc	451	
Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg Lys His Asn Lys Arg		
	105 110 115	
ttc cac cac atc tcc acc gat gaa gtc ttc ggc gat cta gag ctg gat	499	
Phe His His Ile Ser Thr Asp Glu Val Phe Gly Asp Leu Glu Leu Asp		
	120 125 130	
gat cca aac cgc ttc act gaa acc acc gcc tac aag cca tcg tct cca	547	
Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr Lys Pro Ser Ser Pro		
	135 140 145	
tat tct gca acc aag gca ggg tct gat cac ttg gta cac gca tgg atc	595	
Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu Val His Ala Trp Ile		
	150 155 160 165	
cgc tcc ttc gga atc cag gca acc atg tct aac tgc tcc aac aat tac	643	
Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn Cys Ser Asn Asn Tyr		
	170 175 180	
ggt ccc tac cag cac att gaa aag ttc atc ccc cgc cag atc acc aat	691	
Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro Arg Gln Ile Thr Asn		
	185 190 195	
att ctg gcc ggc ctg aca cca aaa ctt tat gga acc ggc gag cag gtc	739	
Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly Thr Gly Glu Gln Val		
	200 205 210	
cgc gac tgg atc cac gtc gat gat cac aat gac gcc gtc cac ctg atc	787	
Arg Asp Trp Ile His Val Asp Asp His Asn Asp Ala Val His Leu Ile		
	215 220 225	

ctg agt aag ggc aag atc ggc gaa acc tac atc atc ggc gcc gac aac 835  
 Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile Ile Gly Ala Asp Asn  
 230 235 240 245  
 gat cat gtg aat aac aag cag gtc atc gag ctt att tgt gaa ctc atg 883  
 Asp His Val Asn Asn Lys Gln Val Ile Glu Leu Ile Cys Glu Leu Met  
 250 255 260  
 ggc ctc gac aaa aac gca tac gag cac gtc gca gac cgc ccc ggc cac 931  
 Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala Asp Arg Pro Gly His  
 265 270 275  
 gat atg cgt tac gcc atg gat tcc acc aag ctg cgc acc gag ctc ggc 979  
 Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu Arg Thr Glu Leu Gly  
 280 285 290  
 tgg gca cct aaa tac acc gac gtt gat tcc ggc atg cgc aaa ggc cta 1027  
 Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly Met Arg Lys Gly Leu  
 295 300 305  
 gag cag acc atc gat tgg tac cgc gaa aac gag gcc tgg tgg cgc cct. 1075  
 Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu Ala Trp Trp Arg Pro  
 310 315 320 325  
 gcc aag aac aac gtc gaa gct acc tac gct aag cag gga caa 1117  
 Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys Gln Gly Gln  
 330 335  
 taatggaata cggtaaacaa ctc 1140

<210> 452  
 <211> 339  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 452  
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 Phe Val Arg Gln Thr Val Glu Gln His Pro Glu Tyr Thr His Ile Thr  
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 Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly  
 35 40 45  
 Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala  
 50 55 60  
 Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe  
 65 70 75 80  
 Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe  
 85 90 95  
 Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg  
 100 105 110  
 Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly  
 115 120 125

Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr  
 130 135 140  
 Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu  
 145 150 155 160  
 Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn  
 165 170 175  
 Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro  
 180 185 190  
 Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly  
 195 200 205  
 Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp  
 210 215 220  
 Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile  
 225 230 235 240  
 Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu  
 245 250 255  
 Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala  
 260 265 270  
 Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu  
 275 280 285  
 Arg Thr Glu Leu Gly Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly  
 290 295 300  
 Met Arg Lys Gly Leu Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu  
 305 310 315 320  
 Ala Trp Trp Arg Pro Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys  
 325 330 335

Gln Gly Gln

<210> 453  
 <211> 909  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(886)  
 <223> RXN00427

<400> 453  
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 aatcaaacct atccggtgaa acacattgtg gtggtggata atg ggg cgg atc cta 115  
 Met Gly Arg Ile Leu  
 1 5  
 gta ttc tat agt gtc act tta gag gtg gcg gga gac cgt ccc gtt tac 163

Val	Phe	Tyr	Ser	Val	Thr	Leu	Glu	Val	Ala	Gly	Asp	Arg	Pro	Val	Tyr		
				10					15					20			
acg	cct	tcg	cgc	acc	aat	ttg	ggc	gac	ggg	ggc	ggg	ttt	gct	ttt	ggg	211	
Thr	Pro	Ser	Arg	Thr	Asn	Leu	Gly	Asp	Gly	Gly	Gly	Phe	Ala	Phe	Gly		
			25					30					35				
ttt	ttg	acg	gcg	ttg	gcg	ctg	ggg	gcg	aac	gcg	gtg	tgg	tgc	aca	gac	259	
Phe	Leu	Thr	Ala	Leu	Ala	Leu	Gly	Ala	Asn	Ala	Val	Trp	Cys	Thr	Asp		
			40				45					50					
gat	gac	ggc	cgg	ccg	gag	ggg	cca	ggg	gtg	ttg	aag	acg	ctt	atc	gac	307	
Asp	Asp	Gly	Arg	Pro	Glu	Gly	Pro	Gly	Val	Leu	Lys	Thr	Leu	Ile	Asp		
	55					60					65						
gcc	gct	tct	cgg	cat	aat	ctg	gag	gag	gtt	tct	ccg	gtg	gta	tgc	aat	355	
Ala	Ala	Ser	Arg	His	Asn	Leu	Glu	Glu	Val	Ser	Pro	Val	Val	Cys	Asn		
	70				75				80						85		
gct	gat	gat	ccg	gag	cgg	ttg	gca	ttt	ccg	ctg	cgt	cgg	ggc	ttg	gag	403	
Ala	Asp	Asp	Pro	Glu	Arg	Leu	Ala	Phe	Pro	Leu	Arg	Arg	Gly	Leu	Glu		
			90						95					100			
tgg	cgt	cgg	atg	cgc	agt	gag	ttg	att	gat	cca	gcc	aac	ccg	gag	gat	451	
Trp	Arg	Arg	Met	Arg	Ser	Glu	Leu	Ile	Asp	Pro	Ala	Asn	Pro	Glu	Asp		
			105					110					115				
gat	ttg	ctg	ccg	ggc	atc	gcc	tcc	ttg	ttc	aat	ggg	gcc	ctg	atc	agc	499	
Asp	Leu	Leu	Pro	Gly	Ile	Ala	Ser	Leu	Phe	Asn	Gly	Ala	Leu	Ile	Ser		
			120				125					130					
gct	tat	gca	atg	gag	cgc	att	ggc	gtg	ccg	gac	tat	cga	ctg	ttt	att	547	
Ala	Tyr	Ala	Met	Glu	Arg	Ile	Gly	Val	Pro	Asp	Tyr	Arg	Leu	Phe	Ile		
	135					140					145						
cgc	ggc	gat	gag	gtg	gag	tat	cac	cgc	cgt	ttg	gtg	cgt	tcc	ggg	ttg	595	
Arg	Gly	Asp	Glu	Val	Glu	Tyr	His	Arg	Arg	Leu	Val	Arg	Ser	Gly	Leu		
	150				155					160					165		
ccg	ttt	ggg	acg	tgt	ttg	acc	acg	gcg	tat	ttg	cac	ccg	gat	ggg	tct	643	
Pro	Phe	Gly	Thr	Cys	Leu	Thr	Thr	Ala	Tyr	Leu	His	Pro	Asp	Gly	Ser		
			170					175						180			
gat	gag	ttc	aag	ccg	att	ctg	ggg	ggg	cgg	atg	cat	acg	cag	tat	ccg	691	
Asp	Glu	Phe	Lys	Pro	Ile	Leu	Gly	Gly	Arg	Met	His	Thr	Gln	Tyr	Pro		
			185				190						195				
gat	aat	gat	ttc	aag	agg	ttt	ttc	acc	tac	cgc	aac	cgt	ggc	tac	ctg	739	
Asp	Asn	Asp	Phe	Lys	Arg	Phe	Phe	Thr	Tyr	Arg	Asn	Arg	Gly	Tyr	Leu		
			200				205					210					
atg	agc	cag	ccg	gga	atg	cgc	aag	ctt	ctc	cct	cag	gaa	tat	gcg	cgc	787	
Met	Ser	Gln	Pro	Gly	Met	Arg	Lys	Leu	Leu	Pro	Gln	Glu	Tyr	Ala	Arg		
	215					220					225						
ttt	gcg	tgg	ttc	ttc	ctg	gtt	cag	aaa	cgg	gat	gtg	aag	gga	ttc	cgg	835	
Phe	Ala	Trp	Phe	Phe	Leu	Val	Gln	Lys	Arg	Asp	Val	Lys	Gly	Phe	Arg		
	230				235					240					245		
gag	tgg	ctg	cgc	ctg	cac	aaa	ctg	ggc	cgc	gac	gag	aaa	ttc	aat	agg	883	
Glu	Trp	Leu	Arg	Leu	His	Lys	Leu	Gly	Arg	Asp	Glu	Lys	Phe	Asn	Arg		



250

255

260

ccc tagatcagtt ttagtagttc ctc  
Pro

909

&lt;210&gt; 454

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 454

Met Gly Arg Ile Leu Val Phe Tyr Ser Val Thr Leu Glu Val Ala Gly  
1 5 10 15

Asp Arg Pro Val Tyr Thr Pro Ser Arg Thr Asn Leu Gly Asp Gly Gly  
20 25 30

Gly Phe Ala Phe Gly Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala  
35 40 45

Val Trp Cys Thr Asp Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu  
50 55 60

Lys Thr Leu Ile Asp Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser  
65 70 75 80

Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu  
85 90 95

Arg Arg Gly Leu Glu Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro  
100 105 110

Ala Asn Pro Glu Asp Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn  
115 120 125

Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp  
130 135 140

Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu  
145 150 155 160

Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu  
165 170 175

His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met  
180 185 190

His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg  
195 200 205

Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro  
210 215 220

Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp  
225 230 235 240

Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp  
245 250 255

Glu Lys Phe Asn Arg Pro  
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<210> 455  
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<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(532)  
<223> FRXA00427

<400> 455  
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Leu Leu Pro Gly Ile  
1 5  
gcc tcc ttg ttc aat ggt gcc ctg atc agc gct tat gca atg gag cgc 163  
Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg  
10 15 20  
att ggc gtg ccg gac tat cga ctg ttt att cgc ggc gat gag gtg gag 211  
Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu  
25 30 35  
tat cac cgc cgt ttg gtg cgt tcc ggt ttg ccg ttt ggt acg tgt ttg 259  
Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu  
40 45 50  
acc acg gcg tat ttg cac ccg gat ggt tct gat gag ttc aag ccg att 307  
Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile  
55 60 65  
ctg ggt ggg cgg atg cat acg cag tat ccg gat aat gat ttc aag agg 355  
Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg  
70 75 80 85  
ttt ttc acc tac cgc aac cgt ggc tac ctg atg agc cag ccg gga atg 403  
Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met  
90 95 100  
cgc aag ctt ctc cct cag gaa tat gcg cgc ttt gcg tgg ttc ttc ctg 451  
Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu  
105 110 115  
gtt cag aaa cgg gat gtg aag gga ttc cgg gag tgg ctg cgc ctg cac 499  
Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His  
120 125 130  
aaa ctg ggc cgc gac gag aaa ttc aat agg ccc tagatcagtt ttagtagttc 552  
Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro  
135 140  
ctc 555

<210> 456

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 456

Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala  
 1 5 10 15

Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg  
 20 25 30

Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro  
 35 40 45

Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp  
 50 55 60

Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp  
 65 70 75 80

Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met  
 85 90 95

Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe  
 100 105 110

Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu  
 115 120 125

Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro  
 130 135 140

&lt;210&gt; 457

&lt;211&gt; 507

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(484)

&lt;223&gt; RXA00327

&lt;400&gt; 457

aacgattttc gccgtcgcaa ccgtgatcac cggtcgcttt ccggcatcgt gtcgtcgcg 60

ctagggggcc aggcgcggga tgattgggtt tgtcacgccg atg.att cag gcg gcg 115  
 Met Ile Gln Ala Ala  
 1 5

ttg tgg atc gtg ctc ttt tta ttc gct gat cgc ctg tcc aat ccg ctg 163  
 Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg Leu Ser Asn Pro Leu  
 10 15 20

gtt ttt gtc agc gcc atc atg ttc gcg att tcc ttt agc tcc ccc gtg 211  
 Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser Phe Ser Ser Pro Val  
 25 30 35

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<400> 458
Met Ile Gln Ala Ala Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg
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Leu Ser Asn Pro Leu Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser
          20           25           30

Phe Ser Ser Pro Val Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys
          35           40           45

Leu Asp Arg Arg Val Met Val Ala Gly Thr Gly Met Ala Asn Met Ser
  50           55           60

Ala Tyr Ile Cys Ala Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu
  65           70           75           80

Asp Trp Asn Ala Asp Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val
          85           90           95

Ala Trp Leu Gly Leu Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu
          100          105          110

Ala Val Cys Leu Leu Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg
      115           120           125

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$\langle 210 \rangle$  460

<211> 164  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 460  
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 Leu Thr Ala Met Cys Val Tyr Ile Val Ala Ile Ala Gly Arg Thr Ser  
           20                    25                    30  
 Phe Gly Val Ala Gly Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala  
           35                    40                    45  
 Ser Arg Leu Ala Val Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu  
           50                    55                    60  
 Ala Gln Ile Pro Met Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys  
           65                    70                    75                    80  
 Leu Leu Leu Ala Gly Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu  
                     85                    90                    95  
 Gly Phe Thr Asp Ser Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile  
                     100                    105                    110  
 Ser Val Gly Asp Ser Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro  
           115                    120                    125  
 Asn Trp Phe Pro Met Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly  
           130                    135                    140  
 Ala Phe Gly Phe Val Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr  
           145                    150                    155                    160  
 Tyr Ser Thr Pro

<210> 461  
 <211> 1347  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1324)  
 <223> RXA00329

<400> 461  
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 ccgcgccttc atagtttggg cagcagcctg tcttgtgtat atg gca gcc att acc 115  
   Met Ala Ala Ile Thr  
   1                    5  
 agc cgc acc agc ttt ggt gtg gct gga gtg gag gcc att gat cgt ttt 163  
 Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu Ala Ile Asp Arg Phe  
                     10                    15                    20  
 cag gta gac gcc aca cgc att gca gta ttc act tct gtt cag gtt ggt 211

Gln Val Asp Ala Thr Arg Ile Ala Val Phe Thr Ser Val Gln Val Gly	
25 30 35	
gtg tac gcg ttt gct cag att ccg atg ggc att ttg atc gat aag ttt	259
Val Tyr Ala Phe Ala Gln Ile Pro Met Gly Ile Leu Ile Asp Lys Phe	
40 45 50	
ggg cct cgg aag ctc ctt gcc att ggt gct ttg gtg atg ggt atc ggc	307
Gly Pro Arg Lys Leu Leu Ala Ile Gly Ala Leu Val Met Gly Ile Gly	
55 60 65	
cag ctc att ttg ggc ttt acg gat agc tat tcc atc gcg att att gcc	355
Gln Leu Ile Leu Gly Phe Thr Asp Ser Tyr Ser Ile Ala Ile Ile Ala	
70 75 80 85	
cgc gtg ttt atc ggc gcc ggc gat gca tcg atc ttc ctt tcg gtt atg	403
Arg Val Phe Ile Gly Ala Gly Asp Ala Ser Ile Phe Leu Ser Val Met	
90 95 100	
cgc atc ctg ccg ttt tgg ttc cca ctg aag cac acc cct att ttc acg	451
Arg Ile Leu Pro Phe Trp Phe Pro Leu Lys His Thr Pro Ile Phe Thr	
105 110 115	
cag tta act acc tgc ctt ggc cag ttg ggc cag ttc ttt tct gcg gtg	499
Gln Leu Thr Thr Cys Leu Gly Gln Leu Gly Gln Phe Phe Ser Ala Val	
120 125 130	
cct ttc atg gcg ttg ttg ggt gcg cag ggt tgg cct gtg gcg ttt gtc	547
Pro Phe Met Ala Leu Leu Gly Ala Gln Gly Trp Pro Val Ala Phe Val	
135 140 145	
agc ctt ggt tcc gtg gtg gca ctc att gcg atc gca gcg ctg gtg gcc	595
Ser Leu Gly Ser Val Val Ala Leu Ile Ala Ile Ala Ala Leu Val Ala	
150 155 160 165	
gtt cgg gat act cca gat cct cag cca aaa cct gtc gaa tca gct cag	643
Val Arg Asp Thr Pro Asp Pro Gln Pro Lys Pro Val Glu Ser Ala Gln	
170 175 180	
gaa gca gat aaa cca agc ctg cgc gcg agt ttg aag ttg att gtc cgc	691
Glu Ala Asp Lys Pro Ser Leu Arg Ala Ser Leu Lys Leu Ile Val Arg	
185 190 195	
aat ccg att acg tgg cag ggt ttc ttc att cac tac gta ttg atg gtg	739
Asn Pro Ile Thr Trp Gln Gly Phe Phe Ile His Tyr Val Leu Met Val	
200 205 210	
tgg cag acc gtg ttc tcc atg atg tgg ggc gtc ccg ctg atg act ttg	787
Trp Gln Thr Val Phe Ser Met Met Trp Gly Val Pro Leu Met Thr Leu	
215 220 225	
ggc atg gga ctg tct gca acg acg gct ggt ttg gtg ttg agc atc aac	835
Gly Met Gly Leu Ser Ala Thr Thr Ala Gly Leu Val Leu Ser Ile Asn	
230 235 240 245	
acg ctg tgc atg gtg gta tcg gcg cca atc atc gga ata att tcc gca	883
Thr Leu Cys Met Val Val Ser Ala Pro Ile Ile Gly Ile Ile Ser Ala	
250 255 260	
cgc ctt ggg tat cgc cgt gac gtg gtc gcc att gcg ctg tcg ttt gtt	931
Arg Leu Gly Tyr Arg Arg Asp Val Val Ala Ile Ala Leu Ser Phe Val	

265	270	275	
caa tcc gca gta tgg ctg gtg ttc ttg gcc tcc gat gca cct cgt ggt			979
Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly			
280	285	290	
ttg atg gct atc atc ttg gtc aac atc gtc atg ggt ctg act act gcg			1027
Leu Met Ala Ile Ile Leu Val Asn Ile Val Met Gly Leu Thr Thr Ala			
295	300	305	
gct tct ggt tat ggc ttt gac acc att cgt gag cgc cta gat cgc aag			1075
Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu Arg Leu Asp Arg Lys			
310	315	320	325
att ttg gct gcg ggc acg gga ctg gca aac atg ggt gga ttc ttg tca			1123
Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser			
330	335	340	
tcg atg gtt gca gcg cag gtt atg ggg ttc ctt ctt gat cac agc gcg			1171
Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala			
345	350	355	
cat ggt agc acc tat act tgg gtg gac ttc cgt ttt ggt ttc ctt gcg			1219
His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala			
360	365	370	
att ctt gtc aca tgg gcc gtc gga gtc acg gga ttt gtt gta gcc cga			1267
Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly Phe Val Val Ala Arg			
375	380	385	
ctc aag ggt gga ccg ggc cgc aga tta ctc gcc cag att agg tct acc			1315
Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala Gln Ile Arg Ser Thr			
390	395	400	405
aag gac ttt taaagatcgg gtaaaacctg tgg			1347
Lys Asp Phe			

&lt;210&gt; 462

&lt;211&gt; 408

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 462

Met	Ala	Ala	Ile	Thr	Ser	Arg	Thr	Ser	Phe	Gly	Val	Ala	Gly	Val	Glu
1				5					10					15	

Ala	Ile	Asp	Arg	Phe	Gln	Val	Asp	Ala	Thr	Arg	Ile	Ala	Val	Phe	Thr
		20						25					30		

Ser	Val	Gln	Val	Gly	Val	Tyr	Ala	Phe	Ala	Gln	Ile	Pro	Met	Gly	Ile
		35					40					45			

Leu	Ile	Asp	Lys	Phe	Gly	Pro	Arg	Lys	Leu	Leu	Ala	Ile	Gly	Ala	Leu
	50					55					60				

Val	Met	Gly	Ile	Gly	Gln	Leu	Ile	Leu	Gly	Phe	Thr	Asp	Ser	Tyr	Ser
65					70					75					80

Ile	Ala	Ile	Ile	Ala	Arg	Val	Phe	Ile	Gly	Ala	Gly	Asp	Ala	Ser	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



85						90						95			
Phe	Leu	Ser	Val 100	Met	Arg	Ile	Leu	Pro 105	Phe	Trp	Phe	Pro	Leu 110	Lys	His
Thr	Pro	Ile 115	Phe	Thr	Gln	Leu	Thr 120	Thr	Cys	Leu	Gly	Gln 125	Leu	Gly	Gln
Phe	Phe 130	Ser	Ala	Val	Pro	Phe 135	Met	Ala	Leu	Leu	Gly 140	Ala	Gln	Gly	Trp
Pro 145	Val	Ala	Phe	Val	Ser 150	Leu	Gly	Ser	Val	Val 155	Ala	Leu	Ile	Ala	Ile 160
Ala	Ala	Leu	Val	Ala 165	Val	Arg	Asp	Thr	Pro 170	Asp	Pro	Gln	Pro	Lys 175	Pro
Val	Glu	Ser	Ala 180	Gln	Glu	Ala	Asp	Lys 185	Pro	Ser	Leu	Arg	Ala 190	Ser	Leu
Lys	Leu	Ile 195	Val	Arg	Asn	Pro	Ile 200	Thr	Trp	Gln	Gly	Phe 205	Phe	Ile	His
Tyr	Val 210	Leu	Met	Val	Trp	Gln 215	Thr	Val	Phe	Ser	Met 220	Met	Trp	Gly	Val
Pro 225	Leu	Met	Thr	Leu	Gly 230	Met	Gly	Leu	Ser	Ala 235	Thr	Thr	Ala	Gly	Leu 240
Val	Leu	Ser	Ile	Asn 245	Thr	Leu	Cys	Met	Val 250	Val	Ser	Ala	Pro	Ile 255	Ile
Gly	Ile	Ile	Ser 260	Ala	Arg	Leu	Gly	Tyr 265	Arg	Arg	Asp	Val	Val 270	Ala	Ile
Ala	Leu	Ser 275	Phe	Val	Gln	Ser	Ala 280	Val	Trp	Leu	Val	Phe 285	Leu	Ala	Ser
Asp	Ala 290	Pro	Arg	Gly	Leu	Met 295	Ala	Ile	Ile	Leu	Val 300	Asn	Ile	Val	Met
Gly 305	Leu	Thr	Thr	Ala 310	Ala	Ser	Gly	Tyr	Gly	Phe 315	Asp	Thr	Ile	Arg	Glu 320
Arg	Leu	Asp	Arg	Lys 325	Ile	Leu	Ala	Ala	Gly 330	Thr	Gly	Leu	Ala	Asn 335	Met
Gly	Gly	Phe 340	Leu	Ser	Ser	Met	Val	Ala 345	Ala	Gln	Val	Met	Gly 350	Phe	Leu
Leu	Asp	His 355	Ser	Ala	His	Gly	Ser 360	Thr	Tyr	Thr	Trp	Val 365	Asp	Phe	Arg
Phe	Gly 370	Phe	Leu	Ala	Ile	Leu 375	Val	Thr	Trp	Ala	Val 380	Gly	Val	Thr	Gly
Phe 385	Val	Val	Ala	Arg	Leu 390	Lys	Gly	Gly	Pro	Gly 395	Arg	Arg	Leu	Leu	Ala 400
Gln	Ile	Arg	Ser	Thr 405	Lys	Asp	Phe								



170								175				180				
tac	gga	gaa	cta	gac	ctg	gta	gag	cac	ttt	tct	tac	gat	ctt	cgc	tcg	691
Tyr	Gly	Glu	Leu	Asp	Leu	Val	Glu	His	Phe	Ser	Tyr	Asp	Leu	Arg	Ser	
185								190				195				
cca	tgg	tct	cca	tca	aac	acc	cac	ttg	ggg	tgt	gat	cct	gaa	agt	gtc	739
Pro	Trp	Ser	Pro	Ser	Asn	Thr	His	Leu	Gly	Cys	Asp	Pro	Glu	Ser	Val	
200								205				210				
aac	ggc	acc	aac	cgt	gca	cct	cgt	gaa	ctt	aaa	cta	gat	gag	tca	ctc	787
Asn	Gly	Thr	Asn	Arg	Ala	Pro	Arg	Glu	Leu	Lys	Leu	Asp	Glu	Ser	Leu	
215								220				225				
gat	ggc	gtg	gag	cac	acc	tgg	act	gtg	agc	acc	acc	cgc	gac	ggc	gtt	835
Asp	Gly	Val	Glu	His	Thr	Trp	Thr	Val	Ser	Thr	Thr	Arg	Asp	Gly	Val	
230								240				245				
gag	tac	ttc	att	gat	gat	gag	gcg	att	aac	cgc	cag	tca	tgg	cgc	aac	883
Glu	Tyr	Phe	Ile	Asp	Asp	Glu	Ala	Ile	Asn	Arg	Gln	Ser	Trp	Arg	Asn	
250								255				260				
gat	gtc	act	ttg	ggg	cat	gcc	gaa	att	gat	gat	ttc	ggg	atc	tcc	gcg	931
Asp	Val	Thr	Leu	Gly	His	Ala	Glu	Ile	Asp	Asp	Phe	Gly	Ile	Ser	Ala	
265								270				275				
cag	acg	ttt	gat	gag	atc	gtc	gac	cgc	gaa	tgg	act	ctc	act	ctt	aat	979
Gln	Thr	Phe	Asp	Glu	Ile	Val	Asp	Arg	Glu	Trp	Thr	Leu	Thr	Leu	Asn	
280								285				290				
caa	aag	gta	gaa	agc	gcc	gac	tgg	gca	aaa	cca	cgt	tcc	tct	gag	gaa	1027
Gln	Lys	Val	Glu	Ser	Ala	Asp	Trp	Ala	Lys	Pro	Arg	Ser	Ser	Glu	Glu	
295								300				305				
gat	ttc	cca	gtc	cgg	tcc	atg	gtg	att	gac	cgc	atc	gag	gtc	acc	gga	1075
Asp	Phe	Pro	Val	Arg	Ser	Met	Val	Ile	Asp	Arg	Ile	Glu	Val	Thr	Gly	
310								315				320				
tct	ccc	gca	gta	tct	gaa	gac	acc	ccc	atg	cca	gat	acc	acc	cag	ctt	1123
Ser	Pro	Ala	Val	Ser	Glu	Asp	Thr	Pro	Met	Pro	Asp	Thr	Thr	Gln	Leu	
330								335				340				
ttg	acc	caa	gac	act	ctg	gaa	tac	ctc	ggg	cgc	atg	cca	gtg	ctg	gaa	1171
Leu	Thr	Gln	Asp	Thr	Leu	Glu	Tyr	Leu	Gly	Arg	Met	Pro	Val	Leu	Glu	
345								350				355				
cgc	tac	gag	cca	gca	agt	gct	gat	ttt	gcc	gat	ggc	cgc	agg	cct	tcc	1219
Arg	Tyr	Glu	Pro	Ala	Ser	Ala	Asp	Phe	Ala	Asp	Gly	Arg	Arg	Pro	Ser	
360								365				370				
tgg	aac	tac	ttc	aat	ttg	aag	gaa	tcg	tgg	cag	aat	cca	gaa	ctc	gag	1267
Trp	Asn	Tyr	Phe	Asn	Leu	Lys	Glu	Ser	Trp	Gln	Asn	Pro	Glu	Leu	Glu	
375								380				385				
caa	cgc	cca	gaa	gct	gtc	gaa	ttc	gtt	gat	gga	cgc	atg	gat	atc	gtg	1315
Gln	Arg	Pro	Glu	Ala	Val	Glu	Phe	Val	Asp	Gly	Arg	Met	Asp	Ile	Val	
390								395				400				
acc	cgt	cgc	cac	tgt	ctg	gcc	acc									

aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc	1411
Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser	
425 430 435	
tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc	1459
Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu	
440 445 450	
acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc	1507
Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg	
455 460 465	
ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat	1555
Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp	
470 475 480 485	
gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt	1603
Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg	
490 495 500	
gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc	1651
Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg	
505 510 515	
cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg	1699
Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly	
520 525 530	
gat tgg cat gac tgg ggc gtc gaa gtc ttc gac ggc cag atc gta ttc	1747
Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe	
535 540 545	
acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc	1795
Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly	
550 555 560 565	
aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag	1843
Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg Pro Ala His Phe Lys	
570 575 580	
ttg tcg gaa gag gaa tac cgt gaa gtc atc ggg cag cct tgg cac ctt	1891
Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu	
585 590 595	
att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca	1939
Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr	
600 605 610	
gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac	1987
Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp	
615 620 625	
cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct	2035
His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro	
630 635 640 645	
gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat	2083
Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp	
650 655 660	

gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag 2131  
 Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu  
 665 670 675  
 acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc 2179  
 Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe  
 680 685 690  
 aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc 2227  
 Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe  
 695 700 705  
 atg aga cag ttc aag taatccttgt gggcgctttg tct 2265  
 Met Arg Gln Phe Lys  
 710

<210> 464

<211> 714

<212> PRT

<213> Corynebacterium glutamicum

<400> 464

Leu Lys Lys His Val Thr Ser Ala Val Thr Ala Val Val Thr Ala Phe  
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 Ser Thr Ala Ala Leu Gly Leu Ser Ile Ala Val Ser Pro Ala Val Ala  
 20 25 30  
 Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val  
 35 40 45  
 Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg  
 50 55 60  
 Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu  
 65 70 75 80  
 Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val  
 85 90 95  
 Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn  
 100 105 110  
 Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys  
 115 120 125  
 Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe  
 130 135 140  
 Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val  
 145 150 155 160  
 Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala  
 165 170 175  
 Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser  
 180 185 190  
 Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys  
 195 200 205

Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys  
 210 215 220  
 Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr  
 225 230 235 240  
 Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg  
 245 250 255  
 Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp  
 260 265 270  
 Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp  
 275 280 285  
 Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro  
 290 295 300  
 Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg  
 305 310 315 320  
 Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro  
 325 330 335  
 Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg  
 340 345 350  
 Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp  
 355 360 365  
 Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln  
 370 375 380  
 Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly  
 385 390 395 400  
 Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp  
 405 410 415  
 Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu  
 420 425 430  
 Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala  
 435 440 445  
 Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu  
 450 455 460  
 Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe  
 465 470 475 480  
 Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu  
 485 490 495  
 Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly  
 500 505 510  
 Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu  
 515 520 525

Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp  
 530 535 540  
 Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly  
 545 550 555 560  
 Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg  
 565 570 575  
 Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly  
 580 585 590  
 Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys  
 595 600 605  
 Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His  
 610 615 620  
 Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val  
 625 630 635 640  
 Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly  
 645 650 655  
 Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly  
 660 665 670  
 Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu  
 675 680 685  
 Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn  
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 Leu Ile Asn Gln Phe Met Arg Gln Phe Lys  
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 <211> 389  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(382)  
 <223> RXN03015

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 Leu Gly Val Gly Thr  
 1 5  
 cct cag cag aag ggt act tat gcg gcg gat ctg acg tat gtt cgt cag 163  
 Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu Thr Tyr Val Arg Gln  
 10 15 20  
 gtt gtt gag gat ttg gtg ccg ctg ctt gag ggc gag cac att att ttc 211  
 Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly Glu His Ile Ile Phe  
 25 30 35

ggc aag tct acg gtt ccg gtt ggt act gct gag cag ttg cag gag ctt 259  
 Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu Gln Leu Gln Glu Leu  
           40                          45                          50  
 gct gat tct ctg gtc aag cct ggt tcg cac gtg gag atc gcg tgg aat 307  
 Ala Asp Ser Leu Val Lys Pro Gly Ser His Val Glu Ile Ala Trp Asn  
           55                          60                          65  
 ccg gag ttc ttg cgt gag ggc tac gcg gtc aaa gac acc atc act ccg 355  
 Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys Asp Thr Ile Thr Pro  
           70                          75                          80                          85  
 gac cgc atc gtg gtg ggt gtg cgt gaa taagaca 389  
 Asp Arg Ile Val Val Gly Val Arg Glu  
                           90

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 466  
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 Thr Tyr Val Arg Gln Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly  
           20                          25                          30  
 Glu His Ile Ile Phe Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu  
           35                          40                          45  
 Gln Leu Gln Glu Leu Ala Asp Ser Leu Val Lys Pro Gly Ser His Val  
           50                          55                          60  
 Glu Ile Ala Trp Asn Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys  
           65                          70                          75                          80  
 Asp Thr Ile Thr Pro Asp Arg Ile Val Val Gly Val Arg Glu  
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<210> 467  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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   Leu Asp Ala Ala Gly  
   1                          5  
 att tca ctt tca gcc gtt gga tcc gac ttc ggc aag atc aac atc acc 163



Ile	Ser	Leu	Ser	Ala	Val	Gly	Ser	Asp	Phe	Gly	Lys	Ile	Asn	Ile	Thr		
				10					15					20			
gat	cct	ttt	gaa	gat	cac	ttg	gag	cgc	gca	cgc	cac	ggt	gtt	gag	gtc	211	
Asp	Pro	Phe	Glu	Asp	His	Leu	Glu	Arg	Ala	Arg	His	Gly	Val	Glu	Val		
			25					30					35				
gct	aag	ctc	ttc	ggc	gcg	aaa	tac	atc	cgc	atg	ttc	tcc	ttc	ttt	att	259	
Ala	Lys	Leu	Phe	Gly	Ala	Lys	Tyr	Ile	Arg	Met	Phe	Ser	Phe	Phe	Ile		
		40					45					50					
gca	gaa	ggc	gac	aac	cct	gaa	agc	ttc	cgc	aaa	gaa	gta	ctc	tcc	cgc	307	
Ala	Glu	Gly	Asp	Asn	Pro	Glu	Ser	Phe	Arg	Lys	Glu	Val	Leu	Ser	Arg		
		55					60					65					
acc	cac	gca	atg	gtc	gaa	ctc	gca	gaa	gcc	ggc	ggc	atc	acc	ctc	ctc	355	
Thr	His	Ala	Met	Val	Glu	Leu	Ala	Glu	Ala	Gly	Gly	Ile	Thr	Leu	Leu		
		70				75				80					85		
cac	gaa	aat	gaa	aag	gga	atc	tat	ggc	gac	tcc	ccg	cag	cgc	gtg	aag	403	
His	Glu	Asn	Glu	Lys	Gly	Ile	Tyr	Gly	Asp	Ser	Pro	Gln	Arg	Val	Lys		
				90					95					100			
gat	tta	atc	acc	agc	atc	gac	tcc	cct	aac	tac	cgc	gca	atc	tac	gac	451	
Asp	Leu	Ile	Thr	Ser	Ile	Asp	Ser	Pro	Asn	Tyr	Arg	Ala	Ile	Tyr	Asp		
			105					110					115				
gca	gct	aac	tac	gtg	caa	acc	gga	ttc	aag	cct	ttt	gat	gag	gca	tgg	499	
Ala	Ala	Asn	Tyr	Val	Gln	Thr	Gly	Phe	Lys	Pro	Phe	Asp	Glu	Ala	Trp		
		120					125						130				
ccg	atc	gtt	aag	gac	tac	gtc	gac	tac	gtc	cac	atc	aag	gac	gcg	acc	547	
Pro	Ile	Val	Lys	Asp	Tyr	Val	Asp	Tyr	Val	His	Ile	Lys	Asp	Ala	Thr		
		135					140					145					
att	cca	gat	gca	gag	cac	ccc	atc	gga	atc	atc	aag	cca	gca	gga	caa	595	
Ile	Pro	Asp	Ala	Glu	His	Pro	Ile	Gly	Ile	Ile	Lys	Pro	Ala	Gly	Gln		
		150			155					160					165		
ggc	gac	ggc	caa	tac	cca	gag	ctc	ctt	gcc	gcg	cta	aac	gcc	gac	ggt	643	
Gly	Asp	Gly	Gln	Tyr	Pro	Glu	Leu	Leu	Ala	Ala	Leu	Asn	Ala	Asp	Gly		
				170					175					180			
tac	aac	gga	ttc	gtc	tcc	atc	gag	cct	cac	ctg	ggt	gac	ttc	gat	gaa	691	
Tyr	Asn	Gly	Phe	Val	Ser	Ile	Glu	Pro	His	Leu	Gly	Asp	Phe	Asp	Glu		
			185					190					195				
ttc	ggc	gga	ctc	tgc	gga	cct	gac	ctg	tgg	acc	agc	gca	tgc	gac	gct	739	
Phe	Gly	Gly	Leu	Cys	Gly	Pro	Asp	Leu	Trp	Thr	Ser	Ala	Cys	Asp	Ala		
		200					205					210					
ctc	gca	gga	atc	ctg	aac	aac	atc	aac	gcc	gag	tac	aac	taaggacaac			788	
Leu	Ala	Gly	Ile	Leu	Asn	Asn	Ile	Asn	Ala	Glu	Tyr	Asn					
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&lt;210&gt; 468

&lt;211&gt; 226

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 468

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Lys Ile Asn Ile Thr Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg  
20 25 30

His Gly Val Glu Val Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met  
35 40 45

Phe Ser Phe Phe Ile Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys  
50 55 60

Glu Val Leu Ser Arg Thr His Ala Met Val Glu Leu Ala Glu Ala Gly  
65 70 75 80

Gly Ile Thr Leu Leu His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser  
85 90 95

Pro Gln Arg Val Lys Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr  
100 105 110

Arg Ala Ile Tyr Asp Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro  
115 120 125

Phe Asp Glu Ala Trp Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His  
130 135 140

Ile Lys Asp Ala Thr Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile  
145 150 155 160

Lys Pro Ala Gly Gln Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala  
165 170 175

Leu Asn Ala Asp Gly Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu  
180 185 190

Gly Asp Phe Asp Glu Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr  
195 200 205

Ser Ala Cys Asp Ala Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu  
210 215 220

Tyr Asn  
225

<210> 469

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXN03030

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Thr Gly Arg	Thr Lys Ile Asp Glu Val	Gln Leu Gln Leu Glu Ala Ala	
	20	25	30
Ile Arg Ala	Glu Leu Pro Gly Val Thr Leu Val Ser Ser Glu Ser Glu		
	35	40	45
Ala Asp Leu	Ala Ile Val Trp Ala Arg Pro Glu Ile Ala Leu Phe Glu		
	50	55	60
Asp Asp Leu	Glu Gly Val Ser Leu Ser Val Asp Pro Arg Ala Asn Gly		
	65	70	75
Val Asp Val	Glu Arg Val Gln Ala Val Glu Ala Ala Val Pro Thr Ile		
	85	90	95
Leu Ala Val	Asn Phe Thr Asn Pro Trp Val Leu Ser Glu Ile Glu Pro		
	100	105	110
Gly Ala Ala	Ala Val Val Gly Thr Phe Glu Ile Lys Pro Glu Phe Leu		
	115	120	125
Leu Lys Ala	Leu Thr Gly Gln Glu Gly Gly Pro Lys Gly Lys Leu Pro		
	130	135	140
Leu Thr Val	Pro Ala Ser Met Gln Ala Ile Ala Asp Ser Pro Arg Asp		
	145	150	155
Ile Pro Gly	Lys Phe Leu Asp Glu Ser Tyr Thr Tyr Val Asp Ser Ala		
	165	170	175
Gly Met Ala	Tyr Lys Tyr Gly His Gly Leu Asn Phe		
	180	185	

<210> 471  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1039)  
 <223> RXN00401

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 Met Ala Arg Phe Ser  
 1 5  
 cca caa gat ctc gca gac cac ctc aag gat gga ctg ctc tct ttc ccg 163  
 Pro Gln Asp Leu Ala Asp His Leu Lys Asp Gly Leu Leu Ser Phe Pro  
 10 15 20  
 gcc acc gct ttc caa gat gac ctc gaa gta gat gaa gct gct tat gtc 211  
 Ala Thr Ala Phe Gln Asp Asp Leu Glu Val Asp Glu Ala Ala Tyr Val  
 25 30 35

gag	cac	att	gaa	tgg	cag	tcc	agc	tac	cca	gtc	gcc	ggc	ctc	ttc	gca	259
Glu	His	Ile	Glu	Trp	Gln	Ser	Ser	Tyr	Pro	Val	Ala	Gly	Leu	Phe	Ala	
		40					45					50				
gct	ggc	ggg	act	ggc	gaa	gga	ttc	agc	ctt	acc	gtt	gag	gaa	aac	cac	307
Ala	Gly	Gly	Thr	Gly	Glu	Gly	Phe	Ser	Leu	Thr	Val	Glu	Glu	Asn	His	
	55					60					65					
cgt	gtc	act	caa	ctt	gca	gtt	cag	gcg	tcc	agc	ccg	gaa	gtt	ccc	gtg	355
Arg	Val	Thr	Gln	Leu	Ala	Val	Gln	Ala	Ser	Ser	Pro	Glu	Val	Pro	Val	
70					75					80					85	
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Leu	Gly	Ser	Ala	Thr	Gly	Ser	Thr	Lys	Ser	Ala	Ile	Ala	Asn	Ala	Gln	
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ggc	gca	gag	gca	gca	ggc	gct	gaa	ggg	gtc	ctc	ctg	ctt	cct	ccc	tac	451
Gly	Ala	Glu	Ala	Ala	Gly	Ala	Glu	Gly	Val	Leu	Leu	Leu	Pro	Pro	Tyr	
			105					110					115			
ctc	acc	gaa	tgc	gac	gca	gaa	ggc	ctg	tac	aac	cat	gca	gcc	gca	gtc	499
Leu	Thr	Glu	Cys	Asp	Ala	Glu	Gly	Leu	Tyr	Asn	His	Ala	Ala	Ala	Val	
		120					125					130				
tgt	gaa	tcc	act	tct	ctt	ggg	gtc	atc	gtg	tac	aac	cgt	gcc	aat	gcc	547
Cys	Glu	Ser	Thr	Ser	Leu	Gly	Val	Ile	Val	Tyr	Asn	Arg	Ala	Asn	Ala	
	135					140					145					
atc	tac	tcc	cca	gag	gtt	atc	gct	cga	ctc	tct	gag	cgc	tac	ccc	aac	595
Ile	Tyr	Ser	Pro	Glu	Val	Ile	Ala	Arg	Leu	Ser	Glu	Arg	Tyr	Pro	Asn	
150					155				160						165	
ttc	att	gga	ttt	aaa	gat	ggc	acc	gga	aac	atc	gag	cac	cta	gca	aag	643
Phe	Ile	Gly	Phe	Lys	Asp	Gly	Thr	Gly	Asn	Ile	Glu	His	Leu	Ala	Lys	
			170					175						180		
atc	acc	acg	cta	tgc	gga	gat	cgc	ctg	ttc	tac	ctc	ggg	gga	ctt	ccc	691
Ile	Thr	Thr	Leu	Cys	Gly	Asp	Arg	Leu	Phe	Tyr	Leu	Gly	Gly	Leu	Pro	
			185					190					195			
acc	gct	gag	acc	ttt	gca	cta	cca	ctg	ctt	cag	atg	ggc	atg	agc	acc	739
Thr	Ala	Glu	Thr	Phe	Ala	Leu	Pro	Leu	Leu	Gln	Met	Gly	Met	Ser	Thr	
		200					205					210				
tac	tcc	tct	gca	atg	ttc	aac	ttc	att	cca	gat	ttc	gca	ctg	agc	ttc	787
Tyr	Ser	Ser	Ala	Met	Phe	Asn	Phe	Ile	Pro	Asp	Phe	Ala	Leu	Ser	Phe	
	215					220					225					
tac	gcc	gat	gtt	cgt	gcg	cag	gac	agc	gca	gca	gta	aag	cag	aag	ctg	835
Tyr	Ala	Asp	Val	Arg	Ala	Gln	Asp	Ser	Ala	Ala	Val	Lys	Gln	Lys	Leu	
230					235				240						245	
agc	gat	ttt	gtg	ctc	ccc	tac	ttg	gat	atc	cgc	gat	cgc	gca	caa	ggc	883
Ser	Asp	Phe	Val	Leu	Pro	Tyr	Leu	Asp	Ile	Arg	Asp	Arg	Ala	Gln	Gly	
			250					255					260			
tac	ggg	gtc	tcc	att	ggg	aag	ggc	gga	ctc	aag	gct	gtt	ggc	cgc	aac	931
Tyr	Gly	Val	Ser	Ile	Gly	Lys	Gly	Gly	Leu	Lys	Ala	Val	Gly	Arg	Asn	
			265				270						275			
gct	ggc	ggc	gtt	cgc	cca	cca	ctg	cgt	aac	ctt	tcc	gag	caa	gat	atc	979

Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu Ser Glu Gln Asp Ile  
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gcg gac ctg tcg gat ttg ctt gcc acc tct ggc gca ggt tcc tac cgc 1027  
 Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly Ala Gly Ser Tyr Arg  
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Glu Ala Ala Tyr Val Glu His Ile Glu Trp Gln Ser Ser Tyr Pro Val  
 35 40 45

Ala Gly Leu Phe Ala Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr  
 50 55 60

Val Glu Glu Asn His Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser  
 65 70 75 80

Pro Glu Val Pro Val Leu Gly Ser Ala Thr Gly Ser Thr Lys Ser Ala  
 85 90 95

Ile Ala Asn Ala Gln Gly Ala Glu Ala Ala Gly Ala Glu Gly Val Leu  
 100 105 110

Leu Leu Pro Pro Tyr Leu Thr Glu Cys Asp Ala Glu Gly Leu Tyr Asn  
 115 120 125

His Ala Ala Ala Val Cys Glu Ser Thr Ser Leu Gly Val Ile Val Tyr  
 130 135 140

Asn Arg Ala Asn Ala Ile Tyr Ser Pro Glu Val Ile Ala Arg Leu Ser  
 145 150 155 160

Glu Arg Tyr Pro Asn Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile  
 165 170 175

Glu His Leu Ala Lys Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr  
 180 185 190

Leu Gly Gly Leu Pro Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln  
 195 200 205

Met Gly Met Ser Thr Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp  
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Phe Ala Leu Ser Phe Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala

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Val Lys Gln Lys Leu Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg						
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Asp Arg Ala Gln Gly Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys						
		260		265		270
Ala Val Gly Arg Asn Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu						
		275		280		285
Ser Glu Gln Asp Ile Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly						
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Ala Gly Ser Tyr Arg Leu Gln Leu Arg						
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 Met Val Ala Thr Ser  
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 cag ttt atc gat gac agc gag gct gcc cag gcg gta cgc gca gct att 163  
 Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala Val Arg Ala Ala Ile  
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 gtt gca gga tac cga aac att gat act gcc cta gcg tat gga aac gag 211  
 Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu Ala Tyr Gly Asn Glu  
 25 30 35  
 cgc gcc gtt ggc gaa gcc att cgc acc gct gga gtg ccc cgc gag gag 259  
 Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly Val Pro Arg Glu Glu  
 40 45 50  
 ctc ttt att tcc acc aag cta gct gca gaa atc aaa gat tac gat gga 307  
 Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile Lys Asp Tyr Asp Gly  
 55 60 65  
 gca gtc gcc gcg att gat gag tct ttg gcg aaa att ggc ttg gat tat 355  
 Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys Ile Gly Leu Asp Tyr  
 70 75 80 85  
 gtc gat ctg atg ctc att cac tcc cca caa cca tgg agt gat ttc cgt 403  
 Val Asp Leu Met Leu Ile His Ser Pro Gln Pro Trp Ser Asp Phe Arg  
 90 95 100  
 ggt ggg gac tat tca gag gga aac cgt gaa gcg tgg cgc gcg ctg gaa 451  
 Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala Trp Arg Ala Leu Glu

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ctg gag gcc gat ctg gag aat atc tta gac tcc gcg acg gtt gct cct Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser Ala Thr Val Ala Pro 135 140 145			547
cac gtt aat cag ctt ctt gtg cat gtt gga aac acc cca agc gag tta His Val Asn Gln Leu Leu Val His Val Gly Asn Thr Pro Ser Glu Leu 150 155 160 165			595
atc agt ttc tgc gat tcc aag ggc att ctg gtc gaa gca tat tca ccc Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val Glu Ala Tyr Ser Pro 170 175 180			643
atc gcc cac gga gag atg ctg aag aac cag cag gtc aag gcg att gct Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln Val Lys Ala Ile Ala 185 190 195			691
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caa ctg gga acg gtg tct ttg cca aag act gcc aac cca gat cat atg Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala Asn Pro Asp His Met 215 220 225			787
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gca ctt caa gaa gtg acc gcc cgc gat tat ggc gag cac agc ggt ttt Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly Glu His Ser Gly Phe 250 255 260			883
cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac Pro Val Tyr Ser Gly Lys 265			924

&lt;210&gt; 474

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 474

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		20					25					30			

Ala	Tyr	Gly	Asn	Glu	Arg	Gly	Val	Gly	Glu	Gly	Ile	Arg	Thr	Ala	Gly
		35					40				45				

Val	Pro	Arg	Glu	Glu	Leu	Phe	Ile	Ser	Thr	Lys	Leu	Ala	Ala	Glu	Ile
	50					55					60				



Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys  
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 Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro  
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 Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala  
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 Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile  
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 Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser  
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 Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn  
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 Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val  
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 Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln  
 180 185 190  
 Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys  
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 Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala  
 210 215 220  
 Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser  
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 Met Arg Gln Val Gly  
 1 5  
 ggt aat ggg ggc cat caa cta gac tcg atc aac gtg tca gat gta gtt 163  
 Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn Val Ser Asp Val Val  
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Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu Pro Pro Gln Val Ala	
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ccg ggc tgg ctg aag aaa ctg gct atc tca tca ggt ctg ctt ggc ctg	259
Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser Gly Leu Leu Gly Leu	
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Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val Asn Gln Val Gln Ser	
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Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser Ser Val Asn Ala Pro	
70 75 80 85	
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Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala Ser Ile Pro Val Ser	
90 95 100	
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Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly Leu Phe Val Arg Thr	
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Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly Glu Val Leu Leu Asp	
135 140 145	
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Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp Asp Ala Ile Leu Glu	
150 155 160 165	
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Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu Ile Thr Gly Thr Ala	
170 175 180	
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Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro Gln Val Thr Gly Val	
185 190 195	
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Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala Ser Ala Leu Ala Ser	
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Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser Arg Phe Thr Ser Ser	
215 220 225	
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Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile Gly Leu Ala Ser Val	
230 235 240 245	
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Leu Val Ser Leu Trp Thr Leu His Arg Met Asp Ile Leu Asp Gly Arg	
250 255 260	
aaa gca cac cgc ttc ctg cct gcc aac tgg tac aag ctg aag cca ctt	931

Lys	Ala	His	Arg	Phe	Leu	Pro	Ala	Asn	Trp	Tyr	Lys	Leu	Lys	Pro	Leu		
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Asp	Gly	Val	Val	Val	Ala	Ile	Leu	Val	Phe	Trp	His	Phe	Leu	Gly	Ala		
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aac	acc	tct	gac	gac	ggc	ttc	atc	atg	acc	atg	gcc	cgc	gtg	tcc	cag	1027	
Asn	Thr	Ser	Asp	Asp	Gly	Phe	Ile	Met	Thr	Met	Ala	Arg	Val	Ser	Gln		
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Ser	Pro	Phe	Gly	Ala	Pro	Tyr	Tyr	Asp	Leu	Leu	Ala	Leu	Met	Ala	Tyr		
				330					335					340			
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Ile	Ser	Thr	Ser	Ser	Ile	Trp	Leu	Arg	Leu	Pro	Ala	Leu	Leu	Ala	Gly		
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ctg	atc	atg	tgg	ttc	gtg	atc	acc	aga	gag	gtc	atg	cca	cgg	ttt	ggc	1219	
Leu	Ile	Met	Trp	Phe	Val	Ile	Thr	Arg	Glu	Val	Met	Pro	Arg	Phe	Gly		
		360					365					370					
tca	ttg	gtt	aac	ggt	cgc	cgc	gtt	gcg	cac	tgg	tct	gca	gcc	atg	gtg	1267	
Ser	Leu	Val	Asn	Gly	Arg	Arg	Val	Ala	His	Trp	Ser	Ala	Ala	Met	Val		
	375					380					385						
ttc	ctg	gcg	ttc	tgg	ctt	cca	tac	aac	aac	ggc	act	cgc	cca	gag	cca	1315	
Phe	Leu	Ala	Phe	Trp	Leu	Pro	Tyr	Asn	Asn	Gly	Thr	Arg	Pro	Glu	Pro		
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Ile	Ile	Ala	Met	Gly	Ala	Leu	Leu	Ala	Trp	Val	Ser	Phe	Glu	Arg	Ala		
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Ile	Ala	Thr	Ser	Arg	Leu	Leu	Pro	Ala	Ala	Ile	Gly	Val	Ile	Ile	Ala		
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Thr	Ile	Ser	Leu	Ala	Ser	Gly	Pro	Thr	Gly	Leu	Met	Ala	Val	Ala	Ala		
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	455					460					465						
ccg	ctt	att	ggg	gcg	tcg	agg	ggg	gcg	tcg	aaa	agc	aaa	gtc	ttt	ggc	1555	
Pro	Leu	Ile	Gly	Ala	Ser	Arg	Gly	Ala	Ser	Lys	Ser	Lys	Val	Phe	Gly		
470					475					480					485		
gct	tcg	atg	gct	atg	ctt	gcc	cca	ttc	ctt	gcg	tct	ggc	acc	gcg	att	1603	
Ala	Ser	Met	Ala	Met	Leu	Ala	Pro	Phe	Leu	Ala	Ser	Gly	Thr	Ala	Ile		
				490					495					500			
ctc	atc	gcc	gtt	ttt	ggc	gat	cag	act	ctg	tca	acc	gtc	atg	gaa	tcc	1651	
Leu	Ile	Ala	Val	Phe	Gly	Asp	Gln	Thr	Leu	Ser	Thr	Val	Met	Glu	Ser		

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Tyr	Val	Arg	Tyr	Gln	Thr	Val	Met	Glu	Gln	Thr	Val	Asp	Gly	Ser	Phe	
		535					540					545				
acc	cgc	cgt	ttt	gct	gtg	ctg	atg	ctc	atg	gcg	tgt	ctg	gct	att	gtg	1795
Thr	Arg	Arg	Phe	Ala	Val	Leu	Met	Leu	Met	Ala	Cys	Leu	Ala	Ile	Val	
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gtc	atc	gcg	atc	ctg	cgt	tac	ggc	cgc	att	cca	ggc	gct	gcg	aag	gga	1843
Val	Ile	Ala	Ile	Leu	Arg	Tyr	Gly	Arg	Ile	Pro	Gly	Ala	Ala	Lys	Gly	
				570					575					580		
cca	tca	ctg	cgt	ttg	atg	atg	gtc	att	ttc	ggc	acc	atg	ttc	ttc	atg	1891
Pro	Ser	Leu	Arg	Leu	Met	Met	Val	Ile	Phe	Gly	Thr	Met	Phe	Phe	Met	
			585						590					595		
atg	ttc	acc	cca	acc	aag	tgg	act	cac	cac	ttc	ggt	gtc	tac	gca	gga	1939
Met	Phe	Thr	Pro	Thr	Lys	Trp	Thr	His	His	Phe	Gly	Val	Tyr	Ala	Gly	
		600					605					610				
ctt	gcc	ggc	gca	ttg	gcc	gga	ctt	gct	gcc	gtg	ggg	ctg	tcc	tat	gtt	1987
Leu	Ala	Gly	Ala	Leu	Ala	Gly	Leu	Ala	Ala	Val	Gly	Leu	Ser	Tyr	Val	
		615					620				625					
gcg	gtg	aaa	tca	cca	cgc	atg	cgc	acc	att	tcc	atc	ggt	gcg	ttc	ctc	2035
Ala	Val	Lys	Ser	Pro	Arg	Met	Arg	Thr	Ile	Ser	Ile	Gly	Ala	Phe	Leu	
		630					635				640				645	
ttc	ctg	ctg	gcg	ctg	gct	ctc	gca	ggc	gtg	aac	gga	ttc	tgg	tac	acc	2083
Phe	Leu	Leu	Ala	Leu	Ala	Leu	Ala	Gly	Val	Asn	Gly	Phe	Trp	Tyr	Thr	
				650					655					660		
tcc	agc	tac	gcc	gtg	cca	tgg	tgg	gat	aaa	acc	atc	cag	atc	aag	ggc	2131
Ser	Ser	Tyr	Ala	Val	Pro	Trp	Trp	Asp	Lys	Thr	Ile	Gln	Ile	Lys	Gly	
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Ile	Glu	Ala	Ser	Thr	Val	Val	Leu	Val	Ile	Ala	Val	Ile	Val	Leu	Ile	
			680				685					690				
atc	ggt	gtt	att	caa	tcc	ttt	gtc	cac	gat	gtg	aaa	acc	gcg	caa	gcc	2227
Ile	Gly	Val	Ile	Gln	Ser	Phe	Val	His	Asp	Val	Lys	Thr	Ala	Gln	Ala	
		695					700					705				
gaa	acc	aat	cac	tcc	atg	ggc	gaa	ctc	gtg	gcg	gaa	gat	gaa	gca	aag	2275
Glu	Thr	Asn	His	Ser	Met	Gly	Glu	Leu	Val	Ala	Glu	Asp	Glu	Ala	Lys	
		710					715				720				725	
cgc	gag	cgt	gcc	tcc	agg	ttc	acc	ggc	ctt	gcg	gcc	tcc	cct	atc	gca	2323
Arg	Glu	Arg	Ala	Ser	Arg	Phe	Thr	Gly	Leu	Ala	Ala	Ser	Pro	Ile	Ala	
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gga	gtg	tcc	gcc	ctc	gtt	gtg	ctg	att	acc	tgc	gca	tcc	atg	ggc	aaa	2371
Gly	Val	Ser	Ala	Leu	Val	Val	Leu	Ile	Thr	Cys	Ala	Ser	Met	Gly	Lys	
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cgc tcc ctg acc ggc aac aca tgt ggc ctt gcc tcc gac gcc atg ctg Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala Ser Asp Ala Met Leu 775 780 785	2467
gaa acc aac tcc aac gat tcc ttc ctc act cca gtg aac tcc aca ctt Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro Val Asn Ser Thr Leu 790 795 800 805	2515
ggc gag tcc ctg gaa tcc gaa gat att cgc ggc ttt agt gct gcc ggc Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly Phe Ser Ala Ala Gly 810 815 820	2563
atc cca cca tca atc agc cag gac caa gca gac ctg tct gct gtt ggt Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp Leu Ser Ala Val Gly 825 830 835	2611
gcc att gcc aac act gac gac tcc acc gaa acc ggc gga tcc gac gaa Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr Gly Gly Ser Asp Glu 840 845 850	2659
tca tcc gga caa tcc acc ggc aac acc ggc ggt gtc cga ggc tcc gaa Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly Val Arg Gly Ser Glu 855 860 865	2707
ggc atc aac ggc tcc aac gcc cgc ctg cca ttc aac ctg gac tac acc Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe Asn Leu Asp Tyr Thr 870 875 880 885	2755
caa gtt cca gtc gtc ggc tcc tgg tcc gct ggc acc caa aac cca gca Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly Thr Gln Asn Pro Ala 890 895 900	2803
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ccc atc atc gtg gta tct gca gca ggt cgc atc gaa cac tac gac atc Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile Glu His Tyr Asp Ile 920 925 930	2899
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gac atc ggc ccc gag cca tcc tgg cgc aac ctc cgc tac cca ctt gac Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu Arg Tyr Pro Leu Asp 970 975 980	3043
caa ctc cca gaa gaa gcg gac gtc gtg cgc atc gtc gcc acc gac gtc Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile Val Ala Thr Asp Val 985 990 995	3091

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tac tcg ctg cgc acc aac tcc aac ggc gat gca cct aag gtt gca gac 3475  
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Asn Gln Val Gln Ser Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser  
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Ser Val Asn Ala Pro Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala  
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 Val Met Gly Thr Leu Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly  
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 Glu Val Leu Leu Asp Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp  
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 Asp Ala Ile Leu Glu Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu  
 165 170 175  
 Ile Thr Gly Thr Ala Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro  
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 Gln Val Thr Gly Val Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala  
 195 200 205  
 Ser Ala Leu Ala Ser Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser  
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 Arg Phe Thr Ser Ser Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile  
 225 230 235 240  
 Gly Leu Ala Ser Val Leu Val Ser Leu Trp Thr Leu His Arg Met Asp  
 245 250 255  
 Ile Leu Asp Gly Arg Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr  
 260 265 270  
 Lys Leu Lys Pro Leu Asp Gly Val Val Val Ala Ile Leu Val Phe Trp  
 275 280 285  
 His Phe Leu Gly Ala Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met  
 290 295 300  
 Ala Arg Val Ser Gln Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp  
 305 310 315 320  
 Phe Gly Val Pro Glu Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu  
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 340 345 350  
 Ala Leu Leu Ala Gly Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val  
 355 360 365  
 Met Pro Arg Phe Gly Ser Leu Val Asn Gly Arg Arg Val Ala His Trp  
 370 375 380  
 Ser Ala Ala Met Val Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly  
 385 390 395 400

Thr Arg Pro Glu Pro Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val  
 405 410 415  
 Ser Phe Glu Arg Ala Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile  
 420 425 430  
 Gly Val Ile Ile Ala Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu  
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 Met Ala Val Ala Ala Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile  
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 Leu Tyr Arg Arg Leu Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys  
 465 470 475 480  
 Ser Lys Val Phe Gly Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala  
 485 490 495  
 Ser Gly Thr Ala Ile Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser  
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 Thr Val Met Glu Ser Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu  
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 Val Asp Gly Ser Phe Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala  
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 Cys Leu Ala Ile Val Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro  
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 Gly Ala Ala Lys Gly Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly  
 580 585 590  
 Thr Met Phe Phe Met Met Phe Thr Pro Thr Lys Trp Thr His His Phe  
 595 600 605  
 Gly Val Tyr Ala Gly Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val  
 610 615 620  
 Gly Leu Ser Tyr Val Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser  
 625 630 635 640  
 Ile Gly Ala Phe Leu Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn  
 645 650 655  
 Gly Phe Trp Tyr Thr Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr  
 660 665 670  
 Ile Gln Ile Lys Gly Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala  
 675 680 685  
 Val Ile Val Leu Ile Ile Gly Val Ile Gln Ser Phe Val His Asp Val  
 690 695 700  
 Lys Thr Ala Gln Ala Glu Thr Asn His Ser Met Gly Glu Leu Val Ala  
 705 710 715 720  
 Glu Asp Glu Ala Lys Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala



725										730					735				
Ala	Ser	Pro	Ile	Ala	Gly	Val	Ser	Ala	Leu	Val	Val	Leu	Ile	Thr	Cys				
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Ala	Ser	Met	Gly	Lys	Gly	Phe	Val	Asp	Gln	Tyr	Pro	Ala	Tyr	Ser	Val				
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Gly	Leu	Gly	Asn	Leu	Arg	Ser	Leu	Thr	Gly	Asn	Thr	Cys	Gly	Leu	Ala				
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Ser	Asp	Ala	Met	Leu	Glu	Thr	Asn	Ser	Asn	Asp	Ser	Phe	Leu	Thr	Pro				
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Ala	Thr	Glu	Glu	Ala	Pro	Ile	Ile	Val	Val	Ser	Ala	Ala	Gly	Arg	Ile				
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Glu	His	Tyr	Asp	Ile	Asn	Gly	Val	Arg	Gln	Ser	Gly	Gln	Ser	Val	Met				
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Leu	Glu	Tyr	Gly	Arg	Leu	Arg	Asp	Asn	Gly	Asp	Val	Glu	Asp	Leu	Gly				
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Glu	Ala	Met	Met	Tyr	Asp	Ile	Gly	Pro	Glu	Pro	Ser	Trp	Arg	Asn	Leu				
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Arg	Tyr	Pro	Leu	Asp	Gln	Leu	Pro	Glu	Glu	Ala	Asp	Val	Val	Arg	Ile				
		980						985					990						
Val	Ala	Thr	Asp	Val	Asn	Leu	Asp	Glu	Asp	Gln	Trp	Val	Ala	Leu	Thr				
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Pro	Pro	Arg	Val	Pro	Asn	Leu	Asp	Ser	Leu	Asn	Asn	Val	Ile	Gly	Ser				
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Gln	Arg	Thr	Phe	Asp	His	Tyr	Ala	Gly	Val	Thr	Glu	Ile	Pro	Glu	Tyr				
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Arg Ile Ser Pro Asp His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln  
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Asp Trp Ala Gly Gly Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn  
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Ala Tyr Glu Ile Pro Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp  
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Gly Ser Ile Glu Arg Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala  
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 Val Ser Trp Thr Val  
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gat atc cct aaa gaa gtt ctc cct gat ttg cca cca ttg cca gaa ggc 163  
 Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro Pro Leu Pro Glu Gly  
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 Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg Asp Ala Lys Gln Gln  
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cct acg tgg gat cgt gca cag gca gaa aac gtg cgc aag atc ctt gag 259  
 Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val Arg Lys Ile Leu Glu  
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tcg gtt cct cca atc gtt gtt gcc cct gag gta ctt gag ctg aag cag 307  
 Ser Val Pro Pro Ile Val Val Ala Pro Glu Val Leu Glu Leu Lys Gln  
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aag ctt gct gat gtt gcc aac ggt aag gcc ttc ctc ttg cag ggt ggt 355  
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gac tgt gcg gaa act ttc gag tca aac act gag ccg cac att cgc gcc 403  
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Asn Val Lys Thr Leu Leu Gln Met Ala Val Val Leu Thr Tyr Gly Ala	
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tcc act cct gtg atc aag atg gct cgt att gct ggt cag tac gca aag	499
Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala Gly Gln Tyr Ala Lys	
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cct cgc tct tct gat ctg gat gga aat ggt ctg cca aac tac cgt ggc	547
Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu Pro Asn Tyr Arg Gly	
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Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu Ala Arg Arg His Asp	
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Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala Ser Ala Ala Met Asn	
170 175 180	
ttg gtg cgc gcg ctc acc agc tct ggc acc gct gat ctt tac cgt ctc	691
Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala Asp Leu Tyr Arg Leu	
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Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser Pro Ala Gly Ala Arg	
200 205 210	
tac gag gct ctt gct cgt gag atc gac tcc ggt ctg cgc ttc atg gaa	787
Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly Leu Arg Phe Met Glu	
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Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala Ala Asp Ile Tyr Cys	
230 235 240 245	
tcc cac gag gct ttg ctg gtg gat tac gag cgt tcc atg ctg cgt ctt	883
Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg Ser Met Leu Arg Leu	
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gca acc gat gag gaa ggc aac gag gaa ctt tac gat ctt tca gct cac	931
Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr Asp Leu Ser Ala His	
265 270 275	
cag ctg tgg atc ggc gag cgc acc cgt ggc atg gat gat ttc cat gtg	979
Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met Asp Asp Phe His Val	
280 285 290	
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Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly Ile Lys Ile Gly Pro	
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ggg atc acc cct gaa gag gct gtt gca tac gct gac aag ctc gat ccg	1075
Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala Asp Lys Leu Asp Pro	
310 315 320 325	
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Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala Arg Met Gly His Asp	
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Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln Ala Val Glu Ala Ser  
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 Gly His Lys Val Ile Trp Gln Ser Asp Pro Met His Gly Asn Thr Phe  
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 acc gca tcc aat ggc tac aag acc cgt cac ttc gac aag gtt atc gat 1267  
 Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe Asp Lys Val Ile Asp  
 375 380 385  
 gag gtc cag ggc ttc ttc gag gtc cac cgc gca ttg ggc acc cac cca 1315  
 Glu Val Gln Gly Phe Phe Glu Val His Arg Ala Leu Gly Thr His Pro  
 390 395 400 405  
 ggc gga atc cac att gag ttc act ggt gaa gat gtc acc gag tgc ctc 1363  
 Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp Val Thr Glu Cys Leu  
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 Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln Ser Leu Glu Leu Ala  
 440 445 450  
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 Phe Leu Val Ala Glu Met Leu Arg Asn  
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&lt;210&gt; 478

&lt;211&gt; 462

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 478

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 Asp Ala Lys Gln Gln Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val  
 35 40 45  
 Arg Lys Ile Leu Glu Ser Val Pro Pro Ile Val Val Ala Pro Glu Val  
 50 55 60  
 Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe  
 65 70 75 80  
 Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu  
 85 90 95  
 Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val  
 100 105 110

Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala  
 115 120 125  
 Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu  
 130 135 140  
 Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu  
 145 150 155 160  
 Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala  
 165 170 175  
 Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala  
 180 185 190  
 Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser  
 195 200 205  
 Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly  
 210 215 220  
 Leu Arg Phe Met Glu Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala  
 225 230 235 240  
 Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg  
 245 250 255  
 Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr  
 260 265 270  
 Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met  
 275 280 285  
 Asp Asp Phe His Val Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly  
 290 295 300  
 Ile Lys Ile Gly Pro Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala  
 305 310 315 320  
 Asp Lys Leu Asp Pro Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala  
 325 330 335  
 Arg Met Gly His Asp Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln  
 340 345 350  
 Ala Val Glu Ala Ser Gly His Lys Val Ile Trp Gln Ser Asp Pro Met  
 355 360 365  
 His Gly Asn Thr Phe Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe  
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 Asp Lys Val Ile Asp Glu Val Gln Gly Phe Phe Glu Val His Arg Ala  
 385 390 395 400  
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 Val Thr Glu Cys Leu Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu  
 420 425 430  
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Val Thr Tyr Ser Pro
1 5

ggt aaa tac ttg gcg tcg ttc ctg gat tct ttg cct ggt gcg act tca 163
Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu Pro Gly Ala Thr Ser
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cga gac acc cac gtt gtg atg gca gac aat ggt tct gtg gac ggt gtt 211
Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val
25 30 35

cct gag cag gca gca gcc tca cgc agc aac gtg gag ttc ctc tca act 259
Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val Glu Phe Leu Ser Thr
40 45 50

ggc ggc aac tta ggc tac gga acg gct att aat att gcc gcc cga tcg 307
Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn Ile Ala Ala Arg Ser
55 60 65

ttg cgt gcg cgc cgg gag gca gga gag atc gat ggg gag ttc ttc ctc 355
Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp Gly Glu Phe Phe Leu
70 75 80 85

gtc tca aac cct gat gtt gtt ttt gac gaa gac tct att gat caa ttg 403
Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp Ser Ile Asp Gln Leu
90 95 100

ctt gaa tgt gcg aaa cgt cac cct gaa gca gga gcg gtt ggc ccg ttg 451
Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly Ala Val Gly Pro Leu
105 110 115

atc cgt gag gcg gac ggt tcg gcg tat ccg tcg gct cgg gcg gta ccc 499
Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser Ala Arg Ala Val Pro
120 125 130

act ttg gcg aat ggc att ggt cac gct ttg ttg ggt gct gtg tgg aaa 547
Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu Gly Ala Val Trp Lys
135 140 145

tcc aat ccg tgg tcg gcg gct tac cgt gac gat gaa gat atg gac act 595
Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp Glu Asp Met Asp Thr

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Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys Leu Leu Leu Arg Trp				
170		175	180	
gat gcg ttt gat cga gtt ggt ggt ttt gat gag cgc tac ttc atg tac				691
Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu Arg Tyr Phe Met Tyr				
185		190	195	
atg gaa gac gtt gac ctg gga gat cgg ctg gtt cgc gcc ggt ttc acc				739
Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val Arg Ala Gly Phe Thr				
200		205	210	
aac gtc ttt tgc cca agt gcg cag atc atc cac gcg aaa ggt cat gtt				787
Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His Ala Lys Gly His Val				
215		220	225	
gcg ggt aaa aac cca gag aac atg ttg ccc gca cac cac gag agc gcg				835
Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala His His Glu Ser Ala				
230		235	240	245
tat cgc ttc cag gct gat cgc ctg gcg aag ccg tgg caa gcc cca att				883
Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro Trp Gln Ala Pro Ile				
250		255	260	
cgg ttg gct ctg cga att ggt ttg aaa tta cga gcc gga gtc gcg gtt				931
Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg Ala Gly Val Ala Val				
265		270	275	
ggt gtc tct aag atg aga acg aaa gcc tct tagaccgtcg acgaccaccg				981
Gly Val Ser Lys Met Arg Thr Lys Ala Ser				
280		285		
gac				984

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Ser Val Asp Gly Val Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val  
 35 40 45  
 Glu Phe Leu Ser Thr Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn  
 50 55 60  
 Ile Ala Ala Arg Ser Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp  
 65 70 75 80  
 Gly Glu Phe Phe Leu Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp  
 85 90 95

Ser Ile Asp Gln Leu Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly  
 100 105 110  
 Ala Val Gly Pro Leu Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser  
 115 120 125  
 Ala Arg Ala Val Pro Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu  
 130 135 140  
 Gly Ala Val Trp Lys Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp  
 145 150 155 160  
 Glu Asp Met Asp Thr Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys  
 165 170 175  
 Leu Leu Leu Arg Trp Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu  
 180 185 190  
 Arg Tyr Phe Met Tyr Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val  
 195 200 205  
 Arg Ala Gly Phe Thr Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His  
 210 215 220  
 Ala Lys Gly His Val Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala  
 225 230 235 240  
 His His Glu Ser Ala Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro  
 245 250 255  
 Trp Gln Ala Pro Ile Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg  
 260 265 270  
 Ala Gly Val Ala Val Gly Val Ser Lys Met Arg Thr Lys Ala Ser  
 275 280 285

<210> 481  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <222> (101)..(979)  
 <223> RXN01631

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 Met Lys Pro Gln Leu  
 1 5  
 att gca tct tgc tgg acc agc gcg gga gac gcc gca ccc gat cgt gac 163  
 Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala Ala Pro Asp Arg Asp  
 10 15 20  
 gat ctc agc agc cca gta gca atc gat gag cgc atc gct cta gtc gct 211  
 Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg Ile Ala Leu Val Ala  
 25 30 35



gaa acc ggt tgg gca ggc att ggg ctt gtt cac gcc gat ctc atc aaa	259
Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His Ala Asp Leu Ile Lys	
40 45 50	
gca cgc gac acc att ggc tac gag gaa ttg cgc cga cgc atc cac gct	307
Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg Arg Arg Ile His Ala	
55 60 65	
gca gga att gaa atc att gag gtg gag ttc ctc aat ggt tgg tgg gcg	355
Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu Asn Gly Trp Trp Ala	
70 75 80 85	
act ggt gcg gaa cgc caa gag tcc gat gcc gtt cgt gcg gat ctg ttt	403
Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val Arg Ala Asp Leu Phe	
90 95 100	
gct gcg gcg caa gct ctt ggt tcc cca cac att aag gtc gga gca gga	451
Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile Lys Val Gly Ala Gly	
105 110 115	
gag ggc acc aat ggt gtg gtt ccc att gct cac atg gcc agt gcg ttt	499
Glu Gly Thr Asn Gly Val Val Pro Ile Ala His Met Ala Ser Ala Phe	
120 125 130	
act gat ctc gct gcg gaa gct gaa gct cat ggc gtc aag ctc gcg ttg	547
Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly Val Lys Leu Ala Leu	
135 140 145	
gaa gca act ccg ttt tct cac ctg aag acc atc tac gac gcg ctg gaa	595
Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile Tyr Asp Ala Leu Glu	
150 155 160 165	
gtt gtc agc cat tcc gat agc cca tcg gct gga ctc atg gtt gat atc	643
Val Val Ser His Ser Asp Ser Pro Ser Ala Gly Leu Met Val Asp Ile	
170 175 180	
tgg cac acc gcg aaa atc gga atc ccc aac gat gaa ctg tgg cgc aac	691
Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp Glu Leu Trp Arg Asn	
185 190 195	
att cca ctg tcc aag gtc aac gca gtg gag gtt gat gat ggt ttc att	739
Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val Asp Asp Gly Phe Ile	
200 205 210	
gac acc cca att gat ctt ttc gat gac tcc acc aac cgt cgc gcg tac	787
Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr Asn Arg Arg Ala Tyr	
215 220 225	
tgc ggt gaa ggc gaa ttt gat ccc gca agc ttc atc cgt ggc gcc atc	835
Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe Ile Arg Gly Ala Ile	
230 235 240 245	
gac gcc ggt tgg acg ggc gca tat ggt gtg gaa att att tcc gca gag	883
Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu Ile Ile Ser Ala Glu	
250 255 260	
cac cga agc ctc ccg gtg aaa gaa ggg ctg caa cgt gct ttc gac acc	931
His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln Arg Ala Phe Asp Thr	
265 270 275	

979

1002

<400> 482																
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Ala	Pro	Asp	Arg	Asp	Asp	Leu	Ser	Ser	Pro	Val	Ala	Ile	Asp	Glu	Arg	
			20					25					30			
Ile	Ala	Leu	Val	Ala	Glu	Thr	Gly	Trp	Ala	Gly	Ile	Gly	Leu	Val	His	
		35					40					45				
Ala	Asp	Leu	Ile	Lys	Ala	Arg	Asp	Thr	Ile	Gly	Tyr	Glu	Glu	Leu	Arg	
	50					55					60					
Arg	Arg	Ile	His	Ala	Ala	Gly	Ile	Glu	Ile	Ile	Glu	Val	Glu	Phe	Leu	
65					70					75					80	
Asn	Gly	Trp	Trp	Ala	Thr	Gly	Ala	Glu	Arg	Gln	Glu	Ser	Asp	Ala	Val	
				85					90					95		
Arg	Ala	Asp	Leu	Phe	Ala	Ala	Ala	Gln	Ala	Leu	Gly	Ser	Pro	His	Ile	
			100					105					110			
Lys	Val	Gly	Ala	Gly	Glu	Gly	Thr	Asn	Gly	Val	Val	Pro	Ile	Ala	His	
		115					120					125				
Met	Ala	Ser	Ala	Phe	Thr	Asp	Leu	Ala	Ala	Glu	Ala	Glu	Ala	His	Gly	
	130					135						140				
Val	Lys	Leu	Ala	Leu	Glu	Ala	Thr	Pro	Phe	Ser	His	Leu	Lys	Thr	Ile	
145					150					155					160	
Tyr	Asp	Ala	Leu	Glu	Val	Val	Ser	His	Ser	Asp	Ser	Pro	Ser	Ala	Gly	
				165					170					175		
Leu	Met	Val	Asp	Ile	Trp	His	Thr	Ala	Lys	Ile	Gly	Ile	Pro	Asn	Asp	
			180					185					190			
Glu	Leu	Trp	Arg	Asn	Ile	Pro	Leu	Ser	Lys	Val	Asn	Ala	Val	Glu	Val	
		195					200					205				
Asp	Asp	Gly	Phe	Ile	Asp	Thr	Pro	Ile	Asp	Leu	Phe	Asp	Asp	Ser	Thr	
	210					215					220					
Asn	Arg	Arg	Ala	Tyr	Cys	Gly	Glu	Gly	Glu	Phe	Asp	Pro	Ala	Ser	Phe	
225					230					235					240	
Ile	Arg	Gly	Ala	Ile	Asp	Ala	Gly	Trp	Thr	Gly	Ala	Tyr	Gly	Val	Glu	
				245					250					255		

Ile Ile Ser Ala Glu His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln  
260 265 270

Arg Ala Phe Asp Thr Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu  
275 280 285

Ala Pro Ser Thr Asn  
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<210> 483

<211> 990

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(967)

<223> RXN01593

<400> 483

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gcacgtagtt tctgcgctct ctggcgccgg cctaccgctc atg tat gtc acc aat 115  
Met Tyr Val Thr Asn  
1 5

aat gcc tcc cgt gct ccg gag gtg gtg gct gcg caa ctc cgt gag att 163  
Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala Gln Leu Arg Glu Ile  
10 15 20

ggc ctt gcc gac acc act gcg gac aat gtg atg aca tct gct caa gct 211  
Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met Thr Ser Ala Gln Ala  
25 30 35

gcc tgc aag atg gcg gcg gag aag att ccc gct gga tcc aag gtg tat 259  
Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala Gly Ser Lys Val Tyr  
40 45 50

gtt ttg ggt tca gaa tcc ttc cgc gag cta gct act gaa gct ggt ttt 307  
Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala Thr Glu Ala Gly Phe  
55 60 65

gtg gtg gtt gat tcg gct gat gat aaa cct gtg gct gtg ctt cac ggc 355  
Val Val Val Asp Ser Ala Asp Asp Lys Pro Val Ala Val Leu His Gly  
70 75 80 85

cac aac cct gag acc ggt tgg gct cag ttg agc gag gct gcg ctg tca 403  
His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser Glu Ala Ala Leu Ser  
90 95 100

att aat gct ggc gcg cag tat ttt gca tca aat ttg gat tcc acc ctt 451  
Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn Leu Asp Ser Thr Leu  
105 110 115

ccc atg gaa cgc ggt cgt cac att ggc aac ggt tcc atg gtg gct gcc 499  
Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly Ser Met Val Ala Ala  
120 125 130

gtg gtc aac gcg act ggc gta aag cct ctt tcc gca ggt aag cca ggc 547  
Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser Ala Gly Lys Pro Gly

135	140	145	
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Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu Asn Ser Ser Lys Pro			
150	155	160	165
ttg gct gtc ggc gat cgt ctc gat acc gat atc gcc ggc gga aac gct			643
Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile Ala Gly Gly Asn Ala			
	170	175	180
gca ggc atg gac aca ttc cag gtc ctg acc ggc gtc agc ggc tac tac			691
Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly Val Ser Gly Tyr Tyr			
	185	190	195
gat ttg gtg cgc gcc att ccc aga gca gcg ccc cac cta tat cgc cac			739
Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro His Leu Tyr Arg His			
	200	205	210
ctc gat gca gga tct cta cag cga tcc ggg cga gct caa gcc agg tgc			787
Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg Ala Gln Ala Arg Cys			
	215	220	225
cca ggg cgg ttt ttc agc gct tat cga cgg cga cac cct ggt cat ttc			835
Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg His Pro Gly His Phe			
	230	235	240
cgg cgg cga tgc cgg cgc aac tcc ggt tgc agc act ccg cac tgc gtt			883
Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser Thr Pro His Cys Val			
	250	255	260
gga tgt ggc ctg ggc ggc cac aga gca gtc acc gag gta cgc gct gat			931
Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr Glu Val Arg Ala Asp			
	265	270	275
tca gag gta gct gct act gca ttg cag agc tgg tgg taaacgggtga			977
Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp Trp			
	280	285	
attcaccaaaa gcc			990

&lt;210&gt; 484

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 484

Met Tyr Val Thr Asn Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala
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Gln Leu Arg Glu Ile Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met
20 25 30

Thr Ser Ala Gln Ala Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala
35 40 45

Gly Ser Lys Val Tyr Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala
50 55 60

Thr Glu Ala Gly Phe Val Val Val Asp Ser Ala Asp Asp Lys Pro Val
65 70 75 80

Ala	Val	Leu	His	Gly 85	His	Asn	Pro	Glu	Thr 90	Gly	Trp	Ala	Gln	Leu 95	Ser
Glu	Ala	Ala	Leu 100	Ser	Ile	Asn	Ala	Gly 105	Ala	Gln	Tyr	Phe	Ala 110	Ser	Asn
Leu	Asp	Ser 115	Thr	Leu	Pro	Met	Glu 120	Arg	Gly	Arg	His	Ile 125	Gly	Asn	Gly
Ser	Met 130	Val	Ala	Ala	Val	Val 135	Asn	Ala	Thr	Gly	Val 140	Lys	Pro	Leu	Ser
Ala 145	Gly	Lys	Pro	Gly	Pro 150	Ala	Met	Phe	Tyr	Ala 155	Gly	Ala	Glu	Thr	Leu 160
Asn	Ser	Ser	Lys	Pro 165	Leu	Ala	Val	Gly	Asp 170	Arg	Leu	Asp	Thr	Asp 175	Ile
Ala	Gly	Gly	Asn 180	Ala	Ala	Gly	Met	Asp 185	Thr	Phe	Gln	Val	Leu 190	Thr	Gly
Val	Ser 195	Gly	Tyr	Tyr	Asp	Leu 200	Val	Arg	Ala	Ile	Pro 205	Arg	Ala	Ala	Pro
His 210	Leu	Tyr	Arg	His	Leu	Asp 215	Ala	Gly	Ser	Leu	Gln 220	Arg	Ser	Gly	Arg
Ala 225	Gln	Ala	Arg	Cys	Pro 230	Gly	Arg	Phe	Phe	Ser 235	Ala	Tyr	Arg	Arg	Arg 240
His	Pro	Gly	His	Phe 245	Arg	Arg	Arg	Cys	Arg 250	Arg	Asn	Ser	Gly	Cys 255	Ser
Thr	Pro	His	Cys 260	Val	Gly	Cys	Gly	Leu 265	Gly	Gly	His	Arg	Ala 270	Val	Thr
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Trp

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<210> 485
<211> 1173
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1150)  
<223> RXN00337
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Met Leu Leu Thr Tyr  
1 5

gcg ttt gtg gat gtg gag gga ggc gtc gaa aag cat tct tta agc act	163
Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr	
10 15 20	
gcg gac att gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt	211
Ala Asp Ile Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val	
25 30 35	
ttg ggg cgg cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc	259
Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala	
40 45 50	
cgg ttg ggc ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg	307
Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser	
55 60 65	
cgt gac aca aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag	355
Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu	
70 75 80 85	
ggg gtg ggg ctg ggt gaa aat tcc gcc atg gat gtg gcg ctc gca ttg	403
Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu	
90 95 100	
gcg ctg tat cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att	451
Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile	
105 110 115	
gcg gag att tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg	499
Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val	
120 125 130	
ttg cgt gcg cgg cac acc gtg gcg ttg ccg ggt gaa act gga cag att	547
Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly Glu Thr Gly Gln Ile	
135 140 145	
tcg gtg gtt gat tac gcc gat ggt tcg gtc act cag gcg cca cat ccg	595
Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr Gln Ala Pro His Pro	
150 155 160 165	
gtg agt cgt tcc gct ggt ttg tcg gca ttt gtt gtt gct gcg caa act	643
Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val Val Ala Ala Gln Thr	
170 175 180	
gaa act gat ccg agc att tac cgc gag atc tat gct cga cat gcg ttt	691
Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr Ala Arg His Ala Phe	
185 190 195	
atc gat gaa gct gcg cgc gct ttc agt gtg gaa tct ttg ccg ttg ctt	739
Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu Ser Leu Arg Leu Leu	
200 205 210	
ccc gac gct tcc act cgt gtt gtg gat tgg ttg cag gcc gtg att gag	787
Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu Gln Ala Val Ile Glu	
215 220 225	
gtg act ggt cga gag gat ctg ccc tcg att gaa caa gcc cag cgc tgg	835
Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu Gln Ala Gln Arg Trp	
230 235 240 245	
ttg aat ctg tgg gaa aac gaa acc ccg cgc gct cag agg aca gcc aat	883

Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala Gln Arg Thr Ala Asn  
 250 255 260  
 gcc ctg cgt tcg aga agg ctg agt gag ttt tct gag ctg ctg atg gaa 931  
 Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser Glu Leu Leu Met Glu  
 265 270 275  
 tcc caa gat gat ttg agc gac acc ttc gat ttc ccc cct gct gat ttg 979  
 Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe Pro Pro Ala Asp Leu  
 280 285 290  
 gcg ctt gct cgt ttg tgc gtc gag cgg ggt gcc aca gct gct cgg tcc 1027  
 Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala Thr Ala Ala Arg Ser  
 295 300 305  
 acg tca gcg cgc ggt gtg att gcg ttg gtt gat gcc cat cat gcg cac 1075  
 Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp Ala His His Ala His  
 310 315 320 325  
 aat ttt gct gcg gat ctc agc gag gat ggc ttg ttg gtg gtt cct ctc 1123  
 Asn Phe Ala Ala Asp Leu Ser Glu Asp Gly Leu Leu Val Val Pro Leu  
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 Gly His Gly Asp Val Ala Glu Gln Gly  
 345 350  
 cct 1173

<210> 486  
 <211> 350  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 486  
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 Lys Ser His Asp Val Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu  
 35 40 45  
 Gly Gly Val Ala Ala Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His  
 50 55 60  
 Lys Gln Met Leu Ser Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu  
 65 70 75 80  
 Ser Thr Ile Pro Glu Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp  
 85 90 95  
 Val Ala Leu Ala Leu Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro  
 100 105 110  
 Thr Lys Ala Arg Ile Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe  
 115 120 125  
 Ser Glu Thr Ser Val Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly

130	135	140
Glu Thr Gly Gln Ile Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr 145 150 155 160		
Gln Ala Pro His Pro Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val 165 170 175		
Val Ala Ala Gln Thr Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr 180 185 190		
Ala Arg His Ala Phe Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu 195 200 205		
Ser Leu Arg Leu Leu Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu 210 215 220		
Gln Ala Val Ile Glu Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu 225 230 235 240		
Gln Ala Gln Arg Trp Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala 245 250 255		
Gln Arg Thr Ala Asn Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser 260 265 270		
Glu Leu Leu Met Glu Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe 275 280 285		
Pro Pro Ala Asp Leu Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala 290 295 300		
Thr Ala Ala Arg Ser Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp 305 310 315 320		
Ala His His Ala His Asn Phe Ala Ala Asp Leu Ser Glu Asp Gly Leu 325 330 335		
Leu Val Val Pro Leu Gly His Gly Asp Val Ala Glu Gln Gly 340 345 350		

&lt;210&gt; 487

&lt;211&gt; 1248

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1225)

&lt;223&gt; RXS00584

&lt;400&gt; 487

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agaggggctg cttttttggt tcctaaattc accccatccc atg cat agc cct gaa	115
Met His Ser Pro Glu	
1 5	

agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca	163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser	



10								15				20				
acc	agc	aac	aag	cgc	gtc	gtg	gct	ttc	cac	gag	ctg	cct	agc	cct	aca	211
Thr	Ser	Asn	Lys	Arg	Val	Val	Ala	Phe	His	Glu	Leu	Pro	Ser	Pro	Thr	
25				30				35								
gat	ctc	atc	gcc	gca	aac	cca	ctg	aca	cca	aag	cag	gct	tcc	aag	gtg	259
Asp	Leu	Ile	Ala	Ala	Asn	Pro	Leu	Thr	Pro	Lys	Gln	Ala	Ser	Lys	Val	
40				45				50								
gag	cag	gat	cgc	cag	gac	atc	gct	gat	atc	ttc	gct	ggc	gac	gat	gac	307
Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe	Ala	Gly	Asp	Asp	Asp	
55				60				65								
cgc	ctc	gtt	gtc	gtt	gtg	gga	cct	tgc	tca	gtt	cac	gat	cct	gaa	gca	355
Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val	His	Asp	Pro	Glu	Ala	
70				75				80				85				
gcc	atc	gat	tac	gca	aac	cgc	ctg	gct	ccg	ctg	gca	aag	cgc	ctt	gat	403
Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu	Ala	Lys	Arg	Leu	Asp	
90				95				100								
cag	gac	ctc	aag	att	gtc	atg	cgc	gtg	tac	ttc	gag	aag	cct	cgc	acc	451
Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe	Glu	Lys	Pro	Arg	Thr	
105				110				115								
atc	gtc	gga	tgg	aag	gga	ttg	atc	aat	gat	cct	cac	ctc	aac	gaa	acc	499
Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro	His	Leu	Asn	Glu	Thr	
120				125				130								
tac	gac	atc	cca	gag	ggc	ttg	cgc	att	gcg	cgc	aaa	gtg	ctt	atc	gac	547
Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg	Lys	Val	Leu	Ile	Asp	
135				140				145								
gtt	gtg	aac	ctt	gat	ctc	cca	gtc	ggc	tgc	gaa	ttc	ctc	gaa	cca	aac	595
Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu	Phe	Leu	Glu	Pro	Asn	
150				155				160				165				
agc	cct	cag	tac	tac	gcc	gac	act	gtc	gca	tgg	gga	gca	atc	ggc	gct	643
Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp	Gly	Ala	Ile	Gly	Ala	
170				175				180								
cgt	acc	acc	gaa	tct	cag	gtg	cac	cgc	cag	ctg	gct	tct	ggg	atg	tct	691
Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu	Ala	Ser	Gly	Met	Ser	
185				190				195								
atg	cca	att	ggc	ttc	aag	aac	gga	act	gac	gga	aac	atc	cag	gtt	gca	739
Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly	Asn	Ile	Gln	Val	Ala	
200				205				210								
gtc	gac	gcg	gta	cag	gct	gcc	cag	aac	cca	cac	ttc	ttc	ttc	gga	acc	787
Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His	Phe	Phe	Phe	Gly	Thr	
215				220				225								
tcc	gac	gac	ggc	gcg	ctg	agc	gtc	gtg	gag	acc	gca	ggc	aac	agc	aac	835
Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr	Ala	Gly	Asn	Ser	Asn	
230				235				240				245				
tcc	cac	atc	att	ttg	cgc	ggc	ggc	acc								

gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931  
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu  
 265 270 275  
 atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979  
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln  
 280 285 290  
 gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa 1027  
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu  
 295 300 305  
 gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag 1075  
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln  
 310 315 320 325  
 aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg 1123  
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val  
 330 335 340  
 tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc 1171  
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile  
 345 350 355  
 gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca 1219  
 Asp Leu Leu Ala Glu Leu Ala Ala Val Arg Glu Arg Arg Ala Ala  
 360 365 370  
 gcc aag taattaaggg cgctagactg tta 1248  
 Ala Lys  
 375

&lt;210&gt; 488

&lt;211&gt; 375

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 488

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu  
 1 5 10 15  
 Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu  
 20 25 30  
 Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys  
 35 40 45  
 Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe  
 50 55 60  
 Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val  
 65 70 75 80  
 His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu  
 85 90 95  
 Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe  
 100 105 110

Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro  
 115 120 125  
 His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg  
 130 135 140  
 Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu  
 145 150 155 160  
 Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp  
 165 170 175  
 Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu  
 180 185 190  
 Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly  
 195 200 205  
 Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His  
 210 215 220  
 Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr  
 225 230 235 240  
 Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly  
 245 250 255  
 Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly  
 260 265 270  
 Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys  
 275 280 285  
 Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile  
 290 295 300  
 Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu  
 305 310 315 320  
 Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly  
 325 330 335  
 Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp  
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 Glu Arg Arg Ala Ala Ala Lys  
 370 375

<210> 489  
 <211> 1131  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1108)  
 <223> RXS02574

&lt;400&gt; 489

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Leu Ala Arg Ala Gln
1 5
atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163
Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly
10 15 20
gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211
Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly
25 30 35
ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259
Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro
40 45 50
ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307
Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser
55 60 65
gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355
Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile
70 75 80 85
ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403
Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro
90 95 100
gaa caa gta gaa gat ctc gca gaa atc cta ggc act ggt tta gct gca 451
Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly Thr Gly Leu Ala Ala
105 110 115
cat ggt gtg aca gtt aac ttt gca cct gtt gta gat gta gat gct tgg 499
His Gly Val Thr Val Asn Phe Ala Pro Val Val Asp Val Asp Ala Trp
120 125 130
ggg ctc ccc gtc gtt ggc gat cgt tcc ttt tcc aac gac cca gcc gta 547
Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser Asn Asp Pro Ala Val
135 140 145
gca gct act tat gcc aca gct ttt gca aag ggc tta agc aaa gta gga 595
Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly Leu Ser Lys Val Gly
150 155 160 165
att acc cca gta ttc aaa cat ttc cca ggt cac ggt cgt gca agt ggc 643
Ile Thr Pro Val Phe Lys His Phe Pro Gly His Gly Arg Ala Ser Gly
170 175 180
gat tcg cac acc caa gat gtg gtg acc ccc gca ctt gat gag ctt aaa 691
Asp Ser His Thr Gln Asp Val Val Thr Pro Ala Leu Asp Glu Leu Lys
185 190 195
act tac gac ctc atc cct tat ggt caa gca ctt tct gaa act gac gga 739
Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu Ser Glu Thr Asp Gly
200 205 210
gcc gtc atg gtg ggc cac atg att gtt cca ggt ctt ggc acc gac gga 787

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Ala Val Met Val Gly His Met Ile Val Pro Gly Leu Gly Thr Asp Gly  
 215 220 225

gtt cca tcc tct atc gac ccc gcc acc tat caa ctg ctc cgc agt ggc 835  
 Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln Leu Leu Arg Ser Gly  
 230 235 240 245

gat tac cca ggt ggc gtg cct ttc gat ggc gtg atc tac acc gac gat 883  
 Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val Ile Tyr Thr Asp Asp  
 250 255 260

ctc tct gga atg agt gcc att tcc gcc acc cat tca ccc gca gaa gca 931  
 Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His Ser Pro Ala Glu Ala  
 265 270 275

gtg ctt gcc tcc ctc aaa gca ggc gca gac caa gca cta tgg atc gac 979  
 Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln Ala Leu Trp Ile Asp  
 280 285 290

tat ggg tcg ttg ggc tcc gcg att gat cgc gtt gat gct gcc gtt agc 1027  
 Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val Asp Ala Ala Val Ser  
 295 300 305

agc ggt gaa tac cct caa gaa caa atg ctg gca tct gcg tta aga gtc 1075  
 Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala Ser Ala Leu Arg Val  
 310 315 320 325

caa ttg ctc tac atc aca cgt ctc gaa caa aag tgaagttacc agtccgtaac 1128  
 Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys  
 330 335

ccc 1131

&lt;210&gt; 490

&lt;211&gt; 336

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 490

Leu Ala Arg Ala Gln Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser  
 1 5 10 15

Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu  
 20 25 30

Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn  
 35 40 45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val  
 50 55 60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln  
 65 70 75 80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala  
 85 90 95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly  
 100 105 110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val  
 115 120 125  
 Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser  
 130 135 140  
 Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly  
 145 150 155 160  
 Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His  
 165 170 175  
 Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala  
 180 185 190  
 Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu  
 195 200 205  
 Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly  
 210 215 220  
 Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln  
 225 230 235 240  
 Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val  
 245 250 255  
 Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His  
 260 265 270  
 Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln  
 275 280 285  
 Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val  
 290 295 300  
 Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala  
 305 310 315 320  
 Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys  
 325 330 335

<210> 491  
 <211> 1038  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1008)  
 <223> RXS03215

<400> 491  
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 1 5 10 15

gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca	96
Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro	
20 25 30	
ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc	144
Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly	
35 40 45	
cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc	192
Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg	
50 55 60	
cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag	240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu	
65 70 75 80	
ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga	288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly	
85 90 95	
tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc	336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly	
100 105 110	
tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa	384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu	
115 120 125	
ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc	432
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser	
130 135 140	
acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac	480
Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His	
145 150 155 160	
gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac	528
Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp	
165 170 175	
att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc	576
Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu	
180 185 190	
cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa	624
Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu	
195 200 205	
gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc	672
Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly	
210 215 220	
gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa	720
Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu	
225 230 235 240	
gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc	768
Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg	
245 250 255	
ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa	816

Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
 260 265 270  
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 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
 275 280 285  
 tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912  
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
 290 295 300  
 cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960  
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
 305 310 315 320  
 ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008  
 Gly Glu Thr Val Ala Val Pro Ala Ala Leu Ile Pro Ala Asn Asn  
 325 330 335  
 tagaaactat tcagaaagca tcaccatgaa 1038

<210> 492  
 <211> 336  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 492  
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 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
 35 40 45  
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
 50 55 60  
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu  
 65 70 75 80  
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  
 85 90 95  
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly  
 100 105 110  
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu  
 115 120 125  
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser  
 130 135 140  
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
 145 150 155 160  
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
 165 170 175



Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
 180 185 190  
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
 195 200 205  
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
 210 215 220  
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
 225 230 235 240  
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
 245 250 255  
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
 260 265 270  
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
 275 280 285  
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
 290 295 300  
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
 305 310 315 320  
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn  
 325 330 335

<210> 493  
 <211> 1031  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1008)  
 <223> FRXA01915

<400> 493  
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 gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca 96  
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
 20 25 30  
 ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc 144  
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
 35 40 45  
 cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc 192  
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
 50 55 60

cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag	240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu	
65 70 75 80	
ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga	288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly	
85 90 95	
tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc	336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly	
100 105 110	
tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa	384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu	
115 120 125	
ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc	432
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser	
130 135 140	
acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac	480
Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His	
145 150 155 160	
gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac	528
Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp	
165 170 175	
att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc	576
Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu	
180 185 190	
cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa	624
Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu	
195 200 205	
gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc	672
Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly	
210 215 220	
gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa	720
Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu	
225 230 235 240	
gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc	768
Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg	
245 250 255	
ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa	816
Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu	
260 265 270	
ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc	864
Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile	
275 280 285	
tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta	912
Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu	
290 295 300	
cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt	960

His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly  
 305 310 315 320

ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008  
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn  
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<210> 494

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 494

Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile  
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Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro  
 20 25 30

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly  
 35 40 45

Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg  
 50 55 60

Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu  
 65 70 75 80

Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly  
 85 90 95

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly  
 100 105 110

Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu  
 115 120 125

Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser  
 130 135 140

Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His  
 145 150 155 160

Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp  
 165 170 175

Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu  
 180 185 190

Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu  
 195 200 205

Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly  
 210 215 220

Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu  
 225 230 235 240

Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg  
 245 250 255

Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu  
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Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile  
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Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu  
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 Met Ser Phe Ala Glu  
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cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163  
 His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro  
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 Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu  
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att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259  
 Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met  
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ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307  
 Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp  
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ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355  
 Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala  
 70 75 80 85

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Pro	Ser	Ile	Tyr	Tyr	Gly	Asp	Glu	Gln	Gly	Phe	Thr	Gly	Leu	Lys	Glu				
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                   345                                  350                                  355

ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219  
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg  
                   360                                  365                                  370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268  
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<213> Corynebacterium glutamicum

<400> 496

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                   20                                  25                                  30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly  
                   35                                  40                                  45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly  
                   50                                  55                                  60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu  
   65                                  70                                  75                                  80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly  
                   85                                  90                                  95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr  
                   100                                  105                                  110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala  
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Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val  
                   130                                  135                                  140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala  
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Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val  
                   165                                  170                                  175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly  
                   180                                  185                                  190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu  
                   195                                  200                                  205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe  
 210 215 220  
 Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr  
 225 230 235 240  
 Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala  
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 Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe  
 260 265 270  
 Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe  
 275 280 285  
 Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro  
 290 295 300  
 Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile  
 305 310 315 320  
 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln  
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 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys  
 340 345 350  
 Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu  
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 Met Ser Phe Ala Glu  
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 cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163  
 His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro  
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 atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211  
 Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu  
 25 30 35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met 40 45 50	259
ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp 55 60 65	307
ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala 70 75 80 85	355
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gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc Val Phe Asn His Val Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr 105 110 115	451
ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr 120 125 130	499
aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu 135 140 145	547
gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala 150 155 160 165	595
cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro 170 175 180	643
cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr 185 190 195	691
gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys 200 205 210	739
gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp 215 220 225	787
act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr 230 235 240 245	835
ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln 250 255 260	883
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cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979  
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu  
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gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027  
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu  
 295 300 305

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 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile  
 310 315 320 325

gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123  
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val  
 330 335 340

ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171  
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ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219  
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg  
 360 365 370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268  
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala  
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&lt;210&gt; 498

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 498

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Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His  
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Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly  
 35 40 45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly  
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Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu  
 65 70 75 80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly  
 85 90 95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr  
 100 105 110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala  
 115 120 125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val  
 130 135 140  
 Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala  
 145 150 155 160  
 Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val  
 165 170 175  
 Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly  
 180 185 190  
 Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu  
 195 200 205  
 Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe  
 210 215 220  
 Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr  
 225 230 235 240  
 Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala  
 245 250 255  
 Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe  
 260 265 270  
 Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe  
 275 280 285  
 Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro  
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 Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile  
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 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln  
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 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys  
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 Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu  
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Ala Asp Leu Asn Ala Val Glu Glu Gln Leu Gly Arg Ala Pro Arg Gly															20	
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Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly Val Pro Gly Val Val															35	
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Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro Phe Pro Thr Leu Tyr															50	
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Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala Ser Arg Leu Glu Val															65	
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Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu Ser Thr Asp Glu Glu															85	
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Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His Phe Leu Ala Lys Arg															100	
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Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser Gly Gly Gly Met Pro															115	
															105	
gac cga gtg aag tgc ctt cac gtc ctc att gac tat gca ctg gca gaa															499	
Asp Arg Val Lys Cys Leu His Val Leu Ile Asp Tyr Ala Leu Ala Glu															130	
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Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro
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Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala

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Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu		
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Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His		
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Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser		
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Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp		
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Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu		
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 Met Val Ile Ser Phe  
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 Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln  
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 Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg  
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 Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala  
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 Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro  
 70 75 80 85  
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 Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu  
 90 95 100  
 acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg 451  
 Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu

105										110					115					
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Asp	Glu	Asn	Gly	Val	Ala	Thr	Pro	Pro	Ile	Ile	Gly	Val	Pro	Leu	Asp					
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ggt	tca	ccg	ggg	ttt	gcg	gaa	att	ccc	gac	act	gat	ggt	ggg	gaa	tta	547				
Gly	Ser	Pro	Gly	Phe	Ala	Glu	Ile	Pro	Asp	Thr	Asp	Gly	Gly	Glu	Leu					
135				140					145											
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Asp	Gly	Asp	Thr	Glu	Tyr	Asp	Arg	Ala	Val	Gly	Pro	Met	Gln	Phe	Ile					
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Pro	Glu	Thr	Trp	Arg	Leu	Met	Gly	Leu	Asp	Ala	Asn	Gly	Asp	Gly	Val					
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gcg	gac	ccc	aac	caa	att	gat	gac	gca	gca	ttg	agt	gcc	gca	aac	ctg	691				
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&lt;210&gt; 502

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 502

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 Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys  
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Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val	
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Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser	
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Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val	
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Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser	
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Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala  
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Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu  
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Ile Ile His His Pro Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala  
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Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val  
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Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile  
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Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu  
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Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala  
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Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val  
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Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro  
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Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro  
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Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser

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253035

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Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile Asp Ala Val Val Asp
404550

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                                     130                                    135                                    140  
 Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met  
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 Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln  
                                     165                                    170                                    175  
 Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg  
                                     180                                    185                                    190  
 Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr  
                                     195                                    200                                    205  
 Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp  
                                     210                                    215                                    220  
 Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr  
                                     225                                    230                                    235                                    240  
 Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser  
                                     245                                    250                                    255  
 Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr  
                                     260                                    265                                    270  
 Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala  
                                     275                                    280                                    285  
 His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val  
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 Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu  
                                     305                                    310                                    315                                    320  
 Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu  
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 Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val  
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 Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro  
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 Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile  
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 Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val  
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 Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr

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Lys	Met	Phe	Val	Pro	Leu	Ile	Thr	Tyr	Phe	Val	Val	Pro	Met	Ile	Leu
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 Val Ser His Thr Ala 5  
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 Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln 20  
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 ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat 211  
 Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn 35  
 25 30  
 aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa 259  
 Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu 50  
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 Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser 65  
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 Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser 85  
 70 75 80  
 ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg 403  
 Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu 100  
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 cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg 451  
 Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu 115  
 105 110  
 ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt 499  
 Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val 130  
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gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu 135 140 145	547
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gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu 200 205 210	739
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tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu 230 235 240 245	835
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att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu 345 350 355	1171
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 Val Phe Ser Asn Asn Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val  
           35                  40                  45  
 Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser  
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 Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser  
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 Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met  
                   85                  90                  95  
 Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe  
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 Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu  
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 Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg  
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 Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala  
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 Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr  
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 Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg  
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 Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu  
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 Gly Lys, Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro  
           245                  250                  255  
 Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr  
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 Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu  
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 Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala

290	295	300
Arg Ala Ala Glu Gln Gly	Ala Phe Val Asn Ile	Val His Gly Gly Val
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Thr Thr Leu Gln Arg Gln Ser Phe Gly	Lys Met Thr Val Arg Leu Thr	
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Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr		
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 Met Ser Leu Ile Glu  
 1 5  
 atg cga aat att gtc aag acc tac aac att gga tct gaa ggt gaa ctc 163  
 Met Arg Asn Ile Val Lys Thr Tyr Asn Ile Gly Ser Glu Gly Glu Leu  
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 Thr Val Leu His Gly Val Asp Phe His Val Asp Arg Gly Glu Phe Val  
 25 30 35  
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 Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser Thr Met Met Asn Ile  
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 Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr Tyr Thr Leu Asp Gly  
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 Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu Ala Ser His Arg Ala  
 70 75 80 85  
 aaa tcg att ggt ttt gtg ttt cag aac ttc aat ctg att ggc cgc atc 403  
 Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn Leu Ile Gly Arg Ile  
 90 95 100  
 gat gcg ttg aag aat gtg gaa atg ccc atg atg tat gcg ggc att ccg 451  
 Asp Ala Leu Lys Asn Val Glu Met Pro Met Met Tyr Ala Gly Ile Pro  
 105 110 115  
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Met	Gly	Glu	Arg	Leu	Asn	His	Glu	Pro	Asn	Glu	Leu	Ser	Gly	Gly	Gln		
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aag	cag	cgc	gtg	gcc	att	gct	cgc	gcg	ttg	gcg	aac	gat	cct	gag	atc	595	
Lys	Gln	Arg	Val	Ala	Ile	Ala	Arg	Ala	Leu	Ala	Asn	Asp	Pro	Glu	Ile		
		150			155				160						165		
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Ile	Leu	Ala	Asp	Glu	Pro	Thr	Gly	Ala	Leu	Asp	Ser	Ala	Thr	Gly	Arg		
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Met	Val	Met	Asp	Ile	Phe	His	Gln	Leu	Asn	Lys	Glu	Gln	Gly	Lys	Thr		
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Ile	Val	Phe	Ile	Thr	His	Asn	Pro	Glu	Leu	Ala	Asp	Glu	Ser	Asp	Arg		
		200					205					210					
gtg	gtc	acc	atg	gtt	gac	ggg	cgc	atc	att	ggg	tct	gag	gtg	aaa	cac	787	
Val	Val	Thr	Met	Val	Asp	Gly	Arg	Ile	Ile	Gly	Ser	Glu	Val	Lys	His		
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Ser																	
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Arg	Gly	Glu	Phe	Val	Ser	Val	Val	Gly	Thr	Ser	Gly	Ser	Gly	Lys	Ser		
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Thr	Met	Met	Asn	Ile	Ile	Gly	Leu	Leu	Asp	Lys	Pro	Thr	Asp	Gly	Thr		
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Tyr	Thr	Leu	Asp	Gly	Val	Asp	Val	Leu	Asp	Ile	Ser	Asp	Asp	Ala	Leu		
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Ala	Ser	His	Arg	Ala	Lys	Ser	Ile	Gly	Phe	Val	Phe	Gln	Asn	Phe	Asn		
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Leu	Ile	Gly	Arg	Ile	Asp	Ala	Leu	Lys	Asn	Val	Glu	Met	Pro	Met	Met		
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Tyr	Ala	Gly	Ile	Pro	Ala	Lys	Gln	Arg	Arg	Ser	Arg	Ala	Val	Glu	Leu		
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 Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala  
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 Asn Asp Pro Glu Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp  
 165 170 175  
 Ser Ala Thr Gly Arg Met Val Met Asp Ile Phe His Gln Leu Asn Lys  
 180 185 190  
 Glu Gln Gly Lys Thr Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala  
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 Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser  
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 Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr  
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 gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc 307  
 Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val  
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 Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe  
 70 75 80 85  
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Pro	Ile	Ser	Phe	Val	Ile	Ala	Leu	Ala	Ile	Ile	Thr	Trp	Leu	His	Ile		
			105					110					115				
ctc	ttt	ggg	gaa	atg	gtg	cca	aag	aac	atc	gct	att	gct	ggc	cct	gaa	499	
Leu	Phe	Gly	Glu	Met	Val	Pro	Lys	Asn	Ile	Ala	Ile	Ala	Gly	Pro	Glu		
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acc	tta	ggc	atg	tgg	ctt	gct	cca	gtg	ctc	att	gcg	ttt	gtg	aag	att	547	
Thr	Leu	Gly	Met	Trp	Leu	Ala	Pro	Val	Leu	Ile	Ala	Phe	Val	Lys	Ile		
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Arg	Ala	Phe	Gly	Val	Glu	Gln	Lys	Asn	Glu	Leu	Asp	Ser	Thr	Val	Asp		
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cca	gag	cag	ctg	gca	tca	atg	att	tcc	gag	tcc	cgt	tcc	gaa	ggc	ctc	691	
Pro	Glu	Gln	Leu	Ala	Ser	Met	Ile	Ser	Glu	Ser	Arg	Ser	Glu	Gly	Leu		
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ctt	gat	gct	gaa	gag	cac	gcc	cgc	ctg	tcc	aag	gcg	ctg	cgc	tct	gag	739	
Leu	Asp	Ala	Glu	Glu	His	Ala	Arg	Leu	Ser	Lys	Ala	Leu	Arg	Ser	Glu		
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cag	cgt	tcc	atc	aag	gaa	ctg	gtg	att	aag	gat	gag	gac	gtg	cgc	acg	787	
Gln	Arg	Ser	Ile	Lys	Glu	Leu	Val	Ile	Lys	Asp	Glu	Asp	Val	Arg	Thr		
	215					220				225							
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Leu	Ala	Phe	Gly	Lys	Ser	Gly	Pro	Thr	Leu	His	Gln	Leu	Glu	Glu	Ala		
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Val	Arg	Glu	Thr	Gly	Phe	Ser	Arg	Phe	Pro	Val	Thr	Gly	Arg	Asp	Gly		
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Ser	Tyr	Leu	Gly	Tyr	Ile	His	Ile	Lys	Asp	Ile	Leu	Pro	Arg	Leu	Ala		
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gat	cct	gag	atg	gat	ccc	tcc	gag	acc	att	ccg	cgt	tct	gca	ctg	cgc	979	
Asp	Pro	Glu	Met	Asp	Pro	Ser	Glu	Thr	Ile	Pro	Arg	Ser	Ala	Leu	Arg		
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cct	ttg	agc	aat	gtg	gat	gcc	gac	ggc	ctc	atg	gat	gac	gtc	ttg	gat	1027	
Pro	Leu	Ser	Asn	Val	Asp	Ala	Asp	Gly	Leu	Met	Asp	Asp	Val	Leu	Asp		
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Phe	Met	His	Tyr	Arg	Ser	Ala	His	Met	Ala	Gln	Val	Arg	Leu	Lys	Gly		
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Glu	Leu	Leu	Gly	Val	Ile	Thr	Leu	Glu	Asp	Leu	Ile	Glu	Glu	Tyr	Val		

330 335 340  
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Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys  
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Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln  
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Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro  
 65 70 75 80

Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro  
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Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile  
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Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala  
 115 120 125

Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile  
 130 135 140

Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile  
 145 150 155 160

Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu  
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Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser  
 180 185 190

Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys  
 195 200 205

Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp  
 210 215 220

Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His  
 225 230 235 240

Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val

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Leu	Pro	Arg	Leu	Ala	Asp	Pro	Glu	Met	Asp	Pro	Ser	Glu	Thr	Ile	Pro				
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Arg	Ser	Ala	Leu	Arg	Pro	Leu	Ser	Asn	Val	Asp	Ala	Asp	Gly	Leu	Met				
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Asp	Asp	Val	Leu	Asp	Phe	Met	His	Tyr	Arg	Ser	Ala	His	Met	Ala	Gln				
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Val	Arg	Leu	Lys	Gly	Glu	Leu	Leu	Gly	Val	Ile	Thr	Leu	Glu	Asp	Leu				
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Asp Asp

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 <213> Corynebacterium glutamicum

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 <222> (101)..(709)  
 <223> RXC01017

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 Met Ala Gln Lys Val  
 1 5  
 acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc 163  
 Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg  
 10 15 20  
 tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt 211  
 Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val  
 25 30 35  
 cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat 259  
 Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp  
 40 45 50  
 tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca 307  
 Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala  
 55 60 65  
 gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca 355  
 Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala  
 70 75 80 85



atg ggt acc cgc atc cac aac gac ggt cgc gga cca atc gaa ggt tcc 403  
 Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser  
 90 95 100  
  
 ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct 451  
 Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala  
 105 110 115  
  
 gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc 499  
 Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg  
 120 125 130  
  
 gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc 547  
 Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr  
 135 140 145  
  
 cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc 595  
 Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr  
 150 155 160 165  
  
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 Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe  
 170 175 180  
  
 aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act 691  
 Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr  
 185 190 195  
  
 gag aac cca cag ttc gac taattaacgc tgtctctgct tat 732  
 Glu Asn Pro Gln Phe Asp  
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&lt;210&gt; 516

&lt;211&gt; 203

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 516

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 Glu Ile Gln Trp Val Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg  
 35 40 45  
  
 Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro  
 50 55 60  
  
 Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly  
 65 70 75 80  
  
 Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly  
 85 90 95  
  
 Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu  
 100 105 110  
  
 Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp

115	120	125
Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly		
130	135	140
Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe		
145	150	155
Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile		
	165	170
		175
Phe Asp Ala Ser Phe Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile		
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		190
Lys Arg Ser Arg Thr Glu Asn Pro Gln Phe Asp		
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 <213> Corynebacterium glutamicum

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 <223> RXC01021

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 Met Ser Ser Ser Glu 5  
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 agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163  
 Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu 20  
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 Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala 35  
 25 30  
 tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259  
 Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala 50  
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 gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307  
 Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val 65  
 55 60  
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 Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met 85  
 70 75 80  
 aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403  
 Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val 100  
 90 95  
 gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451  
 Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg

105										110					115					
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Gly	Asn	Ser	Gly	Val	Val	Leu	Ser	Gln	Val	Leu	Arg	Ala	Ile	Ala	Gln					
120							125					130								
gca	gct	gct	gac	ggg	gtt	att	gat	ggc	cac	aca	atc	caa	gaa	gcg	cta	547				
Ala	Ala	Ala	Asp	Gly	Val	Ile	Asp	Gly	His	Thr	Ile	Gln	Glu	Ala	Leu					
135							140					145								
tcc	att	gct	cgc	tcc	cta	gtt	gat	cgc	gca	att	aca	gat	cct	gtg	gag	595				
Ser	Ile	Ala	Arg	Ser	Leu	Val	Asp	Arg	Ala	Ile	Thr	Asp	Pro	Val	Glu					
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 <213> Corynebacterium glutamicum

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Trp	Ala	Arg	Thr	Ala	Val	Glu	Gln	Leu	Ser	Glu	Arg	Arg	Ala	Glu	Ile
	50					55					60				
Asn	Ala	Leu	Asn	Val	Phe	Pro	Val	Pro	Asp	Ala	Asp	Thr	Gly	Ser	Asn
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Met	Thr	Tyr	Thr	Met	Thr	Ala	Ala	Leu	Asp	Glu	Ala	Leu	Lys	Leu	Gly
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Glu	Leu	Gly	Asp	Val	Ala	Arg	Ile	Thr	Glu	Ala	Leu	Ala	Val	Gly	Ser
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Val	Arg	Gly	Ala	Arg	Gly	Asn	Ser	Gly	Val	Val	Leu	Ser	Gln	Val	Leu
		115					120					125			
Arg	Ala	Ile	Ala	Gln	Ala	Ala	Ala	Asp	Gly	Val	Ile	Asp	Gly	His	Thr
	130					135					140				
Ile	Gln	Glu	Ala	Leu	Ser	Ile	Ala	Arg	Ser	Leu	Val	Asp	Arg	Ala	Ile
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Thr	Asp	Pro	Val	Glu	Gly	Thr	Val	Val	Thr	Val	Leu	Arg	Ser		
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&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1024)

&lt;223&gt; RXC01212

&lt;400&gt; 519

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                                         1 5

aca cca gca atc gac gta aca gac ctc gtg aga acc tac ggc gac tac 163
Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg Thr Tyr Gly Asp Tyr
                        10 15 20

acc gca gtc aag ggc ctg aat ttc cat gta cag cgc ggt gaa gta ttt 211
Thr Ala Val Lys Gly Leu Asn Phe His Val Gln Arg Gly Glu Val Phe
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Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val
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Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly
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Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile
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Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr
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Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp
                        105 110 115

gtg ctt gcc gac gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc 499
Val Leu Ala Asp Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly
                        120 125 130

gcg ctt tcc gga ggc gaa caa cga cgc ctt gat ttg gcc tgc gca ctg 547
Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu
                        135 140 145

ctt ggc gac ccc tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc 595
Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu
                        150 155 160 165

gac cca gaa tct agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa 643
Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys
                        170 175 180

cag cgc ggc gtc acc atg atg ctg acc acc cac tac ctg gag gaa gcc 691
Gln Arg Gly Val Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala

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185					190					195					
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Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala															
200													210		
gtg gaa ggc acc ttg gat gaa ctg gtg gcc cgc gag aag tcg atc atc														787	
Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile															
215													225		
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Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly															
230													245		
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Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Thr															
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Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly															
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Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val															
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295													305		

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 <213> Corynebacterium glutamicum

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 Ser Thr Leu Glu Val Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr  
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 Val Arg Ile Ser Gly Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg  
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 Pro Glu Leu Gly Ile Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu  
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 Thr Val Ala Glu Thr Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro  
 100 105 110  
 Arg Ala Ile Lys Asp Val Leu Ala Asp Val Asp Leu Leu His Arg Glu

115	120	125
Asn Val Lys Val Gly Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp 130 135 140		
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Pro Thr Thr Gly Leu Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu 165 170 175		
Leu Leu Asp Leu Lys Gln Arg Gly Val Thr Met Met Leu Thr Thr His 180 185 190		
Tyr Leu Glu Glu Ala Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn 195 200 205		
Ala Gly Glu Ile Ala Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg 210 215 220		
Glu Lys Ser Ile Ile Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu 225 230 235 240		
Pro Val Leu Ser Gly Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg 245 250 255		
Ile Ala Thr Thr Thr Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp 260 265 270		
Ala Ala Glu Thr Gly Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala 275 280 285		
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Leu Gln Thr Ala 305		

<210> 521  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1108)  
 <223> RXC01306

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 Met Thr Glu Trp Tyr  
 1 5  
 gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc 163  
 Val Val Leu Pro Ala Thr Ile Leu Leu Ile Ala Leu Ser Ala Phe Phe  
 10 15 20  
 gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag 211

Val	Ile	Ile	Glu	Phe	Ala	Leu	Leu	Ala	Ala	Arg	Arg	Asn	Arg	Leu	Glu		
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Glu	Thr	Val	Glu	Thr	Ser	Arg	Ser	Ser	Arg	Ala	Ala	Leu	Arg	Ser	Leu		
		40					45					50					
aat	gaa	ctt	act	ctc	atg	ctc	gcg	ggc	gcg	cag	ttg	gga	atc	acc	atg	307	
Asn	Glu	Leu	Thr	Leu	Met		Leu	Ala	Gly	Ala	Gln	Leu	Gly	Ile	Thr	Met	
	55					60					65						
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Val	Thr	Phe	Ala	Leu	Gly	Ala	Ile	Thr	Lys	Pro	Trp	Val	His	Tyr	Ala		
	70				75				80						85		
ttg	atg	ccg	ctc	ttc	gaa	tgg	gcg	cgt	ata	ccg	ctg	gtt	atg	gca	gat	403	
Leu	Met	Pro	Leu	Phe	Glu	Trp	Ala	Arg	Ile	Pro	Leu	Val	Met	Ala	Asp		
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gtc	att	gcg	ttt	att	ttg	tcg	ctg	ttt	atc	gta	acg	ttt	ctg	cac	ttg	451	
Val	Ile	Ala	Phe	Ile	Leu	Ser	Leu	Phe	Ile	Val	Thr	Phe	Leu	His	Leu		
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Val	Ile	Gly	Glu	Met	Ala	Pro	Lys	Ser	Trp	Ala	Ile	Ala	His	Pro	Glu		
		120					125					130					
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Thr	Ala	Leu	Arg	Thr	Ile	Ala	Ile	Pro	Ala	Arg	Gly	Phe	Ile	Asn	Leu		
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cgc	aaa	gtt	ggt	gaa	act	ccc	gtt	gat	cga	gct	gca	gct	ggt	ggc	tat	643	
Arg	Lys	Val	Gly	Glu	Thr	Pro	Val	Asp	Arg	Ala	Ala	Ala	Gly	Gly	Tyr		
			170					175						180			
gac	acc	gat	acc	ctc	cat	gcc	ctc	att	gag	cat	tcc	cga	gaa	act	ggc	691	
Asp	Thr	Asp	Thr	Leu	His	Ala	Leu	Ile	Glu	His	Ser	Arg	Glu	Thr	Gly		
			185					190					195				
gct	ctg	gat	cag	caa	tcc	gcc	gcc	caa	atc	agc	gga	att	atc	aag	ctg	739	
Ala	Leu	Asp	Gln	Gln	Ser	Ala	Ala	Gln	Ile	Ser	Gly	Ile	Ile	Lys	Leu		
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Asp	Lys	Ile	Thr	Val	Gly	Gln	Thr	Leu	Thr	Ala	Ser	Pro	Phe	Thr	His		
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Ser	Ala	Ser	Ala	Thr	Val	Ala	Glu	Val	Gln	Ala	Ala	Ala	Gln	Arg	Ser		
	230				235				240						245		
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Gly	Ser	Leu	Arg	Val	Leu	Ile	Asp	Ala	Pro	Ser	His	Leu	Phe	Pro	His		
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gtc	att	cat	gtg	cga	gac	acc	ctt	ggt	gcc	tcg	cca	gac	gag	aag	gct	931	
Val	Ile	His	Val	Arg	Asp	Thr	Leu	Gly	Ala	Ser	Pro	Asp	Glu	Lys	Ala		

265										270										275										
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280					285					290																				
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His	Gln	Ala	Leu	Glu	Tyr	Met	Arg	Glu	His	Asn	Glu	Gln	Ile	Ser	Ala															
295					300					305																				
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310					315					320					325															
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330					335																									
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 <211> 336  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 522															
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Arg	Asn	Arg	Leu	Glu	Glu	Thr	Val	Glu	Thr	Ser	Arg	Ser	Ser	Arg	Ala
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Ala	Leu	Arg	Ser	Leu	Asn	Glu	Leu	Thr	Leu	Met	Leu	Ala	Gly	Ala	Gln
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Leu	Gly	Ile	Thr	Met	Val	Thr	Phe	Ala	Leu	Gly	Ala	Ile	Thr	Lys	Pro
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Trp	Val	His	Tyr	Ala	Leu	Met	Pro	Leu	Phe	Glu	Trp	Ala	Arg	Ile	Pro
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Leu	Val	Met	Ala	Asp	Val	Ile	Ala	Phe	Ile	Leu	Ser	Leu	Phe	Ile	Val
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Thr	Phe	Leu	His	Leu	Val	Ile	Gly	Glu	Met	Ala	Pro	Lys	Ser	Trp	Ala
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Ile	Ala	His	Pro	Glu	Thr	Ala	Leu	Arg	Thr	Ile	Ala	Ile	Pro	Ala	Arg
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Ala	Asn	Asp	Leu	Val	Arg	Lys	Val	Gly	Glu	Thr	Pro	Val	Asp	Arg	Ala
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Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His															



180										185					190				
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		195					200					205							
Gly	Ile	Ile	Lys	Leu	Asp	Lys	Ile	Thr	Val	Gly	Gln	Thr	Leu	Thr	Ala				
	210					215					220								
Ser	Pro	Phe	Thr	His	Ser	Ala	Ser	Ala	Thr	Val	Ala	Glu	Val	Gln	Ala				
225					230					235					240				
Ala	Ala	Gln	Arg	Ser	Gly	Ser	Leu	Arg	Val	Leu	Ile	Asp	Ala	Pro	Ser				
				245					250					255					
His	Leu	Phe	Pro	His	Val	Ile	His	Val	Arg	Asp	Thr	Leu	Gly	Ala	Ser				
			260					265					270						
Pro	Asp	Glu	Lys	Ala	Ser	Lys	Trp	Ser	Arg	Pro	Ile	Leu	Thr	Val	Ala				
	275						280					285							
Glu	Thr	Asp	Thr	Leu	His	Gln	Ala	Leu	Glu	Tyr	Met	Arg	Glu	His	Asn				
	290					295					300								
Glu	Gln	Ile	Ser	Ala	Val	Leu	Ser	Ala	Asp	Gly	Lys	Thr	Val	Leu	Gly				
305					310					315					320				
Val	Ile	Thr	Trp	Asp	His	Ile	Leu	Lys	Tyr	Leu	Trp	Pro	Ala	Ser	Val				
				325					330					335					

&lt;210&gt; 523

&lt;211&gt; 513

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(490)

&lt;223&gt; RXC01366

&lt;400&gt; 523

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gactgtccaa	acctaaacca	aaggtctaaa	ctttggcttc	gtg	agt	cag	ttt	cgt	115
				Val	Ser	Gln	Phe	Arg	
				1				5	

cgt	tgt	tcc	cgc	cct	ggt	tgt	ggc	aag	cct	gcc	gtc	gca	acc	ctc	acc	163
Arg	Cys	Ser	Arg	Pro	Gly	Cys	Gly	Lys	Pro	Ala	Val	Ala	Thr	Leu	Thr	
				10				15						20		

tac	gca	tat	tcg	gat	tcc	act	gcg	gtg	ggt	cct	ttg	gcg	cct	gca	211
Tyr	Ala	Tyr	Ser	Asp	Ser	Thr	Ala	Val	Val	Gly	Pro	Leu	Ala	Pro	Ala
			25				30					35			

gca	gag	ccc	cat	agt	tgg	gat	ctg	tgt	gag	cat	cat	gcc	gag	cgt	att	259
Ala	Glu	Pro	His	Ser	Trp	Asp	Leu	Cys	Glu	His	His	Ala	Glu	Arg	Ile	
		40					45					50				

act gcg ccc ctt ggt tgg gag atg ctg cgg gtg aac gac atc aaa gtc 307  
 Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val Asn Asp Ile Lys Val  
     55                    60                    65

gat gac gat gag gat ctg acg gct ctt gct cag gct gtt cgt gag gct 355  
 Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln Ala Val Arg Glu Ala  
     70                    75                    80                    85

gga cgc act gtg agt ggt ctg gtt cct gaa gac gaa gtg ggc ggc aac 403  
 Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp Glu Val Gly Gly Asn  
                     90                    95                    100

cat ccg gtg aac cgg agt gcg cgg atc gcg gaa cag aag gtt cac cgc 451  
 His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu Gln Lys Val His Arg  
                     105                    110                    115

agg ggt cat ctc tat gtt gtg cct gat cag gac gaa tca taagggtttgc 500  
 Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp Glu Ser  
     120                    125                    130

tattcggatt gga 513

<210> 524  
 <211> 130  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 524  
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Val Ala Thr Leu Thr Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly  
     20                    25                    30

Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His  
     35                    40                    45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val  
     50                    55                    60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln  
     65                    70                    75                    80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp  
                     85                    90                    95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu  
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Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp  
     115                    120                    125

Glu Ser  
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<210> 525  
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 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(591)

&lt;223&gt; RXC01372

&lt;400&gt; 525

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Gln Asp Thr Phe Val Leu Pro Thr Leu Pro Thr Ala Ala Gly Leu Ser	
1 5 10 15	
cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa	96
Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu	
20 25 30	
gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc	144
Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys	
35 40 45	
att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc	192
Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val	
50 55 60	
aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg	240
Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val	
65 70 75 80	
cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc	288
His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala	
85 90 95	
cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc	336
Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro	
100 105 110	
gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc	384
Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr	
115 120 125	
gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta	432
Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val	
130 135 140	
ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat	480
Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp	
145 150 155 160	
gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa	528
Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln	
165 170 175	
gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att	576
Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile	
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gaa gaa aag gac ttg taaatggagc tattggaagg ctc	614
Glu Glu Lys Asp Leu	
195	

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<400> 527  
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 Val Ala Gly Val Ala

	1	5	
cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca			163
Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro			
	10	20	
gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa			211
Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu			
	25	35	
acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg			259
Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro			
	40	50	
ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg			307
Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr			
	55	65	
cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag			355
Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys			
	70	85	
ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa			403
Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu			
	90	100	
gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg			451
Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met			
	105	115	
ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca			499
Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser			
	120	130	
ttg ggt gcg gat gat gtg gag tcg att gcg gag ggc gat cca gag cgt			547
Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg			
	135	145	
ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag			595
Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln			
	150	165	
tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag			643
Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys			
	170	180	
tggtagaaaaactg gtgttttttcg gcc			669
Trp			

&lt;210&gt; 528

&lt;211&gt; 182

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 528

Val	Ala	Gly	Val	Ala	Gln	Arg	Phe	Val	Asp	Glu	Arg	Ile	His	Val	Gly
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Leu	Asp	Ser	Met	Pro	Glu	Ala	Val	Thr	Ala	Val	Trp	Met	Glu	Ser	Asp
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<211> 981
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(958)  
<223> RXC01663
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c	g	t	g	g	c	t	t	g	a		g	t	a	c	g	c	a	c	t	g		c	c	a	g	t	a	a	g	g	t		g	t	g	t	a	t	g	t	g		a	t	g		115																	
																Met	Glu	Ile	Ser	Val																																												
																1				5																																												
t	t	g		a	t	c		a	t	c		g	c	c		g	c	a		c	t	g		a	t	c		g	t	a		c	t	g		t	g		c	g		c	g		163																			
Leu	Ile	Ile		Ala		Ala		Leu	Ile	Leu		Val		Ala		Gly		Ile		Val		Leu		Trp		Arg																																						
										10											15											20																																
g	c	g		g	a	c		t	c	g		t	c	t		a	a	a		c	a	g		g	c	a		g	c	t		a	a	a		a	a	g		g	c	t		g	t	g		g	c		211													
Ala	Asp	Ser		Ser		Lys		Gln		Ala		Ala		Lys		Lys		Ala		Glu		Ser		Pro		Val		Gly																																				
										25											30											35																																
t	c	a		g	t	c		g	c	a		c	c	t		g	c	g		c	c	c		g	t	g		c	t	g		g	t	t		g	a	a		g	a	a		g	a	g		c	c	g		g	a	c		c	c	t		g	a	g		259
Ser	Val			Ala		Pro		Ala		Pro		Val		Leu		Val		Val		Glu		Glu		Glu		Pro		Asp		Pro		Glu																																
										40											45											50																																

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag	307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu	
55 60 65	
ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag	355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu	
70 75 80 85	
ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat	403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp	
90 95 100	
gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac	451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr	
105 110 115	
ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg	499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala	
120 125 130	
gag gta gct gcg gac gag gag caa cgg ggc gtc gat aag cat tcg ttt	547
Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe	
135 140 145	
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Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala	
150 155 160 165	
gcg aag cac cac ttc gat ttc atc aag gaa gat gcc ttt ttg acc gat	643
Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp	
170 175 180	
gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg	691
Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val	
185 190 195	
gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg	739
Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala	
200 205 210	
ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc	787
Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val	
215 220 225	
att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa	835
Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu	
230 235 240 245	
tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc	883
Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu	
250 255 260	
agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg	931
Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr	
265 270 275	
tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa	978
Ser Val Trp Ile Pro Cys Gln Lys Leu	
280 285	

tct

981

&lt;210&gt; 530

&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 530

Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly  
 1 5 10 15

Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala  
 20 25 30

Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu  
 35 40 45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala  
 50 55 60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro  
 65 70 75 80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp  
 85 90 95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr  
 100 105 110

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln  
 115 120 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val  
 130 135 140

Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu  
 145 150 155 160

Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp  
 165 170 175

Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala  
 180 185 190

Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His  
 195 200 205

Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile  
 210 215 220

Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp  
 225 230 235 240

Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser  
 245 250 255

Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser  
 260 265 270

Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu



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275                                280                                285

<210> 531
<211> 1545
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1522)
<223> RXC01693

<400> 531
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                                         Met Asn Thr Ala Pro
                                         1                               5

ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc 163
Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala
                        10                        15                        20

ccc tgg caa ggt gag gaa gcc ccc aac cct gag ctc gtg att tta aat 211
Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn
                        25                        30                        35

gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca 259
Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr
                        40                        45                        50

cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca 307
Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn Pro Glu Pro Leu Thr
                        55                        60                        65

aaa gca gtt gcg cag gcc tat tcc ggc cac caa ttc gga cag ttt gtg 355
Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln Phe Gly Gln Phe Val
                        70                        75                        80                        85

gca agc ctt ggt gat ggc cga gcg ctt ctt ctc ggc gaa gcc cgc tca 403
Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu Gly Glu Ala Arg Ser
                        90                        95                        100

gct gac ggc gta ctg cat gat atc cac ctc aaa gga tct gga cga acc 451
Ala Asp Gly Val Leu His Asp Ile His Leu Lys Gly Ser Gly Arg Thr
                        105                        110                        115

caa ttc tcc cga gga gcc gat gga cgc gcc gtc ctt ggc ccc gtc tta 499
Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val Leu Gly Pro Val Leu
                        120                        125                        130

cgc gaa tac atc atc tcc gaa gcg atg cat gca ctt ggt gtt ccc acc 547
Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala Leu Gly Val Pro Thr
                        135                        140                        145

acc agg tca ctt gca gta att agc acc ggt agg aaa atc caa cga gga 595
Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg Lys Ile Gln Arg Gly
                        150                        155                        160                        165

agc gta gcc cca ggc gca gtc ctt gtt cga gta gca acc agc ctc att 643

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Ser	Val	Ala	Pro	Gly	Ala	Val	Leu	Val	Arg	Val	Ala	Thr	Ser	Leu	Ile		
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cga	gtc	gga	tcc	ttc	caa	tac	tcc	aac	atc	tct	ggg	ggc	atc	gaa	cta	691	
Arg	Val	Gly	Ser	Phe	Gln	Tyr	Ser	Asn	Ile	Ser	Gly	Gly	Ile	Glu	Leu		
			185					190					195				
tct	caa	cac	ctg	gcg	aac	tat	acg	atc	acc	agg	cat	ttc	cct	tcg	ttg	739	
Ser	Gln	His	Leu	Ala	Asn	Tyr	Thr	Ile	Thr	Arg	His	Phe	Pro	Ser	Leu		
		200					205					210					
gta	gct	gaa	cta	tcc	gca	cca	acc	ccc	gca	act	tat	gta	tca	ctg	ttt	787	
Val	Ala	Glu	Leu	Ser	Ala	Pro	Thr	Pro	Ala	Thr	Tyr	Val	Ser	Leu	Phe		
	215					220					225						
aaa	gcg	att	ctt	cag	cgc	caa	gca	gac	acc	gtt	gga	aaa	tgg	acc	agg	835	
Lys	Ala	Ile	Leu	Gln	Arg	Gln	Ala	Asp	Thr	Val	Gly	Lys	Trp	Thr	Arg		
230					235					240					245		
ctg	ggg	ttc	gtt	cac	gga	gcc	ctc	aac	aca	gac	aac	acg	ttg	ata	tcc	883	
Leu	Gly	Phe	Val	His	Gly	Ala	Leu	Asn	Thr	Asp	Asn	Thr	Leu	Ile	Ser		
				250					255					260			
gga	gaa	act	gtt	gac	tac	ggc	cca	tgc	gct	ttc	atg	gag	cgc	tac	cgt	931	
Gly	Glu	Thr	Val	Asp	Tyr	Gly	Pro	Cys	Ala	Phe	Met	Glu	Arg	Tyr	Arg		
			265					270					275				
ggc	gac	gcg	aaa	ttt	agc	tcc	atc	gac	act	tat	ggg	cgc	tac	aaa	ttt	979	
Gly	Asp	Ala	Lys	Phe	Ser	Ser	Ile	Asp	Thr	Tyr	Gly	Arg	Tyr	Lys	Phe		
		280					285					290					
gaa	aac	caa	cct	atg	atc	ctc	gga	tgg	aac	atg	gcc	cgc	ctc	gta	gaa	1027	
Glu	Asn	Gln	Pro	Met	Ile	Leu	Gly	Trp	Asn	Met	Ala	Arg	Leu	Val	Glu		
	295					300					305						
acc	ctc	ctc	cca	ctc	ctg	ggc	gcc	aca	cca	gac	gaa	ggc	atg	aca	gca	1075	
Thr	Leu	Leu	Pro	Leu	Leu	Gly	Ala	Thr	Pro	Asp	Glu	Gly	Met	Thr	Ala		
	310				315					320					325		
gcc	caa	gaa	gct	ctc	gta	gaa	ttc	gat	gac	ctc	tgc	gaa	caa	gca	atc	1123	
Ala	Gln	Glu	Ala	Leu	Val	Glu	Phe	Asp	Asp	Leu	Cys	Glu	Gln	Ala	Ile		
				330				335						340			
cga	aaa	gaa	ttc	gcc	act	gca	ctg	ggc	ctt	gac	gag	tca	gac	acc	ggc	1171	
Arg	Lys	Glu	Phe	Ala	Thr	Ala	Leu	Gly	Leu	Asp	Glu	Ser	Asp	Thr	Gly		
			345					350					355				
acg	gta	gag	cag	ttc	cgt	gaa	ctg	ctc	tac	ctc	cat	aac	ccc	gac	atc	1219	
Thr	Val	Glu	Gln	Phe	Arg	Glu	Leu	Leu	Tyr	Leu	His	Asn	Pro	Asp	Ile		
		360					365					370					
acc	acg	ctg	ctg	cgc	gca	ctc	acc	gac	aac	acc	gca	cca	ccg	agt	ggc	1267	
Thr	Thr	Leu	Leu	Arg	Ala	Leu	Thr	Asp	Asn	Thr	Ala	Pro	Pro	Ser	Gly		
		375				380					385						
ttt	gaa	gca	ttc	gtt	cac	gac	tgg	aaa	acc	caa	gac	cca	gat	atc	gaa	1315	
Phe	Glu	Ala	Phe	Val	His	Asp	Trp	Lys	Thr	Gln	Asp	Pro	Asp	Ile	Glu		
	390				395					400					405		
gca	atg	cga	gca	gta	aat	cca	ctt	ttc	att	cca	cgc	aat	cac	ctc	gtg	1363	
Ala	Met	Arg	Ala	Val	Asn	Pro	Leu	Phe	Ile	Pro	Arg	Asn	His	Leu	Val		

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gaa gct gct ctc gca gac gca gtt	gaa ggg aat cta gaa aag ttc cac		1411
Glu Ala Ala Leu Ala Asp Ala Val	Glu Gly Asn Leu Glu Lys Phe His		
425	430	435	
gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act gcg ggc ccc			1459
Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro			
440	445	450	
gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg			1507
Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met			
455	460	465	
acc ttc tgc ggt acc taggacagat ggtggggcag acg			1545
Thr Phe Cys Gly Thr			
470			

&lt;210&gt; 532

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 532

Met Asn Thr Ala Pro Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu	
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Pro Thr Met Ala Ala Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu	
20	30
Leu Val Ile Leu Asn Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro	
35	45
Thr Trp Leu Arg Thr Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn	
50	60
Pro Glu Pro Leu Thr Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln	
65	80
Phe Gly Gln Phe Val Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu	
85	95
Gly Glu Ala Arg Ser Ala Asp Gly Val Leu His Asp Ile His Leu Lys	
100	110
Gly Ser Gly Arg Thr Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val	
115	125
Leu Gly Pro Val Leu Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala	
130	140
Leu Gly Val Pro Thr Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg	
145	160
Lys Ile Gln Arg Gly Ser Val Ala Pro Gly Ala Val Leu Val Arg Val	
165	175
Ala Thr Ser Leu Ile Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser	
180	190

Gly Gly Ile Glu Leu Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg  
 195 200 205  
 His Phe Pro Ser Leu Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr  
 210 215 220  
 Tyr Val Ser Leu Phe Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val  
 225 230 235 240  
 Gly Lys Trp Thr Arg Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp  
 245 250 255  
 Asn Thr Leu Ile Ser Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe  
 260 265 270  
 Met Glu Arg Tyr Arg Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr  
 275 280 285  
 Gly Arg Tyr Lys Phe Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met  
 290 295 300  
 Ala Arg Leu Val Glu Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp  
 305 310 315 320  
 Glu Gly Met Thr Ala Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu  
 325 330 335  
 Cys Glu Gln Ala Ile Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp  
 340 345 350  
 Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu  
 355 360 365  
 His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr  
 370 375 380  
 Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln  
 385 390 395 400  
 Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro  
 405 410 415  
 Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn  
 420 425 430  
 Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp  
 435 440 445  
 Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe  
 450 455 460  
 Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr  
 465 470

&lt;210&gt; 533

&lt;211&gt; 1236

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

<221> CDS  
 <222> (101)..(1213)  
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<400> 533

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                                           Val Ala Trp Pro Ser
                                           1           5

aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg  163
Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala
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cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag  211
His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys
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gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc  259
Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg
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aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg  307
Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp
           55           60           65

ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca  355
Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr
           70           75           80           85

cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat  403
Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp
           90           95           100

tcc ctt act ggt gtg ctg ccg tgg cgt tcc ggc gaa acc ttc tac aac  451
Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly Glu Thr Phe Tyr Asn
           105           110           115

gtt ccc tcc aac ggt cct gct gcg atc atg atg gcc cgc acc gac cgt  499
Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met Ala Arg Thr Asp Arg
           120           125           130

ttg gac gag gct atg aaa atc acc gat tgg att ttt gac aac ctg atc  547
Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile Phe Asp Asn Leu Ile
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gat ggc gac ggc ctt gtg atg gac gga ttg cgc atg cgc atg cac gga  595
Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg Met Arg Met His Gly
           150           155           160           165

cct gag ctt gtc cgt tcc atc cac ccg tat tgc caa ggt gtc gcc att  643
Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys Gln Gly Val Ala Ile
           170           175           180

ggg ggc tgt ttg gaa att gct ctc aaa ctg cgt gag cgc gca ggc ttg  691
Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg Glu Arg Ala Gly Leu
           185           190           195

acc act act gtg gtg gat cac tgg tcg gat gcc gat aag gca gaa gac  739
Thr Thr Thr Val Val Asp His Trp Ser Asp Ala Asp Lys Ala Glu Asp

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tcc ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg Ser Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser 215 220 225			787
cgg aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac Arg Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp 230 235 240 245			835
ggc gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp 250 255 260			883
gtg gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys 265 270 275			931
aag att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn 280 285 290			979
cac cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca His Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr 295 300 305			1027
acg gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu 310 315 320 325			1075
agc gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg Ser Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val 330 335 340			1123
caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu 345 350 355			1171
gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg 360 365 370			1213
tagccccgat agtgtatgtg ctg			1236

&lt;210&gt; 534

&lt;211&gt; 371

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 534

Val	Ala	Trp	Pro	Ser	Asn	Ala	Lys	Glu	Lys	Leu	Phe	Ile	His	Trp	His
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Tyr	Trp	Trp	Gln	Ala	His	Tyr	Leu	Asp	Cys	Leu	Val	Asp	Ala	Ala	Arg
			20					25					30		

Arg	Arg	Thr	Thr	Lys	Ala	Arg	Arg	Asp	Arg	Ile	Arg	Asp	Thr	Ile	Arg
		35					40					45			

Gly	Ile	Ser	Val	Arg	Asn	Val	Gly	Lys	Leu	Thr	Ser	Asn	Arg	Tyr	Tyr
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Asp	Asp	Lys	Ala	Trp	Leu	Ala	Leu	Ala	Leu	Gly	Arg	Ala	Gly	Lys	Val
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Arg	Lys	Val	Arg	Thr	Pro	Lys	Ser	Leu	Pro	Ser	Leu	Glu	Gln	Asn	Ile
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Val	Asp	Gly	Ile	Asp	Ser	Leu	Thr	Gly	Val	Leu	Pro	Trp	Arg	Ser	Gly
			100					105					110		
Glu	Thr	Phe	Tyr	Asn	Val	Pro	Ser	Asn	Gly	Pro	Ala	Ala	Ile	Met	Met
		115					120					125			
Ala	Arg	Thr	Asp	Arg	Leu	Asp	Glu	Ala	Met	Lys	Ile	Thr	Asp	Trp	Ile
		130				135					140				
Phe	Asp	Asn	Leu	Ile	Asp	Gly	Asp	Gly	Leu	Val	Met	Asp	Gly	Leu	Arg
145					150					155					160
Met	Arg	Met	His	Gly	Pro	Glu	Leu	Val	Arg	Ser	Ile	His	Pro	Tyr	Cys
			165						170					175	
Gln	Gly	Val	Ala	Ile	Gly	Ala	Cys	Leu	Glu	Ile	Ala	Leu	Lys	Leu	Arg
			180					185					190		
Glu	Arg	Ala	Gly	Leu	Thr	Thr	Thr	Val	Val	Asp	His	Trp	Ser	Asp	Ala
		195					200					205			
Asp	Lys	Ala	Glu	Asp	Ser	Leu	Lys	Tyr	Phe	Ala	His	Ile	His	Ala	Val
	210					215					220				
Val	Gln	Ala	Val	Ser	Arg	Lys	Met	Thr	Asn	Phe	His	Gly	Val	Ile	Asp
225					230					235					240
Trp	Asp	Thr	Gly	Asp	Gly	Asp	Gly	Gly	Leu	Phe	Lys	Gly	Ile	Leu	Val
			245						250					255	
Arg	Tyr	Leu	Ala	Asp	Val	Ala	Ile	Arg	Leu	Pro	Asp	Asp	Ser	Pro	Thr
		260						265					270		
Asn	Arg	Glu	Thr	Lys	Lys	Ile	Ala	Ala	Arg	Leu	Val	Leu	Glu	Ser	Ala
		275					280					285			
Glu	Ser	Val	Trp	Asn	His	Arg	Leu	Glu	Val	Asp	Gly	Leu	Pro	Val	Phe
	290					295					300				
Ala	Thr	Asp	Trp	Thr	Thr	Asp	Ala	Arg	Leu	Pro	Gln	Asn	Phe	Gly	Leu
305						310					315				320
Ser	Ser	Ser	Ser	Leu	Ser	Asp	Leu	Val	Ser	Val	Val	Arg	Val	Asp	Glu
				325					330					335	
Arg	Asp	Leu	Ser	Val	Gln	Leu	Ser	Gly	Trp	Met	Leu	Met	Glu	Ala	Ala
		340						345					350		
Ala	Lys	Val	Ala	Glu	Glu	Leu	Glu	Asn	Asn	Gly	Asn	Ser	Tyr	Thr	Gly
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Arg	Ser	Arg													
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 Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu  
 20 25 30  
 gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt 144  
 Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu  
 35 40 45  
 gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc ccg gta 192  
 Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val  
 50 55 60  
 tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct 240  
 Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser  
 65 70 75 80  
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 Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala  
 85 90 95  
 acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa 336  
 Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu  
 100 105 110  
 ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc 384  
 Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr  
 115 120 125  
 ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc 432  
 Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val  
 130 135 140  
 cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg 480  
 Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val  
 145 150 155 160  
 gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca 528  
 Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala  
 165 170 175  
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 Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val  
 180 185 190



gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc 624  
 Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg  
 195 200 205  
 aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc 672  
 Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe  
 210 215 220  
 cat gat gtc cag gct gaa gat ggc,cgt ggt cga ttc acc agt att cac 720  
 His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His  
 225 230 235 240  
 gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca 768  
 Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala  
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 Arg Lys Arg

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 <213> Corynebacterium glutamicum

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 Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu  
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 Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val  
 50 55 60  
 Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser  
 65 70 75 80  
 Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala  
 85 90 95  
 Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu  
 100 105 110  
 Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr  
 115 120 125  
 Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val  
 130 135 140  
 Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val  
 145 150 155 160  
 Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala  
 165 170 175  
 Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val

180	185	190
Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg		
195	200	205
Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe		
210	215	220
His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His		
225	230	235
Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala		
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Arg Lys Arg		

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 Val Ala Lys Asn Ser 5  
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 gtt cgt gct gcg gaa gtg tct gca att tta agg ttt gct ggt gag atg 163  
 Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg Phe Ala Gly Glu Met 20  
 10 15  
 caa gct gtc ggc ggc aag ctg gtc atc gaa gca aat ttg gac agc atg 211  
 Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala Asn Leu Asp Ser Met 35  
 25 30  
 caa gtc ggt atg agg ctt cag gag ttt atc caa ggt ttg tac aac tct 259  
 Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln Gly Leu Tyr Asn Ser 50  
 40 45  
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 Arg Val Asp Val His Thr Val Asn Pro Thr Val Ser Arg Lys Thr Pro 65  
 55 60  
 cgg tat ttg gtg cgc atc att gac aat gcc gat gaa att gcg cga cgc 355  
 Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp Glu Ile Ala Arg Arg 85  
 70 75 80  
 acc gga ctg gtc acc agg tct gga cat gtg gtt aaa ggt cta gcg cct 403  
 Thr Gly Leu Val Thr Arg Ser Gly His Val Val Lys Gly Leu Ala Pro 100  
 90 95  
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 Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu Ala Ala Trp Arg Gly

105					110					115						
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Leu	Glu	Val	Leu	Cys	Pro	Gly	Gln	Glu	Ser	Ala	Leu	Ala	Leu	Val	Gly	
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Cys	Ala	Arg	Arg	Ile	Gly	Ile	Ala	Ala	Lys	Thr	Lys	Asp	Ser	Arg	Gly	
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Phe	Asp	Arg	Val	Asn	Val	Arg	Asp	Ala	Glu	Ala	Ile	Gly	Ala	Leu	Leu	
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Thr	Arg	Met	Gly	Ala	Gln	Lys	Thr	Arg	Met	Leu	Trp	Glu	Glu	Lys	Arg	
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Ile	Lys	Arg	Glu	Ser	Arg	Thr	Pro	Gln	Thr	Gly	Leu	Ala	Asn	Phe	Asp	
		200					205					210				
gat	gcc	aat	ctg	cgc	agg	tca	gcc	cga	gca	gca	gtt	gcc	gct	gca	gcg	787
Asp	Ala	Asn	Leu	Arg	Arg	Ser	Ala	Arg	Ala	Ala	Val	Ala	Ala	Ala	Ala	
		215				220					225					
agg	gta	gaa	cgc	gcc	atg	aag	att	ctt	ggt	gat	gat	gtt	cct	gag	cat	835
Arg	Val	Glu	Arg	Ala	Met	Lys	Ile	Leu	Gly	Asp	Asp	Val	Pro	Glu	His	
230					235				240						245	
ttg	gct	gag	gct	gga	cag	ctg	cgt	gtg	cag	cac	cgt	cag	gca	tcg	ttg	883
Leu	Ala	Glu	Ala	Gly	Gln	Leu	Arg	Val	Gln	His	Arg	Gln	Ala	Ser	Leu	
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Glu	Glu	Leu	Gly	Arg	Leu	Ala	Asp	Pro	Gln	Met	Thr	Lys	Asp	Ala	Val	
			265				270					275				
gcc	ggt	cgt	att	cgt	cgt	ctt	ttg	acg	atg	gca	gat	aag	cgc	gcc	gaa	979
Ala	Gly	Arg	Ile	Arg	Arg	Leu	Leu	Thr	Met	Ala	Asp	Lys	Arg	Ala	Glu	
		280					285					290				
gat	ctg	aag	att	cct	gat	aca	aat	tct	gtt	gtg	acg	gaa	gat	ttg	ttg	1027
Asp	Leu	Lys	Ile	Pro	Asp	Thr	Asn	Ser	Val	Val	Thr	Glu	Asp	Leu	Leu	
		295				300					305					
gaa	gaa	att	tagatgattg	aagcctaaaa	acg											1059
Glu	Glu	Ile														
310																

&lt;210&gt; 538

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 538

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 Phe Ala Gly Glu Met Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala  
 20 25 30  
 Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln  
 35 40 45  
 Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val  
 50 55 60  
 Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp  
 65 70 75 80  
 Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val  
 85 90 95  
 Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu  
 100 105 110  
 Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro  
 115 120 125  
 Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala  
 130 135 140  
 Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr  
 145 150 155 160  
 Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala  
 165 170 175  
 Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu  
 180 185 190  
 Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly  
 195 200 205  
 Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala  
 210 215 220  
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 225 230 235 240  
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80																
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 Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu  
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Ile Lys Ala Ala Gly Leu Thr Gly Ile Glu Leu Asn Thr Gly Gly Phe
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Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile Ile Asp Leu Glu Asp 35																
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Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr Arg Asn Ile Arg Glu 50																
tcg ggg ttg gat cct aaa cga acc att gtg aga acc gta ggg ccg agc 307																
Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg Thr Val Gly Pro Ser 65																
gat cca cac ttt ttg gct gac gtg gag atg gtg aag tcc acg gat ttc 355																
Asp Pro His Phe Leu Ala Asp Val Glu Met Val Lys Ser Thr Asp Phe 85																
aca ctt gtt atg gtt cct aaa ctt ctt ggc agc gtg cct gag gaa tta 403																
Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser Val Pro Glu Glu Leu 100																
gat ggc ctc aac att atc gcc atg att gaa acc cct cag gct gca acc 451																
Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr Pro Gln Ala Ala Thr 115																
agc att cct cag att gct gcg gac cct aaa gtc gtt gga atg ttc tgg 499																
Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val Val Gly Met Phe Trp 130																
ggc gcg gag gat ctc aca cac ctc ttg gga ggc act cat tct agg ttc 547																
Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly Thr His Ser Arg Phe 145																
ttg ggt gat gag tcc aat gaa ggc tcc tac cga gac acc atg agg ctt 595																
Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg Asp Thr Met Arg Leu 165																
aca cgc gcc ctg atg cac ctc cac gcg gcg gcg aat ggg aag ttc acc 643																
Thr Arg Ala Leu Met His Leu His Ala Ala Ala Asn Gly Lys Phe Thr 180																

att gat gcc atc cat gcg gat ttc cac gat gaa gag ggc ctc tat tta 691  
 Ile Asp Ala Ile His Ala Asp Phe His Asp Glu Glu Gly Leu Tyr Leu  
 185 190 195  
  
 gaa gcg gtc gat gct gcg cgg act ggt ttc gct ggc acc gca tgc att 739  
 Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala Gly Thr Ala Cys Ile  
 200 205 210  
  
 cac ccc aag cag atc gag att gtt cgg aga gcc tat cgg cca gag gct 787  
 His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala Tyr Arg Pro Glu Ala  
 215 220 225  
  
 aac cag ttg gag tgg gcg aag aaa gtg gtg gag gaa gca gaa aac cat 835  
 Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu Glu Ala Glu Asn His  
 230 235 240 245  
  
 cca ggt gcg ttc aaa ctg gat ggt cag atg att gat gct ccg ttg att 883  
 Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile Asp Ala Pro Leu Ile  
 250 255 260  
  
 tcg cag gcg cgg atg gtt att tcg cgt cag cct gct tgattagttc 929  
 Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro Ala  
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 aagcgttttt tcg 942

&lt;210&gt; 548

&lt;211&gt; 273

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 548

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 Arg Ala Glu Ile Ile Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile  
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 Ile Asp Leu Glu Asp Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr  
 35 40 45  
  
 Arg Asn Ile Arg Glu Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg  
 50 55 60  
  
 Thr Val Gly Pro Ser Asp Pro His Phe Leu Ala Asp Val Glu Met Val  
 65 70 75 80  
  
 Lys Ser Thr Asp Phe Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser  
 85 90 95  
  
 Val Pro Glu Glu Leu Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr  
 100 105 110  
  
 Pro Gln Ala Ala Thr Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val  
 115 120 125  
  
 Val Gly Met Phe Trp Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly  
 130 135 140



Thr His Ser Arg Phe Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg  
 145 150 155 160  
 Asp Thr Met Arg Leu Thr Arg Ala Leu Met His Leu His Ala Ala Ala  
 165 170 175  
 Asn Gly Lys Phe Thr Ile Asp Ala Ile His Ala Asp Phe His Asp Glu  
 180 185 190  
 Glu Gly Leu Tyr Leu Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala  
 195 200 205  
 Gly Thr Ala Cys Ile His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala  
 210 215 220  
 Tyr Arg Pro Glu Ala Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu  
 225 230 235 240  
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 Asp Ala Pro Leu Ile Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro  
 260 265 270

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 <223> RXN00519

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 Met Ala Lys Ile Ile  
 1 5  
 tgg acc cgc acc gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag 163  
 Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys  
 10 15 20  
 ccg gtc gtc gag gca ttt gct gct acc gcg ggc att gag gtc gag acc 211  
 Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr  
 25 30 35  
 cgg gac att tca ctc gct gga cgc atc ctc gcc cag ttc cca gag cgc 259  
 Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala Gln Phe Pro Glu Arg  
 40 45 50  
 ctc acc gaa gat cag aag gta ggc aac gca ctc gca gaa ctc ggc gag 307  
 Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu Ala Glu Leu Gly Glu  
 55 60 65

ctt gct aag act cct gaa gca aac atc att aag ctt cca aac atc tcc	355
Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser	
70 75 80 85	
gct tct gtt cca cag ctc aag gct gct att aag gaa ctg cag gac cag	403
Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys Glu Leu Gln Asp Gln	
90 95 100	
ggc tac gac atc cca gaa ctg cct gat aac gcc acc acc gac gag gaa	451
Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala Thr Thr Asp Glu Glu	
105 110 115	
aaa gac atc ctc gca cgc tac aac gct gtt aag ggt tcc gct gtg aac	499
Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys Gly Ser Ala Val Asn	
120 125 130	
cca gtg ctg cgt gaa ggc aac tct gac cgc cgc gca cca atc gct gtc	547
Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro Ile Ala Val	
135 140 145	
aag aac ttt gtt aag aag ttc cca cac cgc atg ggc gag tgg tct gca	595
Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala	
150 155 160 165	
gat tcc aag acc aac gtt gca acc atg gat gca aac gac ttc cgc cac	643
Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala Asn Asp Phe Arg His	
170 175 180	
aac gag aag tcc atc atc ctc gac gct gct gat gaa gtt cag atc aag	691
Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp Glu Val Gln Ile Lys	
185 190 195	
cac atc gca gct gac ggc acc gag acc atc ctc aag gac agc ctc aag	739
His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys	
200 205 210	
ctt ctt gaa ggc gaa gtt cta gac gga acc gtt ctg tcc gca aag gca	787
Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val Leu Ser Ala Lys Ala	
215 220 225	
ctg gac gca ttc ctt ctc gag cag gtc gct cgc gca aag gca gaa ggt	835
Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg Ala Lys Ala Glu Gly	
230 235 240 245	
atc ctc ttc tcc gca cac ctg aag gcc acc atg atg aag gtc tcc gac	883
Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met Met Lys Val Ser Asp	
250 255 260	
cca atc atc ttc ggc cac gtt gtg cgc gct tac ttc gca gac gtt ttc	931
Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr Phe Ala Asp Val Phe	
265 270 275	
gca cag tac ggt gag cag ctg ctc gca gct ggc ctc aac ggc gaa aac	979
Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn	
280 285 290	
ggc ctc gct gca atc ctc tcc ggc ttg gag tcc ctg gac aac ggc gaa	1027
Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu	
295 300 305	
gaa atc aag gct gca ttc gag aag ggc ttg gaa gac ggc cca gac ctg	1075

Glu 310	Ile	Lys	Ala	Ala	Phe 315	Glu	Lys	Gly	Leu	Glu 320	Asp	Gly	Pro	Asp	Leu 325	
gcc	atg	gtt	aac	tcc	gct	cgc	ggc	atc	acc	aac	ctg	cat	gtc	cct	tcc	1123
Ala	Met	Val	Asn	Ser	Ala	Arg	Gly	Ile	Thr	Asn	Leu	His	Val	Pro	Ser	
				330				335						340		
gat	gtc	atc	gtg	gac	gct	tcc	atg	cca	gca	atg	att	cgt	acc	tcc	ggc	1171
Asp	Val	Ile	Val	Asp	Ala	Ser	Met	Pro	Ala	Met	Ile	Arg	Thr	Ser	Gly	
			345					350					355			
cac	atg	tgg	aac	aaa	gac	gac	cag	gag	cag	gac	acc	ctg	gca	atc	atc	1219
His	Met	Trp	Asn	Lys	Asp	Asp	Gln	Glu	Gln	Asp	Thr	Leu	Ala	Ile	Ile	
		360					365					370				
cca	gac	tcc	tcc	tac	gct	ggc	gtc	tac	cag	acc	gtt	atc	gaa	gac	tgc	1267
Pro	Asp	Ser	Ser	Tyr	Ala	Gly	Val	Tyr	Gln	Thr	Val	Ile	Glu	Asp	Cys	
		375				380					385					
cgc	aag	aac	ggc	gca	ttc	gat	cca	acc	acc	atg	ggc	acc	gtc	cct	aac	1315
Arg	Lys	Asn	Gly	Ala	Phe	Asp	Pro	Thr	Thr	Met	Gly	Thr	Val	Pro	Asn	
390					395					400					405	
gtt	ggc	ctg	atg	gct	cag	aag	gct	gaa	gag	tac	ggc	tcc	cat	gac	aag	1363
Val	Gly	Leu	Met	Ala	Gln	Lys	Ala	Glu	Glu	Tyr	Gly	Ser	His	Asp	Lys	
				410				415						420		
acc	ttc	cgc	atc	gaa	gca	gac	ggc	gtg	gtt	cag	gtt	gtt	tcc	tcc	aac	1411
Thr	Phe	Arg	Ile	Glu	Ala	Asp	Gly	Val	Val	Gln	Val	Val	Ser	Ser	Asn	
			425					430					435			
ggc	gac	gtt	ctc	atc	gag	cac	gac	gtt	gag	gca	aat	gac	atc	tgg	cgt	1459
Gly	Asp	Val	Leu	Ile	Glu	His	Asp	Val	Glu	Ala	Asn	Asp	Ile	Trp	Arg	
		440					445					450				
gca	tgc	cag	gtc	aag	gat	gcc	cca	atc	cag	gat	tgg	gta	aag	ctt	gct	1507
Ala	Cys	Gln	Val	Lys	Asp	Ala	Pro	Ile	Gln	Asp	Trp	Val	Lys	Leu	Ala	
		455				460					465					
gtc	acc	cgc	tcc	cgt	ctc	tcc	gga	atg	cct	gca	gtg	ttc	tgg	ttg	gat	1555
Val	Thr	Arg	Ser	Arg	Leu	Ser	Gly	Met	Pro	Ala	Val	Phe	Trp	Leu	Asp	
470					475				480						485	
cca	gag	cgc	gca	cac	gac	cgc	aac	ctg	gct	tcc	ctc	gtt	gag	aag	tac	1603
Pro	Glu	Arg	Ala	His	Asp	Arg	Asn	Leu	Ala	Ser	Leu	Val	Glu	Lys	Tyr	
				490				495						500		
ctg	gct	gac	cac	gac	acc	gag	ggc	ctg	gac	atc	cag	atc	ctc	tcc	cct	1651
Leu	Ala	Asp	His	Asp	Thr	Glu	Gly	Leu	Asp	Ile	Gln	Ile	Leu	Ser	Pro	
			505					510					515			
gtt	gag	gca	acc	cag	ctc	tcc	atc	gac	cgc	atc	cgc	cgt	ggc	gag	gac	1699
Val	Glu	Ala	Thr	Gln	Leu	Ser	Ile	Asp	Arg	Ile	Arg	Arg	Gly	Glu	Asp	
		520					525					530				
acc	atc	tct	gtc	acc	ggc	aac	gtt	ctg	cgt	gac	tac	aac	acc	gac	ctc	1747
Thr	Ile	Ser	Val	Thr	Gly	Asn	Val	Leu	Arg	Asp	Tyr	Asn	Thr	Asp	Leu	
		535				540				545						
ttc	cca	atc	ctg	gag	ctg	ggc	acc	tct	gca	aag	atg	ctg	tct	gtc	gtt	1795
Phe	Pro	Ile	Leu	Glu	Leu	Gly	Thr	Ser	Ala	Lys	Met	Leu	Ser	Val	Val	

550	555	560	565	
cct ttg atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct				1843
Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser	570	575	580	
gct cct aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg				1891
Ala Pro Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp	585	590	595	
gat tcc ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag				1939
Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu	600	605	610	
ctc aac aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg				1987
Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu	615	620	625	
gac aag gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc				2035
Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg	630	635	640	645
aag gtt ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag				2083
Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys	650	655	660	
ttc tgg gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct				2131
Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala	665	670	675	
gct acc ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac				2179
Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp	680	685	690	
atc gat gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt				2227
Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly	695	700	705	
ggc tac tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca				2275
Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro	710	715	720	725
gtc gca cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct				2324
Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys	730	735		
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 <213> Corynebacterium glutamicum

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 35 40 45  
 Gln Phe Pro Glu Arg Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu  
 50 55 60  
 Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys  
 65 70 75 80  
 Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys  
 85 90 95  
 Glu Leu Gln Asp Gln Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala  
 100 105 110  
 Thr Thr Asp Glu Glu Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys  
 115 120 125  
 Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg  
 130 135 140  
 Ala Pro Ile Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met  
 145 150 155 160  
 Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala  
 165 170 175  
 Asn Asp Phe Arg His Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp  
 180 185 190  
 Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu  
 195 200 205  
 Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val  
 210 215 220  
 Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg  
 225 230 235 240  
 Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met  
 245 250 255  
 Met Lys Val Ser Asp Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr  
 260 265 270  
 Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly  
 275 280 285  
 Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser  
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 Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu  
 305 310 315 320  
 Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn  
 325 330 335  
 Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met  
 340 345 350  
 Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp

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Thr	Leu	Ala	Ile	Ile	Pro	Asp	Ser	Ser	Tyr	Ala	Gly	Val	Tyr	Gln	Thr
370						375					380				
Val	Ile	Glu	Asp	Cys	Arg	Lys	Asn	Gly	Ala	Phe	Asp	Pro	Thr	Thr	Met
385					390					395					400
Gly	Thr	Val	Pro	Asn	Val	Gly	Leu	Met	Ala	Gln	Lys	Ala	Glu	Glu	Tyr
				405					410					415	
Gly	Ser	His	Asp	Lys	Thr	Phe	Arg	Ile	Glu	Ala	Asp	Gly	Val	Val	Gln
			420					425					430		
Val	Val	Ser	Ser	Asn	Gly	Asp	Val	Leu	Ile	Glu	His	Asp	Val	Glu	Ala
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Asn	Asp	Ile	Trp	Arg	Ala	Cys	Gln	Val	Lys	Asp	Ala	Pro	Ile	Gln	Asp
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Trp	Val	Lys	Leu	Ala	Val	Thr	Arg	Ser	Arg	Leu	Ser	Gly	Met	Pro	Ala
465					470					475					480
Val	Phe	Trp	Leu	Asp	Pro	Glu	Arg	Ala	His	Asp	Arg	Asn	Leu	Ala	Ser
			485						490					495	
Leu	Val	Glu	Lys	Tyr	Leu	Ala	Asp	His	Asp	Thr	Glu	Gly	Leu	Asp	Ile
			500					505					510		
Gln	Ile	Leu	Ser	Pro	Val	Glu	Ala	Thr	Gln	Leu	Ser	Ile	Asp	Arg	Ile
		515					520					525			
Arg	Arg	Gly	Glu	Asp	Thr	Ile	Ser	Val	Thr	Gly	Asn	Val	Leu	Arg	Asp
	530					535					540				
Tyr	Asn	Thr	Asp	Leu	Phe	Pro	Ile	Leu	Glu	Leu	Gly	Thr	Ser	Ala	Lys
545					550					555					560
Met	Leu	Ser	Val	Val	Pro	Leu	Met	Ala	Gly	Gly	Gly	Leu	Phe	Glu	Thr
			565						570					575	
Gly	Ala	Gly	Gly	Ser	Ala	Pro	Lys	His	Val	Gln	Gln	Val	Gln	Glu	Glu
			580					585					590		
Asn	His	Leu	Arg	Trp	Asp	Ser	Leu	Gly	Glu	Phe	Leu	Ala	Leu	Ala	Glu
		595					600					605			
Ser	Phe	Arg	His	Glu	Leu	Asn	Asn	Asn	Gly	Asn	Thr	Lys	Ala	Gly	Val
	610					615					620				
Leu	Ala	Asp	Ala	Leu	Asp	Lys	Ala	Thr	Glu	Lys	Leu	Leu	Asn	Glu	Glu
625					630					635					640
Lys	Ser	Pro	Ser	Arg	Lys	Val	Gly	Glu	Ile	Asp	Asn	Arg	Gly	Ser	His
			645						650					655	
Phe	Trp	Leu	Thr	Lys	Phe	Trp	Ala	Asp	Glu	Leu	Ala	Ala	Gln	Thr	Glu
			660					665					670		
Asp	Ala	Asp	Leu	Ala	Ala	Thr	Phe	Ala	Pro	Val	Ala	Glu	Ala	Leu	Asn
		675					680					685			

Thr Gly Ala Ala Asp Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly  
 690 695 700

Ala Thr Asp Leu Gly Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr  
 705 710 715 720

Asn Ile Met Arg Pro Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu  
 725 730 735

Lys Lys

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 <223> FRXA00521

<400> 551

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1				5					10					15		
acc	gag	acc	atc	ctc	aag	gac	agc	ctc	aag	ctt	ctt	gaa	ggc	gaa	gtt	96
Thr	Glu	Thr	Ile	Leu	Lys	Asp	Ser	Leu	Lys	Leu	Leu	Glu	Gly	Glu	Val	
			20					25					30			
cta	gac	gga	acc	gtt	ctg	tcc	gca	aag	gca	ctg	gac	gca	ttc	ctt	ctc	144
Leu	Asp	Gly	Thr	Val	Leu	Ser	Ala	Lys	Ala	Leu	Asp	Ala	Phe	Leu	Leu	
		35					40					45				
gag	cag	gtc	gct	cgc	gca	aag	gca	gaa	ggc	atc	ctc	ttc	tcc	gca	cac	192
Glu	Gln	Val	Ala	Arg	Ala	Lys	Ala	Glu	Gly	Ile	Leu	Phe	Ser	Ala	His	
	50					55					60					
ctg	aag	gcc	acc	atg	atg	aag	gtc	tcc	gac	cca	atc	atc	ttc	ggc	cac	240
Leu	Lys	Ala	Thr	Met	Met	Lys	Val	Ser	Asp	Pro	Ile	Ile	Phe	Gly	His	
	65				70					75					80	
gtt	gtg	cgc	gct	tac	ttc	gca	gac	gtt	ttc	gca	cag	tac	ggt	gag	cag	288
Val	Val	Arg	Ala	Tyr	Phe	Ala	Asp	Val	Phe	Ala	Gln	Tyr	Gly	Glu	Gln	
				85					90					95		
ctg	ctc	gca	gct	ggc	ctc	aac	ggc	gaa	aac	ggc	ctc	gct	gca	atc	ctc	336
Leu	Leu	Ala	Ala	Gly	Leu	Asn	Gly	Glu	Asn	Gly	Leu	Ala	Ala	Ile	Leu	
			100					105					110			
tcc	ggc	ttg	gag	tcc	ctg	gac	aac	ggc	gaa	gaa	atc	aag	gct	gca	ttc	384
Ser	Gly	Leu	Glu	Ser	Leu	Asp	Asn	Gly	Glu	Glu	Ile	Lys	Ala	Ala	Phe	
		115					120					125				
gag	aag	ggc	ttg	gaa	gac	ggc	cca	gac	ctg	gcc	atg	gtt	aac	tcc	gct	432
Glu	Lys	Gly	Leu	Glu	Asp	Gly	Pro	Asp	Leu	Ala	Met	Val	Asn	Ser	Ala	
	130					135					140					

cgc ggc atc acc aac ctg cat gtc cct tcc gat gtc atc gtg gac gct	480
Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala	
145 150 155 160	
tcc atg cca gca atg att cgt acc tcc ggc cac atg tgg aac aaa gac	528
Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp	
165 170 175	
gac cag gag cag gac acc ctg gca atc atc cca gac tcc tcc tac gct	576
Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala	
180 185 190	
ggc gtc tac cag acc gtt atc gaa gac tgc cgc aag aac ggc gca ttc	624
Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe	
195 200 205	
gat cca acc acc atg ggt acc gtc cct aac gtt ggt ctg atg gct cag	672
Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln	
210 215 220	
aag gct gaa gag tac ggc tcc cat gac aag acc ttc cgc atc gaa gca	720
Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala	
225 230 235 240	
gac ggt gtg gtt cag gtt gtt tcc tcc aac ggc gac gtt ctc atc gag	768
Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu	
245 250 255	
cac gac gtt gag gca aat gac atc tgg cgt gca tgc cag gtc aag gat	816
His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp	
260 265 270	
gcc cca atc cag gat tgg gta aag ctt gct gtc acc cgc tcc cgt ctc	864
Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu	
275 280 285	
tcc gga atg cct gca gtg ttc tgg ttg gat cca gag cgc gca cac gac	912
Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp	
290 295 300	
cgc aac ctg gct tcc ctc gtt gag aag tac ctg gct gac cac gac acc	960
Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr	
305 310 315 320	
gag ggc ctg gac atc cag atc ctc tac cct gtt gag gca acc cag ctc	1008
Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu	
325 330 335	
tcc atc gac cgc atc cgc cgt ggc gag gac acc atc tct gtc acc ggt	1056
Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly	
340 345 350	
aac	1059
Asn	

&lt;210&gt; 552

&lt;211&gt; 353

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 552

Leu Asp Ala Ala Asp Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly  
 1 5 10 15  
 Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val  
 20 25 30  
 Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu  
 35 40 45  
 Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His  
 50 55 60  
 Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His  
 65 70 75 80  
 Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln  
 85 90 95  
 Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu  
 100 105 110  
 Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe  
 115 120 125  
 Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala  
 130 135 140  
 Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala  
 145 150 155 160  
 Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp  
 165 170 175  
 Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala  
 180 185 190  
 Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe  
 195 200 205  
 Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln  
 210 215 220  
 Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala  
 225 230 235 240  
 Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu  
 245 250 255  
 His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp  
 260 265 270  
 Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu  
 275 280 285  
 Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp  
 290 295 300  
 Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr  
 305 310 315 320

Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu  
 325 330 335

Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly  
 340 345 350

Asn

<210> 553

<211> 1694

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1671)

<223> RXN02209

<400> 553

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 Thr Glu Ser Thr Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln  
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gac cgc atc ctt ctc tcc gag gca aag gag cag ttc cgt aag gat ctg 96  
 Asp Arg Ile Leu Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu  
 20 25 30

cca acc tac acc gac gac gct gtt tcc gta gac acc tcc atc cct gca 144  
 Pro Thr Tyr Thr Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala  
 35 40 45

acc cgc atg gtt aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa 192  
 Thr Arg Met Val Asn Glu Gly Gly Gln Pro Glu Gly Gly Val Glu  
 50 55 60

gct gac aac tac aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct 240  
 Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala  
 65 70 75 80

act ggc gca gaa gga cgt cct tcc aag cca gtc acc gtt gca tcc cca 288  
 Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro  
 85 90 95

cag ggt ggc gag tac acc atc gac cac ggc atg gtt gca att gca tcc 336  
 Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser  
 100 105 110

atc acc tct tgc acc aac acc tct aac cca tcc gtg atg atc ggc gct 384  
 Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala  
 115 120 125

ggc ctg atc gca cgt aag gca gca gaa aag ggc ctc aag tcc aag cct 432  
 Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro  
 130 135 140

tgg gtt aag acc atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac 480  
 Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr  
 145 150 155 160

tac cag cgc gca gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac	528
Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr	
165 170 175	
ctc tcc ggc ttc ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg	576
Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu	
180 185 190	
cca gag gaa atc tcc gct gcg atc aac gag cac gac ctg acc gca acc	624
Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr	
195 200 205	
gca gtt ttg tcc ggt aac cgt aac ttc gag gga cgt atc tcc cct gac	672
Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp	
210 215 220	
gtt aag atg aac tac ctg gca tcc cca atc atg gtc att gct tac gca	720
Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala	
225 230 235 240	
atc gct ggc acc atg gac ttc gac ttc gag aac gaa gct ctt gga cag	768
Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln	
245 250 255	
gac cag gac ggc aac gac gtc ttc ctg aag gac atc tgg cct tcc acc	816
Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr	
260 265 270	
gag gaa atc gaa gac acc atc cag cag gca atc tcc cgt gag ctt tac	864
Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr	
275 280 285	
gaa gct gac tac gca gat gtc ttc aag ggt gac aag cag tgg cag gaa	912
Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu	
290 295 300	
ctc gat gtt cct acc ggt gac acc ttc gag tgg gac gag aac tcc acc	960
Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr	
305 310 315 320	
tac atc cgc aag gca cct tac ttc gac ggc atg cct gtc gag cca gtg	1008
Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val	
325 330 335	
gca gtc acc gac atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac	1056
Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp	
340 345 350	
tct gtc acc acc gac cac atc tcc cct gct tcc tcc att aag cca ggt	1104
Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly	
355 360 365	
acc cct gca gct cag tac ttg gat gag cac ggt gtg gaa cgc cac gac	1152
Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp	
370 375 380	
tac aac tcc ctg ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc	1200
Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg	
385 390 395 400	

ggc acc ttc gcc aac atc cgc ctc cag aac cag ctg gtt gac atc gca 1248  
 Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala  
 405 410 415  
 ggt ggc tac acc cgc gac ttc acc cag gag ggt gct cca cag gcg ttc 1296  
 Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe  
 420 425 430  
 atc tac gac gct tcc gtc aac tac aag gct gct ggc att ccg ctg gtc 1344  
 Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val  
 435 440 445  
 gtc ttg ggc ggc aag gag tac ggc acc ggt tct tcc cgt gac tgg gca 1392  
 Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala  
 450 455 460  
 gct aag ggc act aac ctg ctc gga att cgc gca gtt atc acc gag tcc 1440  
 Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser  
 465 470 475 480  
 ttc gag cgt att cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca 1488  
 Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro  
 485 490 495  
 ctg cag ttc cct gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc 1536  
 Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly  
 500 505 510  
 acc gag acc ttc gac atc acc gga ctg acc gca ctt aac gag ggc gag 1584  
 Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu  
 515 520 525  
 act cct aag act gtc aag gtc acc gca acc aag gag aac ggc gac gtc 1632  
 Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val  
 530 535 540  
 gtc gag ttc gac gca att tgt ccg cat cga cac ccc agg tgaggctgac 1681  
 Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg  
 545 550 555  
 tactaccgcc acg 1694

&lt;210&gt; 554

&lt;211&gt; 557

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 554

Thr Glu Ser Thr Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln  
 1 5 10 15

Asp Arg Ile Leu Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu  
 20 25 30

Pro Thr Tyr Thr Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala  
 35 40 45

Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu  
 50 55 60

Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala  
 65 70 75 80  
 Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro  
 85 90 95  
 Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser  
 100 105 110  
 Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala  
 115 120 125  
 Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro  
 130 135 140  
 Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr  
 145 150 155 160  
 Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr  
 165 170 175  
 Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu  
 180 185 190  
 Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr  
 195 200 205  
 Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp  
 210 215 220  
 Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala  
 225 230 235 240  
 Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln  
 245 250 255  
 Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr  
 260 265 270  
 Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr  
 275 280 285  
 Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu  
 290 295 300  
 Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr  
 305 310 315 320  
 Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val  
 325 330 335  
 Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp  
 340 345 350  
 Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly  
 355 360 365  
 Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp  
 370 375 380  
 Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg

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385              390              395              400
Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala
              405              410              415
Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe
              420              425              430
Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val
              435              440              445
Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala
              450              455              460
Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser
465              470              475              480
Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro
              485              490              495
Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly
              500              505              510
Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu
              515              520              525
Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val
              530              535              540
Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg
545              550              555

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&lt;210&gt; 555

&lt;211&gt; 1682

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1659)

&lt;223&gt; FRXA02209

&lt;400&gt; 555

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gtt gtt cct tcc atc gct ggc cct aag cgc cca cag gac cgc atc ctt      48
Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu
  1              5              10              15
ctc tcc gag gca aag gag cag ttc cgt aag gat ctg cca acc tac acc      96
Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
              20              25              30
gac gac gct gtt tcc gta gac acc tcc atc cct gca acc cgc atg gtt      144
Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
              35              40              45
aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa gct gac aac tac      192
Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
              50              55              60
aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct act ggc gca gaa      240

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Asn 65	Ala	Ser	Trp	Ala	Gly 70	Ser	Gly	Glu	Ser	Leu 75	Ala	Thr	Gly	Ala	Glu 80	
gga	cgt	cct	tcc	aag	cca	gtc	acc	gtt	gca	tcc	cca	cag	ggt	ggc	gag	288
Gly	Arg	Pro	Ser	Lys 85	Pro	Val	Thr	Val	Ala 90	Ser	Pro	Gln	Gly	Gly	Glu 95	
tac	acc	atc	gac	cac	ggc	atg	gtt	gca	att	gca	tcc	atc	acc	tct	tgc	336
Tyr	Thr	Ile	Asp 100	His	Gly	Met	Val	Ala 105	Ile	Ala	Ser	Ile	Thr	Ser	Cys	
acc	aac	acc	tct	aac	cca	tcc	gtg	atg	atc	ggc	gct	ggc	ctg	atc	gca	384
Thr	Asn	Thr	Ser 115	Asn	Pro	Ser	Val	Met 120	Ile	Gly	Ala	Gly	Leu	Ile	Ala 125	
cgt	aag	gca	gca	gaa	aag	ggc	ctc	aag	tcc	aag	cct	tgg	gtt	aag	acc	432
Arg	Lys 130	Ala	Ala	Glu	Lys	Gly 135	Leu	Lys	Ser	Lys	Pro 140	Trp	Val	Lys	Thr	
atc	tgt	gca	cca	ggc	tcc	cag	gtt	gtc	gac	ggc	tac	tac	cag	cgc	gca	480
Ile	Cys	Ala	Pro	Gly 145	Ser	Gln 150	Val	Val	Asp	Gly 155	Tyr	Tyr	Gln	Arg	Ala 160	
gac	ctc	tgg	aag	gac	ctt	gag	gcc	atg	ggc	ttc	tac	ctc	tcc	ggc	ttc	528
Asp	Leu	Trp	Lys 165	Asp	Leu	Glu	Ala	Met 170	Gly	Phe	Tyr	Leu	Ser	Gly	Phe 175	
ggc	tgc	acc	acc	tgt	att	ggc	aac	tcc	ggc	cca	ctg	cca	gag	gaa	atc	576
Gly	Cys	Thr 180	Thr	Cys	Ile	Gly	Asn	Ser 185	Gly	Pro	Leu	Pro	Glu	Glu	Ile 190	
tcc	gct	gcg	atc	aac	gag	cac	gac	ctg	acc	gca	acc	gca	gtt	ttg	tcc	624
Ser	Ala	Ala 195	Ile	Asn	Glu	His	Asp 200	Leu	Thr	Ala	Thr	Ala	Val	Leu	Ser 205	
ggc	aac	cgt	aac	ttc	gag	gga	cgt	atc	tcc	cct	gac	gtt	aag	atg	aac	672
Gly	Asn 210	Arg	Asn	Phe	Glu	Gly 215	Arg	Ile	Ser	Pro	Asp 220	Val	Lys	Met	Asn	
tac	ctg	gca	tcc	cca	atc	atg	gtc	att	gct	tac	gca	atc	gct	ggc	acc	720
Tyr	Leu	Ala	Ser 225	Pro	Ile	Met	Val 230	Ile	Ala	Tyr	Ala 235	Ile	Ala	Gly	Thr 240	
atg	gac	ttc	gac	ttc	gag	aac	gaa	gct	ctt	gga	cag	gac	cag	gac	ggc	768
Met	Asp	Phe	Asp 245	Phe	Glu	Asn	Glu 250	Ala	Leu	Gly	Gln	Asp	Gln	Asp	Gly 255	
aac	gac	gtc	ttc	ctg	aag	gac	atc	tgg	cct	tcc	acc	gag	gaa	atc	gaa	816
Asn	Asp	Val 260	Phe	Leu	Lys	Asp	Ile 265	Trp	Pro	Ser	Thr	Glu	Glu	Ile	Glu 270	
gac	acc	atc	cag	cag	gca	atc	tcc	cgt	gag	ctt	tac	gaa	gct	gac	tac	864
Asp	Thr	Ile 275	Gln	Gln	Ala	Ile	Ser 280	Arg	Glu	Leu	Tyr	Glu	Ala	Asp	Tyr 285	
gca	gat	gtc	ttc	aag	ggc	gac	aag	cag	tgg	cag	gaa	ctc	gat	gtt	cct	912
Ala	Asp 290	Val	Phe	Lys	Gly	Asp 295	Lys	Gln	Trp	Gln	Glu	Leu	Asp	Val	Pro 300	
acc	ggc	gac	acc	ttc	gag	tgg	gac	gag	aac	tcc	acc	tac	atc	cgc	aag	960
Thr	Gly	Asp	Thr	Phe	Glu	Trp	Asp	Glu	Asn	Ser	Thr	Tyr	Ile	Arg	Lys	

305	310	315	320	
gca cct tac ttc gac ggc atg cct gtc gag cca gtg gca gtc acc gac Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp 325 330 335				1008
atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac tct gtc acc acc Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr 340 345 350				1056
gac cac atc tcc cct gct tcc tcc att aag cca ggt acc cct gca gct Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala 355 360 365				1104
cag tac ttg gat gag cac ggt gtg gaa cgc cac gac tac aac tcc ctg Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu 370 375 380				1152
ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc ggc acc ttc gcc Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala 385 390 395 400				1200
aac atc cgc ctc cag aac cag ctg gtt gac atc gca ggt ggc tac acc Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr 405 410 415				1248
cgc gac ttc acc cag gag ggt gct cca cag gcg ttc atc tac gac gct Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala 420 425 430				1296
tcc gtc aac tac aag gct gct ggc att ccg ctg gtc gtc ttg ggc ggc Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly 435 440 445				1344
aag gag tac ggc acc ggt tct tcc cgt gac tgg gca gct aag ggc act Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr 450 455 460				1392
aac ctg ctc gga att cgc gca gtt atc acc gag tcc ttc gag cgt att Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile 465 470 475 480				1440
cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca ctg cag ttc cct His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro 485 490 495				1488
gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc acc gag acc ttc Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe 500 505 510				1536
gac atc acc gga ctg acc gca ctt aac gag ggc gag act cct aag act Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr 515 520 525				1584
gtc aag gtc acc gca acc aag gag aac ggc gac gtc gtc gag ttc gac Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp 530 535 540				1632
gca att tgt ccg cat cga cac ccc agg tgaggctgac tactaccgcc Ala Ile Cys Pro His Arg His Pro Arg 545 550				1679



acg

1682

<210> 556  
 <211> 553  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 556  
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 Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr  
                   20                  25                  30  
 Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val  
           35                  40                  45  
 Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr  
   50                  55                  60  
 Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu  
   65                  70                  75                  80  
 Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu  
                   85                  90                  95  
 Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys  
           100                  105                  110  
 Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala  
   115                  120                  125  
 Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr  
   130                  135                  140  
 Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala  
   145                  150                  155                  160  
 Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe  
           165                  170                  175  
 Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile  
           180                  185                  190  
 Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser  
   195                  200                  205  
 Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn  
   210                  215                  220  
 Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr  
   225                  230                  235                  240  
 Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly  
           245                  250                  255  
 Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu  
           260                  265                  270

Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr  
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 Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys  
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 Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp  
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 Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala  
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 Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu  
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 Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala  
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 Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe  
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&lt;210&gt; 557

&lt;211&gt; 874

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

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                               Val Thr Glu Ser Lys
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Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr
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Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
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Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
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Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
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Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
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Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg
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&lt;210&gt; 558

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 558

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Glu	Lys	Leu	Pro	Tyr	Ser	Leu	Lys	Val	Leu	Gly	Glu	Asn	Leu	Leu	Arg
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Asn	Trp	Asp	Ala	Ser	Ser	Asp	Pro	Ser	Ile	Glu	Ile	Gln	Phe	Thr	Pro
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Ala	Arg	Val	Leu	Met	Gln	Asp	Phe	Thr	Gly	Val	Pro	Cys	Val	Val	Asp
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Leu	Ala	Thr	Met	Arg	Glu	Ala	Val	Ala	Ala	Leu	Gly	Gly	Asp	Pro	Asn
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Asp	Val	Asn	Pro	Leu	Asn	Pro	Ala	Glu	Met	Val	Ile	Asp	His	Ser	Val
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Ile	Glu	Tyr	Glu	Arg	Asn	Glu	Glu	Arg	Tyr	Gln	Phe	Leu	Arg	Trp	Gly
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Ser	Glu	Ser	Phe	Ser	Asn	Phe	Arg	Val	Val	Pro	Pro	Gly	Thr	Gly	Ile
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Val	His	Gln	Val	Asn	Ile	Glu	Tyr	Leu	Ala	Arg	Val	Val	Phe	Asp	Asn
			180					185					190		

Glu	Gly	Leu	Ala	Tyr	Pro	Asp	Thr	Cys	Ile	Gly	Thr	Asp	Ser	His	Thr
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Thr	Met	Glu	Asn	Gly	Leu	Gly	Ile	Leu	Gly	Trp	Gly	Val	Gly	Gly	Ile
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 Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr  
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 Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser  
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 Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg  
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 170 175 180

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Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala  
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Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro  
 65 70 75 80

Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp  
 85 90 95

Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn  
 100 105 110

Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val  
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 130 135 140

Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly  
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 Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile  
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 Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu  
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Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly	
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Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val	
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Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu	
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&lt;210&gt; 562

&lt;211&gt; 956

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 562

Arg His Ser Val Pro Arg Leu Thr Lys Gly Gln Gly Thr Ile Ile Gly  
 1 5 10 15  
 Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp  
 20 25 30  
 Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr  
 35 40 45  
 Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg  
 50 55 60  
 Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe  
 65 70 75 80  
 Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val  
 85 90 95  
 Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu  
 100 105 110  
 Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser  
 115 120 125  
 Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile

130					135					140				
Glu Thr His Asn Leu	Thr Ile Trp Asp Leu	Asp Arg Thr Phe Asn Val	145	150	155	160								
Gly Gly Phe Gly Gly	Lys Glu Thr Met Thr	Leu Arg Glu Val Leu Ser	165	170	175									
Arg Leu Arg Ala Ala	Tyr Thr Leu Lys Val	Gly Ser Glu Tyr Thr His	180	185	190									
Ile Leu Asp Arg Asp	Glu Arg Thr Trp Leu	Gln Asp Arg Leu Glu Ala	195	200	205									
Gly Met Pro Lys Pro	Thr Gln Ala Glu Gln	Lys Tyr Ile Leu Gln Lys	210	215	220									
Leu Asn Ala Ala Glu	Ala Phe Glu Asn Phe	Leu Gln Thr Lys Tyr Val	225	230	235	240								
Gly Gln Lys Arg Phe	Ser Leu Glu Gly Ala	Glu Ala Leu Ile Pro Leu	245	250	255									
Met Asp Ser Ala Ile	Asp Thr Ala Ala Gly	Gln Gly Leu Asp Glu Val	260	265	270									
Val Ile Gly Met Pro	His Arg Gly Arg Leu	Asn Val Leu Phe Asn Ile	275	280	285									
Val Gly Lys Pro Leu	Ala Ser Ile Phe Asn	Glu Phe Glu Gly Gln Met	290	295	300									
Glu Gln Gly Gln Ile	Gly Gly Ser Gly Asp	Val Lys Tyr His Leu Gly	305	310	315	320								
Ser Glu Gly Gln His	Leu Gln Met Phe Gly	Asp Gly Glu Ile Lys Val	325	330	335									
Ser Leu Thr Ala Asn	Pro Ser His Leu Glu	Ala Val Asn Pro Ala Met	340	345	350									
Glu Gly Ile Val Arg	Ala Lys Gln Asp Tyr	Leu Asp Lys Gly Val Asp	355	360	365									
Gly Lys Thr Val Val	Pro Leu Leu Leu His	Gly Asp Ala Ala Phe Ala	370	375	380									
Gly Leu Gly Ile Val	Pro Glu Thr Ile Asn	Leu Ala Lys Leu Arg Gly	385	390	395	400								
Tyr Asp Val Gly Gly	Thr Ile His Ile Val	Val Asn Asn Gln Ile Gly	405	410	415									
Phe Thr Thr Thr Pro	Asp Ser Ser Arg Ser	Met His Tyr Ala Thr Asp	420	425	430									
Tyr Ala Lys Ala Phe	Gly Cys Pro Val Phe	His Val Asn Gly Asp Asp	435	440	445									
Pro Glu Ala Val Val	Trp Val Gly Gln Leu	Ala Thr Glu Tyr Arg Arg	450	455	460									

Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg  
 465 470 475 480  
 Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr  
 485 490 495  
 Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp  
 500 505 510  
 Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val  
 515 520 525  
 Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu  
 530 535 540  
 Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln  
 545 550 555 560  
 Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu  
 565 570 575  
 Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His  
 580 585 590  
 Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu  
 595 600 605  
 Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu  
 610 615 620  
 Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg  
 625 630 635 640  
 Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala  
 645 650 655  
 Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn  
 660 665 670  
 Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met  
 675 680 685  
 Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala  
 690 695 700  
 Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile  
 705 710 715 720  
 Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys  
 725 730 735  
 Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His  
 740 745 750  
 Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser  
 755 760 765  
 Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu  
 770 775 780

Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr  
 785 790 795 800  
 Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ala Ser Ala Pro Glu Asp  
 805 810 815  
 Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val  
 820 825 830  
 Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu  
 835 840 845  
 Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile  
 850 855 860  
 Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile  
 865 870 875 880  
 Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val  
 885 890 895  
 Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His  
 900 905 910  
 Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg  
 915 920 925  
 Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu  
 930 935 940  
 Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala  
 945 950 955

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 <212> DNA  
 <213> *Corynebacterium glutamicum*

<220>  
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 <223> RXA01745

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 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala  
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 cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96  
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala  
 20 25 30  
 gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag 144  
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu  
 35 40 45  
 gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa 192  
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu  
 50 55 60

atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg	240
Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp	
65 70 75 80	
ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag	288
Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu	
85 90 95	
gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc	336
Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly	
100 105 110	
acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc	384
Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly	
115 120 125	
gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc	432
Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala	
130 135 140	
gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag	480
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu	
145 150 155 160	
cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct	528
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala	
165 170 175	
act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac	576
Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn	
180 185 190	
gtt cca tac gtc acc cca ctg gtg cgc aag ctt gct gaa aag cac ggc	624
Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly	
195 200 205	
gtt gac ttg aac acc gtg acc ggt acc ggt atc ggt ggc cgt atc cgc	672
Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg	
210 215 220	
aag cag gat gtt ttg gct gct gcg aac ggc gag gct gca cct gct gag	720
Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu	
225 230 235 240	
gct gct gct cct gtt tcc gct tgg tcc act aag tct gtt gac cct gag	768
Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu	
245 250 255	
aag gct aag ctc cgt ggt acc act cag aag gtc aac cgc atc cgt gag	816
Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu	
260 265 270	
atc acc gcg atg aag acc gtc gag gct ctg cag att tct gct cag ctc	864
Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu	
275 280 285	
acc cag ctg cac gag gtc gat atg act cgc gtt gct gag ctg cgt aag	912
Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys	
290 295 300	
aag aac aag ccc gcg ttc atc gag aag cac ggt gtg aac ctc act tac	960

Lys	Asn	Lys	Pro	Ala	Phe	Ile	Glu	Lys	His	Gly	Val	Asn	Leu	Thr	Tyr		
305					310					315					320		
ctg	cca	ttc	ttc	gtg	aag	gca	gtt	gtc	gag	gct	ttg	gtt	tcc	cat	cca	1008	
Leu	Pro	Phe	Phe	Val	Lys	Ala	Val	Val	Glu	Ala	Leu	Val	Ser	His	Pro		
				325					330					335			
aac	gtc	aac	gcg	tct	ttc	aac	gcg	aag	acc	aag	gag	atg	acc	tac	cac	1056	
Asn	Val	Asn	Ala	Ser	Phe	Asn	Ala	Lys	Thr	Lys	Glu	Met	Thr	Tyr	His		
			340					345					350				
tcc	tcc	gtt	aac	ctc	tcc	atc	gct	gtt	gat	acc	cca	gct	ggt	ctg	ttg	1104	
Ser	Ser	Val	Asn	Leu	Ser	Ile	Ala	Val	Asp	Thr	Pro	Ala	Gly	Leu	Leu		
		355					360					365					
acc	cca	gtc	att	cac	gat	gct	cag	gat	ctc	tcc	atc	cca	gag	atc	gca	1152	
Thr	Pro	Val	Ile	His	Asp	Ala	Gln	Asp	Leu	Ser	Ile	Pro	Glu	Ile	Ala		
	370					375					380						
aag	gca	att	gtt	gac	ctg	gct	gat	cgt	tca	cgc	aac	aac	aag	ctg	aag	1200	
Lys	Ala	Ile	Val	Asp	Leu	Ala	Asp	Arg	Ser	Arg	Asn	Asn	Lys	Leu	Lys		
385					390					395					400		
cca	aac	gat	ctg	tcc	ggt	ggc	acc	ttc	acc	atc	acc	aac	att	ggt	tct	1248	
Pro	Asn	Asp	Leu	Ser	Gly	Gly	Thr	Phe	Thr	Ile	Thr	Asn	Ile	Gly	Ser		
				405					410					415			
gaa	ggc	gca	ctg	tct	gat	acc	cca	atc	ctg	gtt	cca	cca	cag	gct	ggc	1296	
Glu	Gly	Ala	Leu	Ser	Asp	Thr	Pro	Ile	Leu	Val	Pro	Pro	Gln	Ala	Gly		
			420					425					430				
atc	ttg	ggc	acc	ggc	gcg	atc	gtg	aag	cgt	cca	gtt	gtc	atc	acc	gag	1344	
Ile	Leu	Gly	Thr	Gly	Ala	Ile	Val	Lys	Arg	Pro	Val	Val	Ile	Thr	Glu		
		435					440					445					
gat	gga	att	gat	tcc	atc	gcg	atc	cgt	cag	atg	gtc	ttc	cta	cca	ctg	1392	
Asp	Gly	Ile	Asp	Ser	Ile	Ala	Ile	Arg	Gln	Met	Val	Phe	Leu	Pro	Leu		
	450					455					460						
acc	tac	gac	cac	cag	gtt	gta	gat	ggc	gca	gat	gct	ggt	cgc	ttc	ctg	1440	
Thr	Tyr	Asp	His	Gln	Val	Val	Asp	Gly	Ala	Asp	Ala	Gly	Arg	Phe	Leu		
465					470				475						480		
acc	acc	atc	aag	gac	cgc	ctt	gag	acc	gct	aac	ttc	gaa	ggc	gat	ctg	1488	
Thr	Thr	Ile	Lys	Asp	Arg	Leu	Glu	Thr	Ala	Asn	Phe	Glu	Gly	Asp	Leu		
			485					490						495			
cag	ctc	taagatctct	gcaagttaaa	acc												1517	
Gln	Leu																

&lt;210&gt; 564

&lt;211&gt; 498

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 564

Ile	Leu	Ala	Asp	Glu	Asp	Asp	Thr	Val	Asp	Val	Gly	Ala	Val	Ile	Ala
1				5					10					15	



Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala  
 20 25 30  
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu  
 35 40 45  
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu  
 50 55 60  
 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp  
 65 70 75 80  
 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu  
 85 90 95  
 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly  
 100 105 110  
 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly  
 115 120 125  
 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala  
 130 135 140  
 Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu  
 145 150 155 160  
 Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala  
 165 170 175  
 Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn  
 180 185 190  
 Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly  
 195 200 205  
 Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg  
 210 215 220  
 Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu  
 225 230 235 240  
 Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu  
 245 250 255  
 Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu  
 260 265 270  
 Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu  
 275 280 285  
 Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys  
 290 295 300  
 Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr  
 305 310 315 320  
 Leu Pro Phe Phe Val Lys Ala Val Val Glu Ala Leu Val Ser His Pro  
 325 330 335  
 Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His

340	345	350
Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu		
355	360	365
Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala		
370	375	380
Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys		
385	390	400
Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser		
405	410	415
Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly		
420	425	430
Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu		
435	440	445
Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu		
450	455	460
Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu		
465	470	475
Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu		
485	490	495

Gln Leu

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 <213> Corynebacterium glutamicum

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 gttcgcaacc gctaattagt taaggagcac ctgtttaatc atg tct att ttt ctc 115  
 Met Ser Ile Phe Leu  
 1 5  
 aat tca gat tcc cgc atc atc att cag ggc att acc ggt tcg gaa ggt 163  
 Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile Thr Gly Ser Glu Gly  
 10 15 20  
 tca gag cat gcg cgt cga att tta gcc tct ggt gcg aag ctc gtg ggt 211  
 Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly Ala Lys Leu Val Gly  
 25 30 35  
 ggc acc aac ccc cgc aaa gct ggg caa acc att ttg atc aat gac act 259  
 Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile Leu Ile Asn Asp Thr  
 40 45 50

gag ttg cct gta ttt ggc act gtt aag gaa gca atg gag gaa acg ggt	307
Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala Met Glu Glu Thr Gly	
55 60 65	
gcg gat gtc acc gta att ttc gtt cct cca gcc ttt gcc aaa gct gcg	355
Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala Phe Ala Lys Ala Ala	
70 75 80 85	
atc att gaa gct atc gac gct cac atc cca ctg tgc gtg att att act	403
Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu Cys Val Ile Ile Thr	
90 95 100	
gag ggc atc cca gtg cgt gac gct tct gag gcg tgg gct tat gcc aag	451
Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala Trp Ala Tyr Ala Lys	
105 110 115	
aag gtg gga cac acc cgc atc att ggc cct aac tgc cca gcc att att	499
Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn Cys Pro Gly Ile Ile	
120 125 130	
act ccc ggc gaa tct ctt gcg gga att acg ccg gca aac att gca ggt	547
Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro Ala Asn Ile Ala Gly	
135 140 145	
tcc ggc ccg atc ggg ttg atc tca aag tcg gga aca ctg act tat cag	595
Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly Thr Leu Thr Tyr Gln	
150 155 160 165	
atg atg tac gaa ctt tca gat att ggc att tct acg gcg att ggt att	643
Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser Thr Ala Ile Gly Ile	
170 175 180	
ggc ggt gac cca atc atc ggt aca acc cat atc gac gct ctg gag gcc	691
Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile Asp Ala Leu Glu Ala	
185 190 195	
ttt gaa gct gat cct gag acc aag gca atc gtc atg atc ggt gag atc	739
Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val Met Ile Gly Glu Ile	
200 205 210	
ggt gga gat gca gag gaa cgc gct gct gac ttc att tct aag cac gtg	787
Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe Ile Ser Lys His Val	
215 220 225	
aca aaa cca gtt gtg ggt tac gtg gca gcc ttt acc gcc cct gaa gga	835
Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly	
230 235 240 245	
aag acc atg ggg cat gct ggc gcc atc gtg aca ggt tca gaa ggc act	883
Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly Ser Glu Gly Thr	
250 255 260	
gcg cga gca aag aag cat gca ttg gag gcc gtg ggt gtt cgc gtg gga	931
Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly Val Arg Val Gly	
265 270 275	
aca act ccg agt gaa acc gcg aag ctt atg cgt gag gta gtt gca gct	979
Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu Val Val Ala Ala	
280 285 290	

ttg taactaacag gccacagatc tta  
Leu

1005

&lt;210&gt; 566

&lt;211&gt; 294

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 566

Met Ser Ile Phe Leu Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile  
1 5 10 15

Thr Gly Ser Glu Gly Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly  
20 25 30

Ala Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile  
35 40 45

Leu Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala  
50 55 60

Met Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala  
65 70 75 80

Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu  
85 90 95

Cys Val Ile Ile Thr Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala  
100 105 110

Trp Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn  
115 120 125

Cys Pro Gly Ile Ile Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro  
130 135 140

Ala Asn Ile Ala Gly Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly  
145 150 155 160

Thr Leu Thr Tyr Gln Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser  
165 170 175

Thr Ala Ile Gly Ile Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile  
180 185 190

Asp Ala Leu Glu Ala Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val  
195 200 205

Met Ile Gly Glu Ile Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe  
210 215 220

Ile Ser Lys His Val Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe  
225 230 235 240

Thr Ala Pro Glu Gly Lys Thr Met Gly His Ala Gly Ala Ile Val Thr  
245 250 255

Gly Ser Glu Gly Thr Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val  
260 265 270

Gly Val Arg Val Gly Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg  
 275 280 285

Glu Val Val Ala Ala Leu  
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 <211> 1395  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA00783

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 Leu Lys His Leu Leu  
 1 5  
 tta cgg gaa gac ttt gtt aaa gac gca gaa ggc tct aag cat ggg ccg 163  
 Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly Ser Lys His Gly Pro  
 10 15 20  
 gaa atg gaa ttg gca gtg gat ctt ttt gaa tac caa gca cgg gac ctc 211  
 Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr Gln Ala Arg Asp Leu  
 25 30 35  
 ttt gaa acc cat ggt gtg cca gtg ttg aag gga att gtg gca tca aca 259  
 Phe Glu Thr His Gly Val Pro Val Leu Lys Gly Ile Val Ala Ser Thr  
 40 45 50  
 cca gag gcg gcg agg aaa gcg gct gag gaa atc ggc gga ctg acc gtc 307  
 Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile Gly Gly Leu Thr Val  
 55 60 65  
 gtc aag gct cag gtc aag gtg ggc gga cgt ggc aag gcg ggt ggc gtc 355  
 Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val  
 70 75 80 85  
 cgt gtg gca ccg acg tcg gct cag gct ttt gat gct gcg gat gcg att 403  
 Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile  
 90 95 100  
 ctc ggc atg gat atc aaa gga cac act gtt aat cag gtg atg gtg gcg 451  
 Leu Gly Met Asp Ile Lys Gly His Thr Val Asn Gln Val Met Val Ala  
 105 110 115  
 cag ggc gct gac att gct gag gaa tac tat ttc tcc att ttg ttg gat 499  
 Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe Ser Ile Leu Leu Asp  
 120 125 130  
 cgc gcg aat cgt tcg tat ctg gct atg tgc tct gtt gaa ggt ggc atg 547  
 Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser Val Glu Gly Gly Met  
 135 140 145

gag atc gag atc ctg gcg aag gaa aag cct gaa gct ttg gca aag gtg Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val 150 155 160 165	595
gaa gtg gat ccc ctc act ggt att gat gag gac aaa gcg cgg gag att Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile 170 175 180	643
gtc act gct gct ggc ttt gaa act gag gtg gca gag aaa gtc att ccg Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala Glu Lys Val Ile Pro 185 190 195	691
gtg ctg atc aag atc tgg cag gtg tat tac gaa gag gaa gca aca ctc Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Glu Ala Thr Leu 200 205 210	739
gtt gag gtg aac ccg ttg gtg ctc acg gat gac ggc gat gtg att gcg Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp Gly Asp Val Ile Ala 215 220 225	787
ctt gat ggc aag atc acg ctg gat gat aac gct gat ttc cgc cat gat Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala Asp Phe Arg His Asp 230 235 240 245	835
aac cgt ggt gcg ttg gct gaa tct gcc ggt ggc ttg gac att ttg gaa Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu 250 255 260	883
ctg aag gcc aag aag aat gat ctg aac tac gtg aaa ctt gat ggc tct Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser 265 270 275	931
gtg ggc atc att ggc aat ggt gca ggt ttg gtg atg tcc acg ttg gat Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp 280 285 290	979
atc gtg gct gca gct ggt gaa cgc cat ggt ggg cag cgc ccc gcg aac Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn 295 300 305	1027
ttc cta gac att ggt ggc gga gca tca gct gaa tcg atg gct gct ggt Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly 310 315 320 325	1075
ctc gat gtg atc ctt ggg gat agc cag gta cgc agt gtg ttt gtg aat Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn 330 335 340	1123
gtg ttt ggt ggc atc acc gcg tgt gat gtg gtg gca aag gga atc gtt Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val 345 350 355	1171
gga gct ttg gat gtg ctc ggc gat caa gca acg aag cct ctt gtg gtg Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val 360 365 370	1219
cgc ctt gat ggc aac aac gtg gtg gaa ggc aga cga atc ctc gcg gaa Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu 375 380 385	1267
tat aac cac cct ttg gtc acc gtt gtg gag ggt atg gat gca gcg gct	1315

Tyr Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala  
 390 395 400 405

gat cac gct gcc cat ttg gcc aat ctt gcc cag cac ggc cag ttc gca 1363  
 Asp His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala  
 410 415 420

acc gct aat tagttaagga gcacctgttt aat 1395  
 Thr Ala Asn

<210> 568

<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 568

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Ser Lys His Gly Pro Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr  
 20 25 30

Gln Ala Arg Asp Leu Phe Glu Thr His Gly Val Pro Val Leu Lys Gly  
 35 40 45

Ile Val Ala Ser Thr Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile  
 50 55 60

Gly Gly Leu Thr Val Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly  
 65 70 75 80

Lys Ala Gly Gly Val Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp  
 85 90 95

Ala Ala Asp Ala Ile Leu Gly Met Asp Ile Lys Gly His Thr Val Asn  
 100 105 110

Gln Val Met Val Ala Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe  
 115 120 125

Ser Ile Leu Leu Asp Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser  
 130 135 140

Val Glu Gly Gly Met Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu  
 145 150 155 160

Ala Leu Ala Lys Val Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp  
 165 170 175

Lys Ala Arg Glu Ile Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala  
 180 185 190

Glu Lys Val Ile Pro Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu  
 195 200 205

Glu Glu Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp  
 210 215 220

Gly Asp Val Ile Ala Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala

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<211> 1623
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1600)  
<223> RXN01695
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tgttcggcag agaactcgcg gagataaaag gaagttgaac atg tca gat tcc ccg 115
                                         Met Ser Asp Ser Pro
                                         1             5

aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt 163
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly
                        10                        15                        20

gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag 211

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Ala	Gly	Ile	Met	Ser	Ser	Thr	Leu	Gly	Ala	Met	Leu	Arg	Gln	Leu	Glu	
			25					30					35			
cca	agc	tgg	act	cag	atc	gtc	ttc	gag	cgt	ttg	gat	gga	ccg	gca	caa	259
Pro	Ser	Trp	Thr	Gln	Ile	Val	Phe	Glu	Arg	Leu	Asp	Gly	Pro	Ala	Gln	
		40					45					50				
gag	tcg	tcc	tcc	ccg	tgg	aac	aat	gca	gga	acc	ggc	cac	tct	gct	cta	307
Glu	Ser	Ser	Ser	Pro	Trp	Asn	Asn	Ala	Gly	Thr	Gly	His	Ser	Ala	Leu	
	55					60					65					
tgc	gag	ctg	aac	tac	acc	cca	gag	gtt	aag	ggc	aag	gtt	gaa	att	gcc	355
Cys	Glu	Leu	Asn	Tyr	Thr	Pro	Glu	Val	Lys	Gly	Lys	Val	Glu	Ile	Ala	
	70				75					80					85	
aag	gct	gta	gga	atc	aac	gag	aag	ttc	cag	gtt	tcc	cgt	cag	ttc	tgg	403
Lys	Ala	Val	Gly	Ile	Asn	Glu	Lys	Phe	Gln	Val	Ser	Arg	Gln	Phe	Trp	
				90					95					100		
tct	cac	ctc	gtt	gaa	gag	gga	gtg	ctg	tct	gat	cct	aag	gaa	ttc	atc	451
Ser	His	Leu	Val	Glu	Glu	Gly	Val	Leu	Ser	Asp	Pro	Lys	Glu	Phe	Ile	
			105					110					115			
aac	cct	gtt	cct	cac	gta	tct	ttc	ggc	cag	ggc	gca	gat	cag	gtt	gca	499
Asn	Pro	Val	Pro	His	Val	Ser	Phe	Gly	Gln	Gly	Ala	Asp	Gln	Val	Ala	
		120					125					130				
tac	atc	aag	gct	cgc	tac	gaa	gct	ttg	aag	gat	cac	cca	ctc	ttc	cag	547
Tyr	Ile	Lys	Ala	Arg	Tyr	Glu	Ala	Leu	Lys	Asp	His	Pro	Leu	Phe	Gln	
	135					140					145					
ggc	atg	acc	tac	gct	gac	gat	gaa	gct	acc	ttc	acc	gag	aag	ctg	cct	595
Gly	Met	Thr	Tyr	Ala	Asp	Asp	Glu	Ala	Thr	Phe	Thr	Glu	Lys	Leu	Pro	
	150				155					160					165	
ttg	atg	gca	aag	ggc	cgt	gac	ttc	tct	gat	cca	gta	gca	atc	tct	tgg	643
Leu	Met	Ala	Lys	Gly	Arg	Asp	Phe	Ser	Asp	Pro	Val	Ala	Ile	Ser	Trp	
				170					175					180		
atc	gat	gaa	ggc	acc	gac	atc	aac	tac	ggt	gct	cag	acc	aag	cag	tac	691
Ile	Asp	Glu	Gly	Thr	Asp	Ile	Asn	Tyr	Gly	Ala	Gln	Thr	Lys	Gln	Tyr	
			185					190					195			
ctg	gat	gca	gct	gaa	gtt	gaa	ggc	act	gaa	atc	cgc	tat	ggc	cac	gaa	739
Leu	Asp	Ala	Ala	Glu	Val	Glu	Gly	Thr	Glu	Ile	Arg	Tyr	Gly	His	Glu	
		200					205					210				
gtc	aag	agc	atc	aag	gct	gat	ggc	gca	aag	tgg	atc	gtg	acc	gtc	aag	787
Val	Lys	Ser	Ile	Lys	Ala	Asp	Gly	Ala	Lys	Trp	Ile	Val	Thr	Val	Lys	
	215					220					225					
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Asn	Val	His	Thr	Gly	Asp	Thr	Lys	Thr	Ile	Lys	Ala	Asn	Phe	Val	Phe	
	230				235					240					245	
gtc	ggc	gca	ggc	gga	tac	gca	ctg	gat	ctg	ctt	cgc	agc	gca	ggc	atc	883
Val	Gly	Ala	Gly	Gly	Tyr	Ala	Leu	Asp	Leu	Leu	Arg	Ser	Ala	Gly	Ile	
				250					255					260		
cca	cag	gtc	aag	ggc	ttc	gct	gga	ttc	cca	gta	tcc	ggc	ctg	tgg	ctt	931
Pro	Gln	Val	Lys	Gly	Phe	Ala	Gly	Phe	Pro	Val	Ser	Gly	Leu	Trp	Leu	

265								270				275								
cgt	tgc	acc	aac	gag	gaa	ctg	atc	gag	cag	cac	gca	gcc	aag	gta	tat	979				
Arg	Cys	Thr	Asn	Glu	Glu	Leu	Ile	Glu	Gln	His	Ala	Ala	Lys	Val	Tyr					
280				285				290												
ggc	aag	gca	tct	gtt	ggc	gct	cct	cca	atg	tct	gtt	cct	cac	ctt	gac	1027				
Gly	Lys	Ala	Ser	Val	Gly	Ala	Pro	Pro	Met	Ser	Val	Pro	His	Leu	Asp					
295				300				305												
acc	cgc	gtt	atc	gag	ggt	gaa	aag	ggt	ctg	ctc	ttt	gga	cct	tac	ggt	1075				
Thr	Arg	Val	Ile	Glu	Gly	Glu	Lys	Gly	Leu	Leu	Phe	Gly	Pro	Tyr	Gly					
310				315				320												
ggc	tgg	acc	cct	aag	ttc	ttg	aag	gaa	ggc	tcc	tac	ctg	gac	ctg	ttc	1123				
Gly	Trp	Thr	Pro	Lys	Phe	Leu	Lys	Glu	Gly	Ser	Tyr	Leu	Asp	Leu	Phe					
330				335				340												
aag	tcc	atc	cgc	cca	gac	aac	att	cct	tcc	tac	ctt	ggc	gtt	gct	gct	1171				
Lys	Ser	Ile	Arg	Pro	Asp	Asn	Ile	Pro	Ser	Tyr	Leu	Gly	Val	Ala	Ala					
345				350				355												
cag	gaa	ttt	gat	ctg	acc	aag	tac	ctt	gtc	act	gaa	gtt	ctc	aag	gac	1219				
Gln	Glu	Phe	Asp	Leu	Thr	Lys	Tyr	Leu	Val	Thr	Glu	Val	Leu	Lys	Asp					
360				365				370												
cag	gac	aag	cgt	atg	gat	gct	ctt	cgc	gag	tac	atg	cca	gag	gca	caa	1267				
Gln	Asp	Lys	Arg	Met	Asp	Ala	Leu	Arg	Glu	Tyr	Met	Pro	Glu	Ala	Gln					
375				380				385												
aac	ggc	gat	tgg	gag	acc	atc	gtt	gcc	gga	cag	cgt	gtt	cag	gtt	att	1315				
Asn	Gly	Asp	Trp	Glu	Thr	Ile	Val	Ala	Gly	Gln	Arg	Val	Gln	Val	Ile					
390				395				400												
aag	cct	gca	gga	ttc	cct	aag	ttc	ggt	tcc	ctg	gaa	ttc	ggc	acc	acc	1363				
Lys	Pro	Ala	Gly	Phe	Pro	Lys	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Thr	Thr					
410				415				420												
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Leu	Ile	Asn	Asn	Ser	Glu	Gly	Thr	Ile	Ala	Gly	Leu	Leu	Gly	Ala	Ser					
425				430				435												
cct	gga	gca	tcc	atc	gca	cct	tcc	gca	atg	atc	gag	ctg	ctt	gag	cgt	1459				
Pro	Gly	Ala	Ser	Ile	Ala	Pro	Ser	Ala	Met	Ile	Glu	Leu	Leu	Glu	Arg					
440				445				450												
tgc	ttc	ggt	gac	cgc	atg	atc	gag	tgg	ggc	gac	aag	ctg	aag	gac	atg	1507				
Cys	Phe	Gly	Asp	Arg	Met	Ile	Glu	Trp	Gly	Asp	Lys	Leu	Lys	Asp	Met					
455				460				465												
atc	cct	tcc	tac	ggc	aag	aag	ctt	gct	tcc	gag	cca	gca	ctg	ttt	gag	1555				
Ile	Pro	Ser	Tyr	Gly	Lys	Lys	Leu	Ala	Ser	Glu	Pro	Ala	Leu	Phe	Glu					
470				475				480												
cag	cag	tgg	gca	cgc	acc	cag	aag	acc	ctg	aag	ctt	gag	gaa	gcc		1600				
Gln	Gln	Trp	Ala	Arg	Thr	Gln	Lys	Thr	Leu	Lys	Leu	Glu	Glu	Ala						
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taaattcttct aactgctttc ttt															1623					

&lt;210&gt; 570

&lt;211&gt; 500

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 570

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Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp
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Val Val Leu Ile Gly Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met
      20             25             30

Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu
      35             40             45

Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
 50             55             60

Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly
 65             70             75             80

Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val
      85             90             95

Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp
      100            105            110

Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly
 115            120            125

Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp
 130            135            140

His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe
 145            150            155            160

Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro
      165            170            175

Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala
      180            185            190

Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile
 195            200            205

Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp
 210            215            220

Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys
 225            230            235            240

Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu
      245            250            255

Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val
 260            265            270

Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His
 275            280            285

Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser

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<211> 1039
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1039)
<223> FRXA01615
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tgttcggcag agaactcgcg gagataaaag gaagttgaac atg tca gat tcc ccg 115
                                         Met Ser Asp Ser Pro
                                         1                               5

aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt 163
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly

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				10				15				20					
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Ala	Gly	Ile	Met	Ser	Ser	Thr	Leu	Gly	Ala	Met	Leu	Arg	Gln	Leu	Glu		
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Pro	Ser	Trp	Thr	Gln	Ile	Val	Phe	Glu	Arg	Leu	Asp	Gly	Pro	Ala	Gln		
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gag	tcg	tcc	tcc	ccg	tgg	aac	aat	gca	gga	acc	ggc	cac	tct	gct	cta	307	
Glu	Ser	Ser	Ser	Pro	Trp	Asn	Asn	Ala	Gly	Thr	Gly	His	Ser	Ala	Leu		
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tgc	gag	ctg	aac	tac	acc	cca	gag	gtt	aag	ggc	aag	gtt	gaa	att	gcc	355	
Cys	Glu	Leu	Asn	Tyr	Thr	Pro	Glu	Val	Lys	Gly	Lys	Val	Glu	Ile	Ala		
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Lys	Ala	Val	Gly	Ile	Asn	Glu	Lys	Phe	Gln	Val	Ser	Arg	Gln	Phe	Trp		
				90								95				100	
tct	cac	ctc	gtt	gaa	gag	gga	gtg	ctg	tct	gat	cct	aag	gaa	ttc	atc	451	
Ser	His	Leu	Val	Glu	Glu	Gly	Val	Leu	Ser	Asp	Pro	Lys	Glu	Phe	Ile		
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aac	cct	gtt	cct	cac	gta	tct	ttc	ggc	cag	ggc	gca	gat	cag	gtt	gca	499	
Asn	Pro	Val	Pro	His	Val	Ser	Phe	Gly	Gln	Gly	Ala	Asp	Gln	Val	Ala		
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tac	atc	aag	gct	cgc	tac	gaa	gct	ttg	aag	gat	cac	cca	ctc	ttc	cag	547	
Tyr	Ile	Lys	Ala	Arg	Tyr	Glu	Ala	Leu	Lys	Asp	His	Pro	Leu	Phe	Gln		
135								140				145					
ggc	atg	acc	tac	gct	gac	gat	gaa	gct	acc	ttc	acc	gag	aag	ctg	cct	595	
Gly	Met	Thr	Tyr	Ala	Asp	Asp	Glu	Ala	Thr	Phe	Thr	Glu	Lys	Leu	Pro		
150				155								160				165	
ttg	atg	gca	aag	ggc	cgt	gac	ttc	tct	gat	cca	gta	gca	atc	tct	tgg	643	
Leu	Met	Ala	Lys	Gly	Arg	Asp	Phe	Ser	Asp	Pro	Val	Ala	Ile	Ser	Trp		
				170				175				180					
atc	gat	gaa	ggc	acc	gac	atc	aac	tac	ggt	gct	cag	acc	aag	cag	tac	691	
Ile	Asp	Glu	Gly	Thr	Asp	Ile	Asn	Tyr	Gly	Ala	Gln	Thr	Lys	Gln	Tyr		
				185				190				195					
ctg	gat	gca	gct	gaa	gtt	gaa	ggc	act	gaa	atc	cgc	tat	ggc	cac	gaa	739	
Leu	Asp	Ala	Ala	Glu	Val	Glu	Gly	Thr	Glu	Ile	Arg	Tyr	Gly	His	Glu		
200								205				210					
gtc	aag	agc	atc	aag	gct	gat	ggc	gca	aag	tgg	atc	gtg	acc	gtc	aag	787	
Val	Lys	Ser	Ile	Lys	Ala	Asp	Gly	Ala	Lys	Trp	Ile	Val	Thr	Val	Lys		
215								220				225					
aac	gta	cac	act	ggc	gac	acc	aag	acc	atc	aag	gca	aac	ttc	gtg	ttc	835	
Asn	Val	His	Thr	Gly	Asp	Thr	Lys	Thr	Ile	Lys	Ala	Asn	Phe	Val	Phe		
230				235								240</					

cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt 931  
 Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu  
                   265                                  270                                  275

cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat 979  
 Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr  
                   280                                  285                                  290

ggc aag gca tct gtt ggc gct cct cca atg tct gtt cct cac ctt gac 1027  
 Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp  
                   295                                  300                                  305

- acc cgc gtt atc 1039  
 Thr Arg Val Ile  
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<211> 313

<212> PRT

<213> Corynebacterium glutamicum

<400> 572

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                   20                                  25                                  30

Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu  
                   35                                  40                                  45

Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr  
                   50                                  55                                  60

Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly  
   65                                  70                                  75                                  80

Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val  
                   85                                  90                                  95

Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp  
                   100                                  105                                  110

Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly  
                   115                                  120                                  125

Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp  
                   130                                  135                                  140

His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe  
   145                                  150                                  155                                  160

Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro  
                   165                                  170                                  175

Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala  
                   180                                  185                                  190

Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile

195	200	205
Arg Tyr Gly His Glu Val	Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp	
210	215	220
Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys		
225	230	235
Ala Asn Phe Val Phe Val Gly Ala Gly Tyr Ala Leu Asp Leu Leu		
245	250	255
Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val		
260	265	270
Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His		
275	280	285
Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser		
290	295	300
Val Pro His Leu Asp Thr Arg Val Ile		
305	310	

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> FRXA01695

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Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala	
1 5 10 15	
atg atc gag ctg ctt gag cgt tgc ttc ggt gac cgc atg atc gag tgg	96
Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp	
20 25 30	
ggc gac aag ctg aag gac atg atc cct tcc tac ggc aag aag ctt gct	144
Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala	
35 40 45	
tcc gag cca gca ctg ttt gag cag cag tgg gca cgc acc cag aag acc	192
Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr	
50 55 60	
ctg aag ctt gag gaa gcc taaatcttct aactgctttc ttt	233
Leu Lys Leu Glu Glu Ala	
65 70	

<210> 574  
 <211> 70  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 574

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 20 25 30  
 Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala  
 35 40 45  
 Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr  
 50 55 60  
 Leu Lys Leu Glu Glu Ala  
 65 70

&lt;210&gt; 575

&lt;211&gt; 1063

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1063)

&lt;223&gt; RXA00290

&lt;400&gt; 575

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 gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115  
 Met Thr Ile Asp Leu  
 1 5  
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163  
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His  
 10 15 20  
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211  
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met  
 25 30 35  
 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259  
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu  
 40 45 50  
 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307  
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly  
 55 60 65  
 aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355  
 Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly  
 70 75 80 85  
 gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403  
 Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln  
 90 95 100  
 ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451  
 Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp  
 105 110 115



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gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct 499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
      120                      125                      130

tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc 547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
      135                      140                      145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
      150                      155                      160                      165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
      170                      175                      180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att 691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
      185                      190                      195

tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac 739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
      200                      205                      210

gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac 787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
      215                      220                      225

gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag 835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
      230                      235                      240                      245

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
      250                      255                      260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
      265                      270                      275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
      280                      285                      290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
      295                      300                      305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063
Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
      310                      315                      320

```

&lt;210&gt; 576

&lt;211&gt; 321

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 576

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu

1	5	10	15
Ile. Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg	20	25	30
Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val	35	40	45
Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr	50	55	60
His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala	65	70	75
Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met	85	90	95
Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile	100	105	110
Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile	115	120	125
Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser	130	135	140
Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp	145	150	155
Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu	165	170	175
Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp	180	185	190
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val	195	200	205
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser	210	215	220
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala	225	230	235
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn	245	250	255
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn	260	265	270
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe	275	280	285
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys	290	295	300
Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg	305	310	315
Ser			320

<210> 577  
 <211> 1347  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1324)  
 <223> RXN01048

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 Met Thr Ile Asp Leu  
 1 5  
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163  
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His  
 10 15 20  
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211  
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met  
 25 30 35  
 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259  
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu  
 40 45 50  
 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307  
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly  
 55 60 65  
 aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355  
 Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly  
 70 75 80 85  
 gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403  
 Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln  
 90 95 100  
 ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451  
 Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp  
 105 110 115  
 gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct 499  
 Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro  
 120 125 130  
 tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc 547  
 Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe  
 135 140 145  
 gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595  
 Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His  
 150 155 160 165  
 gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643  
 Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn

	170							175						180					
tcc Ser	ctg Leu	aag Lys	ctg Leu 185	ctg Leu	gat Asp	cgc Arg	aag Lys	atc Ile 190	gaa Glu	gac Asp	ctc Leu	aag Lys	att Ile 195	gtt Val	att Ile	691			
tcc Ser	ggc Gly	gca Ala 200	ggc Gly	gca Ala	gcg Ala	ggc Gly	gtt Val 205	gca Ala	gct Ala	gta Val	gat Asp	atg Met 210	ctg Leu	acc Thr	aac Asn	739			
gct Ala	gga Gly 215	gca Ala	acc Thr	gac Asp	atc Ile	gtg Val 220	gtt Val	ctt Leu	gat Asp	tcc Ser	cga Arg 225	ggc Gly	atc Ile	atc Ile	cac His	787			
gac Asp 230	agc Ser	cgt Arg	gag Glu	gat Asp	ctt Leu 235	tcc Ser	cca Pro	gtt Val	aag Lys	gct Ala 240	gct Ala	ctt Leu	gca Ala	gag Glu	aag Lys 245	835			
acc Thr	aac Asn	cct Pro	cgt Arg	ggc Gly 250	atc Ile	agc Ser	ggt Gly	ggc Gly	atc Ile 255	aat Asn	gag Glu	gct Ala	ttc Phe	acc Thr 260	ggc Gly	883			
gcg Ala	gac Asp	ctg Leu	ttc Phe 265	att Ile	ggc Gly	gtg Val	tcc Ser	ggc Gly 270	ggc Gly	aac Asn	atc Ile	ggc Gly	gag Glu 275	gac Asp	gct Ala	931			
ctc Leu	aaa Lys	ctc Leu 280	atg Met	gcc Ala	ccg Pro	gag Glu	cca Pro 285	atc Ile	ctg Leu	ttc Phe	acc Thr	ctg Leu 290	gcg Ala	aac Asn	cca Pro	979			
acc Thr	cca Pro 295	gag Glu	atc Ile	gat Asp	cct Pro	gag Glu 300	ctg Leu	tct Ser	cag Gln	aag Lys	tac Tyr 305	ggc Gly	gcc Ala	atc Ile	gtc Val	1027			
gcg Ala 310	acc Thr	ggg Gly	cgc Arg	tct Ser	gac Asp 315	ctg Leu	cct Pro	aac Asn	cag Gln	atc Ile 320	aac Asn	aac Asn	gtg Val	ctg Leu	gcg Ala 325	1075			
ttc Phe	cca Pro	gga Gly	att Ile	ttc Phe 330	gcc Ala	ggc Gly	gct Ala	ctc Leu	gca Ala 335	gcc Ala	aag Lys	gct Ala	aag Lys	aag Lys 340	atc Ile	1123			
acc Thr	ccc Pro	gag Glu	atg Met 345	aag Lys	ctc Leu	gcc Ala	gct Ala	cag Gln 350	agg Arg	caa Gln	tcg Ser	cag Gln	aca Thr 355	tcg Ser	cag Gln	1171			
ctg Leu	agg Arg	acc Thr 360	tcg Ser	agg Arg	tcg Ser	gcc Ala	gca Ala 365	tcg Ser	tgc Cys	cta Leu	ccg Pro	ccc Pro 370	tgg Trp	atc Ile	ccc Pro	1219			
gcg Ala	ttg Leu 375	ccc Pro	caa Gln	cag Gln	tca Ser	agg Arg 380	cag Gln	ctg Leu	tcc Ser	agg Arg	ccg Pro 385	tcg Ser	cca Pro	aag Lys	cgc Arg	1267			
aaa Lys 390	acg Thr	ctt Leu	aaa Lys	aat Asn 395	ttg Leu	ctt Leu	atc Ile	gac Asp	gcc Ala	tcc Ser 400	ctc Leu	ccc Pro	gtc Val	gag Glu	gcg Ala 405	1315			
cca Pro	ata Ile	ttt Phe	taaagacaaa cttgaggcccc aca													1347			

&lt;210&gt; 578

&lt;211&gt; 408

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 578

Met	Thr	Ile	Asp	Leu	Gln	Arg	Ser	Thr	Gln	Asn	Leu	Thr	His	Glu	Glu
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Ile	Phe	Glu	Ala	His	Glu	Gly	Gly	Lys	Leu	Ser	Ile	Ser	Ser	Thr	Arg
		20						25					30		

Pro	Leu	Arg	Asp	Met	Arg	Asp	Leu	Ser	Leu	Ala	Tyr	Thr	Pro	Gly	Val
		35					40					45			

Ala	Gln	Val	Cys	Glu	Ala	Ile	Lys	Glu	Asp	Pro	Glu	Val	Ala	Arg	Thr
	50					55					60				

His	Thr	Gly	Ile	Gly	Asn	Thr	Val	Ala	Val	Ile	Ser	Asp	Gly	Thr	Ala
65					70					75					80

Val	Leu	Gly	Leu	Gly	Asp	Ile	Gly	Pro	Gln	Ala	Ser	Leu	Pro	Val	Met
			85						90					95	

Glu	Gly	Lys	Ala	Gln	Leu	Phe	Ser	Ser	Phe	Ala	Gly	Leu	Lys	Ala	Ile
		100						105					110		

Pro	Ile	Val	Leu	Asp	Val	His	Asp	Val	Asp	Ala	Leu	Val	Glu	Thr	Ile
		115					120					125			

Ala	Ala	Ile	Ala	Pro	Ser	Phe	Gly	Ala	Ile	Asn	Leu	Glu	Asp	Ile	Ser
	130					135					140				

Ala	Pro	Arg	Cys	Phe	Glu	Val	Glu	Arg	Arg	Leu	Ile	Glu	Arg	Leu	Asp
145				150						155					160

Ile	Pro	Val	Met	His	Asp	Asp	Gln	His	Gly	Thr	Ala	Val	Val	Ile	Leu
			165						170					175	

Ala	Ala	Leu	Arg	Asn	Ser	Leu	Lys	Leu	Leu	Asp	Arg	Lys	Ile	Glu	Asp
		180						185					190		

Leu	Lys	Ile	Val	Ile	Ser	Gly	Ala	Gly	Ala	Ala	Gly	Val	Ala	Ala	Val
	195					200						205			

Asp	Met	Leu	Thr	Asn	Ala	Gly	Ala	Thr	Asp	Ile	Val	Val	Leu	Asp	Ser
	210					215					220				

Arg	Gly	Ile	Ile	His	Asp	Ser	Arg	Glu	Asp	Leu	Ser	Pro	Val	Lys	Ala
225				230						235					240

Ala	Leu	Ala	Glu	Lys	Thr	Asn	Pro	Arg	Gly	Ile	Ser	Gly	Gly	Ile	Asn
			245						250					255	

Glu	Ala	Phe	Thr	Gly	Ala	Asp	Leu	Phe	Ile	Gly	Val	Ser	Gly	Gly	Asn
		260						265					270		

Ile	Gly	Glu	Asp	Ala	Leu	Lys	Leu	Met	Ala	Pro	Glu	Pro	Ile	Leu	Phe
	275						280					285			

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys  
 290 295 300  
 Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile  
 305 310 315 320  
 Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala  
 325 330 335  
 Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln  
 340 345 350  
 Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu  
 355 360 365  
 Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg  
 370 375 380  
 Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser  
 385 390 395 400  
 Leu Pro Val Glu Ala Pro Ile Phe  
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<210> 579  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> FRXA01048

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 1 5 10 15  
 att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96  
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu  
 20 25 30  
 atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144  
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr  
 35 40 45  
 tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192  
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro  
 50 55 60  
 caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240  
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu  
 65 70 75 80  
 aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288  
 Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe  
 85 90 95

taagagcaaa cttgaggccc aca

311

<210> 580

<211> 96

<212> PRT

<213> Corynebacterium glutamicum

<400> 580

Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly  
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Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu  
20 25 30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr  
35 40 45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro  
50 55 60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu  
65 70 75 80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe  
85 90 95

<210> 581

<211> 1063

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1063)

<223> FRXA00290

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gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115  
Met Thr Ile Asp Leu  
1 5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163  
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His  
10 15 20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211  
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met  
25 30 35

cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259  
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu  
40 45 50

gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307

Ala	Ile	Lys	Glu	Asp	Pro	Glu	Val	Ala	Arg	Thr	His	Thr	Gly	Ile	Gly		
55						60					65						
aac	acc	gtc	gcg	gtt	att	tcc	gac	ggc	acc	gct	gtt	ctt	ggc	ctt	ggc	355	
Asn	Thr	Val	Ala	Val	Ile	Ser	Asp	Gly	Thr	Ala	Val	Leu	Gly	Leu	Gly	85	
70					75				80								
gat	atc	gga	cct	cag	gcc	tcc	ctt	ccc	gtc	atg	gag	ggc	aag	gct	cag	403	
Asp	Ile	Gly	Pro	Gln	Ala	Ser	Leu	Pro	Val	Met	Glu	Gly	Lys	Ala	Gln	100	
				90				95									
ctg	ttt	agc	tct	ttc	gct	ggc	ctg	aag	gct	atc	cct	atc	gtt	ttg	gac	451	
Leu	Phe	Ser	Ser	Phe	Ala	Gly	Leu	Lys	Ala	Ile	Pro	Ile	Val	Leu	Asp	115	
			105				110										
gtt	cac	gat	gtt	gac	gct	ttg	gtt	gag	acc	atc	gca	gcc	atc	gcg	cct	499	
Val	His	Asp	Val	Asp	Ala	Leu	Val	Glu	Thr	Ile	Ala	Ala	Ile	Ala	Pro	130	
			120				125										
tct	ttc	ggg	gct	atc	aac	ttg	gag	gac	atc	tcc	gct	cct	cgt	tgc	ttc	547	
Ser	Phe	Gly	Ala	Ile	Asn	Leu	Glu	Asp	Ile	Ser	Ala	Pro	Arg	Cys	Phe	145	
	135					140											
gag	gtg	gag	cgc	cgc	ctc	atc	gag	cggt	ctc	gat	att	cca	gtt	atg	cac	595	
Glu	Val	Glu	Arg	Arg	Leu	Ile	Glu	Arg	Leu	Asp	Ile	Pro	Val	Met	His	165	
	150				155					160							
gat	gac	cag	cac	ggc	acc	gct	gtg	gtt	atc	ctc	gct	gcg	ctg	cggt	aac	643	
Asp	Asp	Gln	His	Gly	Thr	Ala	Val	Val	Ile	Leu	Ala	Ala	Leu	Arg	Asn	180	
				170					175								
tcc	ctg	aag	ctg	ctg	gat	cggt	aag	atc	gaa	gac	ctc	aag	att	gtt	att	691	
Ser	Leu	Lys	Leu	Leu	Asp	Arg	Lys	Ile	Glu	Asp	Leu	Lys	Ile	Val	Ile	195	
			185					190									
tcc	ggc	gca	ggc	gca	gcg	ggc	gtt	gca	gct	gta	gat	atg	ctg	acc	aac	739	
Ser	Gly	Ala	Gly	Ala	Ala	Gly	Val	Ala	Ala	Val	Asp	Met	Leu	Thr	Asn	210	
		200					205										
gct	gga	gca	acc	gac	atc	gtg	gtt	ctt	gat	tcc	cga	ggc	atc	atc	cac	787	
Ala	Gly	Ala	Thr	Asp	Ile	Val	Val	Leu	Asp	Ser	Arg	Gly	Ile	Ile	His	225	
			215				220										
gac	agc	cgt	gag	gat	ctt	tcc	cca	gtt	aag	gct	gct	ctt	gca	gag	aag	835	
Asp	Ser	Arg	Glu	Asp	Leu	Ser	Pro	Val	Lys	Ala	Ala	Leu	Ala	Glu	Lys	245	
					235					240							
acc	aac	cct	cgt	ggc	atc	agc	ggg	ggc	atc	aat	gag	gct	ttc	acc	ggc	883	
Thr	Asn	Pro	Arg	Gly	Ile	Ser	Gly	Gly	Ile	Asn	Glu	Ala	Phe	Thr	Gly	260	
				250					255								
gcg	gac	ctg	ttc	att	ggc	gtg	tcc	ggc	ggc	aac	atc	ggc	gag	gac	gct	931	
Ala	Asp	Leu	Phe	Ile	Gly	Val	Ser	Gly	Gly	Asn	Ile	Gly	Glu	Asp	Ala	275	
			265					270									
ctc	aaa	ctc	atg	gcc	ccg	gag	cca	atc	ctg	ttc	acc	ctg	gcg	aac	cca	979	
Leu	Lys	Leu	Met	Ala	Pro	Glu	Pro	Ile	Leu	Phe	Thr	Leu	Ala	Asn	Pro	290	
			280				285										
acc	cca	gag	atc	gat	cct	gag	ctg	tct	cag	aag	tac	ggc	gcc	atc	gtc	1027	
Thr	Pro	Glu	Ile	Asp	Pro	Glu	Leu	Ser	Gln	Lys	Tyr	Gly	Ala	Ile	Val		



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 <213> Corynebacterium glutamicum

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 Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val  
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 Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr  
 50 55 60  
 His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala  
 65 70 75 80  
 Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met  
 85 90 95  
 Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile  
 100 105 110  
 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile  
 115 120 125  
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser  
 130 135 140  
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp  
 145 150 155 160  
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu  
 165 170 175  
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp  
 180 185 190  
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val  
 195 200 205  
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser  
 210 215 220  
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala  
 225 230 235 240  
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn  
 245 250 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn  
 260 265 270  
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 275 280 285  
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 Ser

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 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala  
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 gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag 144  
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu  
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 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp  
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 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu  
 85 90 95  
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 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly  
 100 105 110  
 acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc 384  
 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly  
 115 120 125  
 gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc 432  
 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala

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Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu			
145	150	155	160
cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct			528
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala			
	165	170	175
act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac			576
Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn			
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ggt cca			582
Val Pro			

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 35 40 45  
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu  
 50 55 60  
 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp  
 65 70 75 80  
 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu  
 85 90 95  
 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly  
 100 105 110  
 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly  
 115 120 125  
 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala  
 130 135 140  
 Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu  
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 Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala  
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 180 185 190

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<213> Corynebacterium glutamicum

<400> 586

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Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile
          35          40          45

Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly
          50          55          60

Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr
          65          70          75          80

Val Pro Gly Ser Thr Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn
          85          90          95

Arg Arg Ala Val Thr Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr
          100          105          110

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Val Ser Arg Leu Pro Glu Ala Pro Lys Glu Asn
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<222> (101)..(1660)

<223> RXN00389

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tctggcgcag gttcctaccg ccttcagttg aggtgaaagc atg atc acc gca acc 115
                                     Met Ile Thr Ala Thr
                                     1          5

gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
          10          15          20

aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
          25          30          35

cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259
Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu Arg Ala Ala Thr Thr
          40          45          50

tcg gcg aag cga gct ttt gaa agc tac cga ctc act act cca gag gtt 307

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Arg	Ala	Asp	Phe	Leu	Asp	Ser	Ile	Ala	Asp	Asn	Ile	Asp	Ala	Leu	Ser	85	
70					75					80							
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Gly	Glu	Ile	Val	Gln	Arg	Ala	Ser	Leu	Glu	Thr	Gly	Leu	Gly	Thr	Thr		
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cga	ctc	aca	ggc	gaa	gta	gcc	cgc	acc	agc	aac	cag	ctc	cgc	ctg	ttt	451	
Arg	Leu	Thr	Gly	Glu	Val	Ala	Arg	Thr	Ser	Asn	Gln	Leu	Arg	Leu	Phe		
			105					110					115				
gca	gaa	acc	gtg	aga	agc	gga	cag	ttc	cac	cga	gta	cgc	att	gaa	cga	499	
Ala	Glu	Thr	Val	Arg	Ser	Gly	Gln	Phe	His	Arg	Val	Arg	Ile	Glu	Arg		
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gga	ccg	cgg	att	gat	ctt	cgc	cag	cgt	cag	ggt	ccg	ttg	gga	cca	gtc	547	
Gly	Pro	Arg	Ile	Asp	Leu	Arg	Gln	Arg	Gln	Val	Pro	Leu	Gly	Pro	Val		
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gcg	gta	ttc	ggg	gca	agc	aac	ttc	ccc	gtc	gct	ttc	tct	act	gct	ggc	595	
Ala	Val	Phe	Gly	Ala	Ser	Asn	Phe	Pro	Val	Ala	Phe	Ser	Thr	Ala	Gly		
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ggc	gat	aca	gca	tca	gcg	ttg	gct	gca	ggc	tgc	cct	gtg	ggt	ttt	aag	643	
Gly	Asp	Thr	Ala	Ser	Ala	Leu	Ala	Ala	Gly	Cys	Pro	Val	Val	Phe	Lys		
				170					175					180			
gcg	cat	aat	gcg	cac	cct	gga	aca	gct	gag	ctc	gtc	ggg	caa	gcg	gtg	691	
Ala	His	Asn	Ala	His	Pro	Gly	Thr	Ala	Glu	Leu	Val	Gly	Gln	Ala	Val		
			185					190					195				
cgg	gga	gcc	gtc	gaa	aag	cat	gag	ttt	gat	gct	ggc	gtg	ttt	aac	ctt	739	
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu		
		200					205					210					
gtc	tac	ggc	cgt	ggc	gtg	gaa	att	ggc	cag	gag	ctg	gct	gcg	gat	ccg	787	
Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro		
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aat	atc	acg	gca	atc	ggt	ttt	acc	ggt	tca	cgc	cag	ggt	ggt	ttg	gca	835	
Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala		
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ctg	tca	cag	act	gcg	ttt	agc	cgc	cca	ggt	ccc	ggt	cca	gtc	ttt	gca	883	
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala		
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gaa	atg	agt	gcc	acc	aac	cct	gtg	ttc	gtc	ttc	ccc	ggc	gcg	ctg	gcg	931	
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala		
			265				270						275				
gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcg	ttt	acc	gct	tcc	gtc	979	
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val		
		280					285					290					
acc	ggc	agt	tcc	ggg	caa	ttg	tgc	acc	aag	cct	ggc	ctc	ggt	ttc	atc	1027	
Thr	Gly	Ser	Ser	Gly	Gln	Leu	Cys	Thr	Lys	Pro	Gly	Leu	Val	Phe	Ile		

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Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys			
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Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln			
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gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa			1171
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys			
	345	350	355
atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg			1219
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro			
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gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg			1267
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu			
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cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc			1315
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser			
390	395	400	405
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca			1363
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr			
	410	415	420
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt			1411
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu			
	425	430	435
atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg			1459
Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp			
	440	445	450
cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat			1507
Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr			
	455	460	465
ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc			1555
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile			
470	475	480	485
gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg			1603
Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu			
	490	495	500
ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa			1651
Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu			
	505	510	515
ata gac cgt taatagctgg tctttacatt tgc			1683
Ile Asp Arg			
520			

&lt;210&gt; 588

&lt;211&gt; 520

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 588

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      20           25           30

Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
      35           40           45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
      50           55           60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
 65           70           75           80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
      85           90           95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
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Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
     115           120           125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
     130           135           140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
    145           150           155           160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
     165           170           175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
     180           185           190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
     195           200           205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
     210           215           220

Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
    225           230           235           240

Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
     245           250           255

Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
     260           265           270

Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
     275           280           285

Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
     290           295           300

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Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala  
 305 310 315 320  
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr  
 325 330 335  
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala  
 340 345 350  
 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu  
 355 360 365  
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu  
 370 375 380  
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val  
 385 390 395 400  
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu  
 405 410 415  
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln  
 420 425 430  
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val  
 435 440 445  
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile  
 450 455 460  
 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val  
 465 470 475 480  
 Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr  
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 Val Val Gly Thr Ala  
 1 5  
 cat tgc gaa tca gca ctt aag gaa gtg act ttg atg tca aac gtt gga 163

His	Cys	Glu	Ser	Ala	Leu	Lys	Glu	Val	Thr	Leu	Met	Ser	Asn	Val	Gly	
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Lys	Pro	Arg	Thr	Ala	Gln	Glu	Ile	Gln	Gln	Asp	Trp	Asp	Thr	Asn	Pro	
			25					30					35			
cgt	tgg	aac	ggc	atc	acc	cgc	gac	tac	acc	gca	gac	cag	gta	gct	gat	259
Arg	Trp	Asn	Gly	Ile	Thr	Arg	Asp	Tyr	Thr	Ala	Asp	Gln	Val	Ala	Asp	
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ctg	cag	ggc	tcc	gtc	atc	gag	gag	cac	act	ctt	gct	cgc	cgc	ggc	tca	307
Leu	Gln	Gly	Ser	Val	Ile	Glu	Glu	His	Thr	Leu	Ala	Arg	Arg	Gly	Ser	
	55					60					65					
gag	atc	ctc	tgg	gac	gca	gtc	acc	cag	gaa	ggc	gac	gga	tac	atc	aac	355
Glu	Ile	Leu	Trp	Asp	Ala	Val	Thr	Gln	Glu	Gly	Asp	Gly	Tyr	Ile	Asn	
	70				75					80					85	
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ggc	ctg	aag	gct	gtc	tac	ctg	tcc	ggc	tgg	cag	gtc	gca	ggc	gac	gcc	451
Gly	Leu	Lys	Ala	Val	Tyr	Leu	Ser	Gly	Trp	Gln	Val	Ala	Gly	Asp	Ala	
			105					110					115			
aac	ctc	tcc	ggc	cac	acc	tac	cct	gac	cag	tcc	ctc	tac	cca	gcg	aac	499
Asn	Leu	Ser	Gly	His	Thr	Tyr	Pro	Asp	Gln	Ser	Leu	Tyr	Pro	Ala	Asn	
		120					125					130				
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Ser	Val	Pro	Ser	Val	Val	Arg	Arg	Ile	Asn	Asn	Ala	Leu	Leu	Arg	Ser	
	135					140					145					
gat	gaa	atc	gca	cgc	acc	gaa	ggc	gac	acc	tcc	gtt	gac	aac	tgg	gtt	595
Asp	Glu	Ile	Ala	Arg	Thr	Glu	Gly	Asp	Thr	Ser	Val	Asp	Asn	Trp	Val	
	150				155					160					165	
gtc	cca	atc	gtc	gcg	gac	ggc	gaa	gct	ggc	ttc	ggc	gga	gca	ctc	aac	643
Val	Pro	Ile	Val	Ala	Asp	Gly	Glu	Ala	Gly	Phe	Gly	Gly	Ala	Leu	Asn	
				170					175					180		
gtc	tac	gaa	ctc	cag	aag	gca	atg	atc	gca	gct	ggc	gct	gca	ggc	acc	691
Val	Tyr	Glu	Leu	Gln	Lys	Ala	Met	Ile	Ala	Ala	Gly	Ala	Ala	Gly	Thr	
		185					190					195				
cac	tgg	gaa	gac	cag	ctc	gct	tct	gaa	aag	aag	tgt	ggc	cac	ctc	ggc	739
His	Trp	Glu	Asp	Gln	Leu	Ala	Ser	Glu	Lys	Lys	Cys	Gly	His	Leu	Gly	
		200					205					210				
ggc	aag	gtt	ctg	atc	cca	acc	cag	cag	cac	atc	cgc	acc	ctg	aac	tct	787
Gly	Lys	Val	Leu	Ile	Pro	Thr	Gln	Gln	His	Ile	Arg	Thr	Leu	Asn	Ser	
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gcc	cgc	ctt	gca	gca	gac	gtt	gca	aac	acc	cca	act	gtt	gtt	atc	gca	835
Ala	Arg	Leu	Ala	Ala	Asp	Val	Ala	Asn	Thr	Pro	Thr	Val	Val	Ile	Ala	
	230				235					240					245	
cgt	acc	gac	gct	gag	gca	gca	acc	ctg	atc	acc	tct	gac	gtt	gat	gag	883
Arg	Thr	Asp	Ala	Glu	Ala	Ala	Thr	Leu	Ile	Thr	Ser	Asp	Val	Asp	Glu	

250								255								260															
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Arg	Asp	Gln	Pro	Phe	Ile	Thr	Gly	Glu	Arg	Thr	Ala	Glu	Gly	Tyr	Tyr																
265								270								275															
cac	gtc	aag	aat	ggt	ctc	gag	cca	tgt	atc	gca	cgt	gca	aag	tcc	tac	979															
His	Val	Lys	Asn	Gly	Leu	Glu	Pro	Cys	Ile	Ala	Arg	Ala	Lys	Ser	Tyr																
280								285								290															
gca	cca	tac	gca	gat	atg	atc	tgg	atg	gag	acc	ggc	acc	cct	gac	ctg	1027															
Ala	Pro	Tyr	Ala	Asp	Met	Ile	Trp	Met	Glu	Thr	Gly	Thr	Pro	Asp	Leu																
295								300								305															
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Glu	Leu	Ala	Lys	Lys	Phe	Ala	Glu	Gly	Val	Arg	Ser	Glu	Phe	Pro	Asp																
310								315								320								325							
cag	ctg	ctg	tcc	tac	aac	tgc	tcc	cca	tcc	ttc	aac	tgg	tct	gca	cac	1123															
Gln	Leu	Leu	Ser	Tyr	Asn	Cys	Ser	Pro	Ser	Phe	Asn	Trp	Ser	Ala	His																
330								335								340															
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Leu	Glu	Ala	Asp	Glu	Ile	Ala	Lys	Phe	Gln	Lys	Glu	Leu	Gly	Ala	Met																
345								350								355															
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Gly	Phe	Lys	Phe	Gln	Phe	Ile	Thr	Leu	Ala	Gly	Phe	His	Ser	Leu	Asn																
360								365								370															
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Tyr	Gly	Met	Phe	Asp	Leu	Ala	Tyr	Gly	Tyr	Ala	Arg	Glu	Gly	Met	Thr																
375								380								385															
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Ser	Phe	Val	Asp	Leu	Gln	Asn	Arg	Glu	Phe	Lys	Ala	Ala	Glu	Glu	Arg																
390								395								400								405							
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Gly	Phe	Thr	Ala	Val	Lys	His	Gln	Arg	Glu	Val	Gly	Ala	Gly	Tyr	Phe																
410								415								420															
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Asp	Gln	Ile	Ala	Thr	Thr	Val	Asp	Pro	Asn	Ser	Ser	Thr	Thr	Ala	Leu																
425								430								435															
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Lys	Gly	Ser	Thr	Glu	Glu	Gly	Gln	Phe	His	Asn																					
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aat																1467															

&lt;210&gt; 590

&lt;211&gt; 448

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 590

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 Trp Asp Thr Asn Pro Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala  
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 Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu  
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 Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly  
 65 70 75 80  
 Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val  
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 Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln  
 100 105 110  
 Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser  
 115 120 125  
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 130 135 140  
 Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser  
 145 150 155 160  
 Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe  
 165 170 175  
 Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala  
 180 185 190  
 Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys  
 195 200 205  
 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile  
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 Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro  
 225 230 235 240  
 Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr  
 245 250 255  
 Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr  
 260 265 270  
 Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala  
 275 280 285  
 Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr  
 290 295 300  
 Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg  
 305 310 315 320  
 Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe  
 325 330 335



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90 95 100	
aac ctc tcc ggc cac acc tac cct gac cag tcc ctc tac cca gcg aac Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn	451
105 110 115	
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120 125 130	
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135 140 145	
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150 155 160 165	
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170 175 180	
cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly	691
185 190 195	
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200 205 210	
gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala	787
215 220 225	
cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu	835
230 235 240 245	
cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr	883
250 255 260	
cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr	931
265 270 275	
gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu	979
280 285 290	
gag ctc gct aag aag ttc gct gaa ggc gtt cgc tct gag ttc cca gac Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp	1027
295 300 305	
cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His	1075
310 315 320 325	

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 Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met  
 330 335 340  
  
 ggc ttc aag ttc cag ttc atc acc ctc gca ggc ttc cac tcc ctc aac 1171  
 Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn  
 345 350 355  
  
 tac ggc atg ttc gac ctg gct tac gga tac gct cgc gaa ggc atg acc 1219  
 Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr  
 360 365 370  
  
 tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt 1267  
 Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg  
 375 380 385  
  
 ggc ttc acc gct gtt aag cac cag cgt gag gtt ggc gca ggc tac ttc 1315  
 Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe  
 390 395 400 405  
  
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 Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu  
 410 415 420  
  
 aag ggt tcc act gaa gaa ggc cag ttc cac aac taggacctac aggttctgac 1416  
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 aat 1419

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 Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu  
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 Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly  
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 Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val  
 65 70 75 80  
  
 Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln  
 85 90 95  
  
 Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser  
 100 105 110  
  
 Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn  
 115 120 125

Ala	Leu	Leu	Arg	Ser	Asp	Glu	Ile	Ala	Arg	Thr	Glu	Gly	Asp	Thr	Ser	130	135	140
Val	Asp	Asn	Trp	Val	Val	Pro	Ile	Val	Ala	Asp	Gly	Glu	Ala	Gly	Phe	145	150	155
Gly	Gly	Ala	Leu	Asn	Val	Tyr	Glu	Leu	Gln	Lys	Ala	Met	Ile	Ala	Ala	165	170	175
Gly	Ala	Ala	Gly	Thr	His	Trp	Glu	Asp	Gln	Leu	Ala	Ser	Glu	Lys	Lys	180	185	190
Cys	Gly	His	Leu	Gly	Gly	Lys	Val	Leu	Ile	Pro	Thr	Gln	Gln	His	Ile	195	200	205
Arg	Thr	Leu	Asn	Ser	Ala	Arg	Leu	Ala	Ala	Asp	Val	Ala	Asn	Thr	Pro	210	215	220
Thr	Val	Val	Ile	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Ala	Thr	Leu	Ile	Thr	225	230	235
Ser	Asp	Val	Asp	Glu	Arg	Asp	Gln	Pro	Phe	Ile	Thr	Gly	Glu	Arg	Thr	245	250	255
Ala	Glu	Gly	Tyr	Tyr	His	Val	Lys	Asn	Gly	Leu	Glu	Pro	Cys	Ile	Ala	260	265	270
Arg	Ala	Lys	Ser	Tyr	Ala	Pro	Tyr	Ala	Asp	Met	Ile	Trp	Met	Glu	Thr	275	280	285
Gly	Thr	Pro	Asp	Leu	Glu	Leu	Ala	Lys	Lys	Phe	Ala	Glu	Gly	Val	Arg	290	295	300
Ser	Glu	Phe	Pro	Asp	Gln	Leu	Leu	Ser	Tyr	Asn	Cys	Ser	Pro	Ser	Phe	305	310	315
Asn	Trp	Ser	Ala	His	Leu	Glu	Ala	Asp	Glu	Ile	Ala	Lys	Phe	Gln	Lys	325	330	335
Glu	Leu	Gly	Ala	Met	Gly	Phe	Lys	Phe	Gln	Phe	Ile	Thr	Leu	Ala	Gly	340	345	350
Phe	His	Ser	Leu	Asn	Tyr	Gly	Met	Phe	Asp	Leu	Ala	Tyr	Gly	Tyr	Ala	355	360	365
Arg	Glu	Gly	Met	Thr	Ser	Phe	Val	Asp	Leu	Gln	Asn	Arg	Glu	Phe	Lys	370	375	380
Ala	Ala	Glu	Glu	Arg	Gly	Phe	Thr	Ala	Val	Lys	His	Gln	Arg	Glu	Val	385	390	395
Gly	Ala	Gly	Tyr	Phe	Asp	Gln	Ile	Ala	Thr	Thr	Val	Asp	Pro	Asn	Ser	405	410	415
Ser	Thr	Thr	Ala	Leu	Lys	Gly	Ser	Thr	Glu	Glu	Gly	Gln	Phe	His	Asn	420	425	430



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 Met Thr Glu Gln Glu  
 1 5  
 ctg ttg tct gct cag act gcc gac aac gct gga act gac agc acc gaa 163  
 Leu Leu Ser Ala Gln Thr Ala Asp Asn Ala Gly Thr Asp Ser Thr Glu  
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 Arg Val Asp Ala Gly Gly Met Gln Val Ala Lys Val Leu Tyr Asp Phe  
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 Val Thr Glu Ala Val Leu Pro Arg Val Gly Val Asp Ala Glu Lys Phe  
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 Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg  
 55 60 65  
 gag ctg ctt gct cgc cgc gat gaa ctg cag atg ctt atc gac gac tac 355  
 Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr  
 70 75 80 85  
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 His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe  
 90 95 100  
 ctc aaa gaa atc gga tac ttg gtt gag gag cca gaa gct gca gaa atc 451  
 Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro Glu Ala Ala Glu Ile  
 105 110 115  
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 Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln  
 120 125 130  
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 135 140 145  
 gct cgc tgg ggt tcc ctc tac gat gcg ttg tac ggc acc aac gcc atc 595  
 Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile  
 150 155 160 165  
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 Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg  
 170 175 180

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cct gtc cac cca atc ggc aag gca gac aag act ggt ctc aaa gac atc Pro Val His Pro Ile Gly Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile 265 270 275	931
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acc aac gag ctc ttc ggc cgc gtt gag gat ctg ctt gat ctg cca cgc	1411

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Asn	Leu	Asp	Ala	Ser	Ile	Met	Glu	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile		
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470					475					480					485		
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Lys	Gln	Ala	Tyr	Glu	Asn	Asn	Asn	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly		
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Leu	Pro	Gly	Lys	Ala	Gln	Ile	Gly	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu		
		520					525					530					
ctc	atg	gca	gaa	atg	ctg	gag	aag	aag	atc	ggc	cag	cca	cgc	gaa	ggc	1747	
Leu	Met	Ala	Glu	Met	Leu	Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly		
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Ala	Asn	Thr	Ala	Trp	Val	Pro	Ser	Pro	Thr	Gly	Ala	Thr	Leu	His	Ala		
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acg	cac	tac	cac	ttg	gtt	gat	gtg	ttc	aag	gtt	caa	gac	gaa	ctg	cgt	1843	
Thr	His	Tyr	His	Leu	Val	Asp	Val	Phe	Lys	Val	Gln	Asp	Glu	Leu	Arg		
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gct	gcc	ggc	cgc	cgc	gac	agc	ctg	cgc	aac	att	ctc	acc	att	tca	acc	1891	
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Asn	Asn	Cys	Gln	Ser	Ile	Leu	Gly	Tyr	Val	Val	Arg	Trp	Val	Glu	His		
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Gly	Val	Gly	Cys	Ser	Lys	Val	Pro	Asp	Ile	His	Asp	Ile	Asp	Leu	Met		
630					635					640					645		
gaa	gac	cgc	gca	acg	ctg	cgt	att	tcc	tcg	cag	atg	ctg	gcc	aac	tgg	2083	
Glu	Asp	Arg	Ala	Thr	Leu	Arg	Ile	Ser	Ser	Gln	Met	Leu	Ala	Asn	Trp		
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atc	cgc	cat	gat	gtt	gtc	tcg	aag	gag	cag	gtc	ttg	gag	tca	ctg	gaa	2131	
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665										670					675					
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Pro	Ile	Leu	His	Ala	Arg	Arg	Arg	Glu	Phe	Lys	Ala	Lys	Asn							
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 Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu  
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Phe	Leu	Asp	Pro	Glu	Ala	Ile	Leu	Leu	Glu	Thr	Asn	Gly	Leu	His	Ile
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Glu	Leu	Gln	Ile	Asp	Pro	Val	His	Pro	Ile	Gly	Lys	Ala	Asp	Lys	Thr
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Gly	Leu	Lys	Asp	Ile	Val	Leu	Glu	Ser	Ala	Ile	Thr	Thr	Ile	Met	Asp
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Phe	Glu	Asp	Ser	Val	Ala	Ala	Val	Asp	Ala	Glu	Asp	Lys	Thr	Leu	Gly
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Ser	Lys	Asn	Gly	Arg	Ile	Phe	Thr	Arg	Glu	Leu	Asn	Lys	Asp	Arg	Val
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Ser	Arg	Lys	Gly	Ser	Ile	Tyr	Ile	Val	Lys	Pro	Lys	Gln	His	Gly	Pro
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Glu	Glu	Val	Ala	Phe	Thr	Asn	Glu	Leu	Phe	Gly	Arg	Val	Glu	Asp	Leu
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Ile	His	Thr	Ser	Met	Glu	Ala	Gly	Ala	Met	Val	Arg	Lys	Ala	Asp	Met
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Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala	
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Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg	
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Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly	
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Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr	
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Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp	
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Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu	
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Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu	
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tac gat gcg ttg tac ggc acc aac gcc atc cca gaa act gat ggc gct	432
Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala	
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Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu	
145 150 155 160	
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Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser	
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cat gcc gat gtt gag aag tac aac atc acc gat gga aag ctt gca gcc	576
His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala	
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cac att gga gat agc gtc tac cga ctg aaa aac cgt gaa tcc tac cgt	624
His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg	
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Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr	
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Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly	
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Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile	
245 250 255	

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Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu	
260 265 270	
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Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu	
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Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu	
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Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu	
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His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln	
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Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met	
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Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln	
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Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro	
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Arg Val Glu Asp Leu Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly	
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Val Met Asp Glu Glu Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile	
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Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu Ala Gly Ala Met Val	
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Arg Lys Ala Asp Met Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn	
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Asn Asn Val Asp Ala Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln	
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Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly	Ala	Asn	Thr	Ala	Trp	Val		
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cct	tca	cca	act	ggt	gcg	acg	ctg	cac	gca	acg	cac	tac	cac	ttg	gtt	1632	
Pro	Ser	Pro	Thr	Gly	Ala		Leu	His	Ala	Thr	His	Tyr	His	Leu	Val		
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Ser	Leu	Arg	Asn	Ile	Leu	Thr	Ile	Ser	Thr	Ala	Pro	Asn	Thr	Asn	Trp		
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Ser	Glu	Glu	Glu	Lys	Lys	Glu	Glu	Met	Asp	Asn	Asn	Cys	Gln	Ser	Ile		
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ctc	gga	tac	gtt	gtg	cgc	tgg	gtt	gag	cac	ggt	gtt	ggt	tgc	tcc	aag	1824	
Leu	Gly	Tyr	Val	Val	Arg	Trp	Val	Glu	His	Gly	Val	Gly	Cys	Ser	Lys		
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Val	Pro	Asp	Ile	His	Asp	Ile	Asp	Leu	Met	Glu	Asp	Arg	Ala	Thr	Leu		
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Ser	Lys	Glu	Gln	Val	Leu	Glu	Ser	Leu	Glu	Arg	Met	Ala	Val	Val	Val		
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gac	aag	caa	aat	gcg	ggc	gac	gag	gcc	tac	cgc	gat	atg	gcg	ccg	aag	2016	
Asp	Lys	Gln	Asn	Ala	Gly	Asp	Glu	Ala	Tyr	Arg	Asp	Met	Ala	Pro	Lys		
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Tyr	Asp	Ala	Ser	Leu	Ala	Phe	Gln	Ala	Ala	Lys	Asp	Leu	Ile	Phe	Glu		
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ggc	acc	aag	tcc	cca	tcg	ggc	tac	acc	gag	ccc	atc	ttg	cac	gca	cgc	2112	
Gly	Thr	Lys	Ser	Pro	Ser	Gly	Tyr	Thr	Glu	Pro	Ile	Leu	His	Ala	Arg		
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cgc	cgc	gag	ttc	aaa	gca	aaa	aac	taagc	cgcgt	tttcg	acgct	tac				2159	
Arg	Arg	Glu	Phe	Lys	Ala	Lys	Asn										
705					710												

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&lt;211&gt; 712

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 596

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 Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly  
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 Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr  
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 Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp  
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 Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu  
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 Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu  
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 Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala  
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 Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu  
 145 150 155 160  
 Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser  
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 His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala  
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 His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg  
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 Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr  
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 Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly  
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 Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile  
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 Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu  
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 Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu  
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 Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu  
 305 310 315 320

His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln  
 325 330 335  
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 Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro  
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 Lys Gln His Gly Pro Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly  
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 Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu Ala Gly Ala Met Val  
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 Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val  
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 Pro Ser Pro Thr Gly Ala Thr Leu His Ala Thr His Tyr His Leu Val  
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 Val Pro Asp Ile His Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu  
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Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys					
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Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu					
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Arg Arg Glu Phe Lys Ala Lys Asn					
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 Ala Asn Leu Ser Leu Thr Phe Thr Glu Leu Asp Phe Leu Asp Arg Phe  
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 Asp Ala Ala Ser Lys His Ala Phe Ser Ala Val Glu Phe Gln Tyr Pro  
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 tac gat ttc gat gtt caa gag att aaa cag cgt gct gat tcc gca ggt 259  
 Tyr Asp Phe Asp Val Gln Glu Ile Lys Gln Arg Ala Asp Ser Ala Gly  
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 Leu Pro Ile Glu Leu Phe Asn Ala Pro Pro Gly Asp Thr Phe Gly Leu  
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 Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln Ser Ile Glu Gln Ala  
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 Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys Met His Val Met Ala  
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 Gly Ile Ala Asp Val Thr Ser Glu Thr Thr Ala Arg Tyr Val Glu Asn  
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Ile Arg Trp Ala Ala Gln Gln Leu Asp Lys Leu Asp Val Val Val Val  
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 Ile Glu Pro Ile Asn His Tyr Ser Val Pro Gly Tyr Phe Leu His Thr  
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 Leu Glu Gln Ala Tyr Trp Leu Ile Asp Ser Ile Ala His Pro Asn Val  
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 aag atc tta ttc gat act ttc cac ctt cag cag att cat ggc aat ctc 643  
 Lys Ile Leu Phe Asp Thr Phe His Leu Gln Gln Ile His Gly Asn Leu  
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 Thr Arg Arg Leu Arg Glu Val His Gly Ala Gly Leu Leu Gly His Val  
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 Gln Val Ala Ser Val Pro Asp Arg His Glu Pro Gly Thr Gly Glu Val  
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 Val Ile Ala Gly Glu Tyr His Pro Ala Gly Glu Thr Thr Ala Gly Leu  
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 Gly Trp Leu Glu Leu  
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 Glu Phe Gln Tyr Pro Tyr Asp Phe Asp Val Gln Glu Ile Lys Gln Arg  
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 Ala Asp Ser Ala Gly Leu Pro Ile Glu Leu Phe Asn Ala Pro Pro Gly  
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 Asp Thr Phe Gly Leu Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln  
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 Ser Ile Glu Gln Ala Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys  
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Ala	His	Pro	Asn	Val	Lys	Ile	Leu	Phe	Asp	Thr	Phe	His	Leu	Gln	Gln
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Ile	His	Gly	Asn	Leu	Thr	Arg	Arg	Leu	Arg	Glu	Val	His	Gly	Ala	Gly
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Leu	Leu	Gly	His	Val	Gln	Val	Ala	Ser	Val	Pro	Asp	Arg	His	Glu	Pro
	195						200					205			
Gly	Thr	Gly	Glu	Val	Asn	Ala	Ala	Tyr	Ile	Phe	Gln	Leu	Leu	Ser	Glu
	210					215					220				
Leu	Gly	Tyr	Asp	Gly	Val	Ile	Ala	Gly	Glu	Tyr	His	Pro	Ala	Gly	Glu
225					230					235					240
Thr	Thr	Ala	Gly	Leu	Gly	Trp	Leu	Glu	Leu						
				245				250							

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA01886

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 gcgcaaccat caaccttgct gaaagcatcg aggtttaacc atg act ttt aaa ctc 115  
 Met Thr Phe Lys Leu 5  
 gca gca tgc gca gag atg atc tac cag gac ctg cct ttc gag gag agg 163  
 Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu Pro Phe Glu Glu Arg 20  
 gtc aag acg atc tct gat cag gga ttc ctc gtg gaa att tgg gac tgg 211  
 Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val Glu Ile Trp Asp Trp 35  
 tcc aca aaa gac atc gat gcg ctc gtg gca aca ggc gcg gaa ttt tcc 259  
 Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr Gly Ala Glu Phe Ser 50  
 tcc atg acg ggc tac ctg cgc ggg gat ctg att act gaa cag ggc cgc 307  
 Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile Thr Glu Gln Gly Arg

55	60	65	
gcg gag ctc ttg gca acc gct tgc gag tcc ttg gcg gtg gcg gaa aag			355
Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu Ala Val Ala Glu Lys			
70	75	80	85
ctc aac tgc ccc cgg ctg aat ctg cat gga act ggc ctt gga ccg cag			403
Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr Gly Leu Gly Pro Gln			
	90	95	100
gga cta cct gtt act ccc att gaa gtg gtt acc cca gaa atg tgg ctc			451
Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr Pro Glu Met Trp Leu			
	105	110	115
tac gct gct gaa acg ctc cgc cag atc gct gag ctg ggg gag cgc gca			499
Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu Leu Gly Glu Arg Ala			
	120	125	130
ggc aag gtt ttc gtg ctg gaa aac ctc aac ctc gca gtc gat cac ccc			547
Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu Ala Val Asp His Pro			
	135	140	145
ggc act cct ttt gcc aag gcc act gac act ttg gcg ctg gtc aag gct			595
Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu Ala Leu Val Lys Ala			
	150	155	160
gtc aat cac ccg aat ctg cgc ctc aac ctg gat ttg tac cac gcc cag			643
Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp Leu Tyr His Ala Gln			
	170	175	180
att ggc gaa gga aac ctc att gag ctg ctc cgt gag gcg cag cca ttc			691
Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg Glu Ala Gln Pro Phe			
	185	190	195
atc ggc gaa atc cag gtt gcc gat gtc ccc ggc cgc atg gaa ccc ggc			739
Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly Arg Met Glu Pro Gly			
	200	205	210
acc ggc gag atc aac tac cag ggc gtc gcg aaa gct ctc gcc gcg atg			787
Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys Ala Leu Ala Ala Met			
	215	220	225
ggc tac gac ggc gtc atc ggc atg gag gcg tgg gca tgc ggc gac tcc			835
Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp Ala Ser Gly Asp Ser			
	230	235	240
agc gac gcg ctg cag gcg ttg aag tca gcg ttc acg gtc taaattgctt			884
Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe Thr Val			
	250	255	
atcgacgcac ccc			897

&lt;210&gt; 600

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 600

Met	Thr	Phe	Lys	Leu	Ala	Ala	Cys	Ala	Glu	Met	Ile	Tyr	Gln	Asp	Leu
1					5				10					15	

Pro Phe Glu Glu Arg Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val  
                   20                                  25                                  30  
 Glu Ile Trp Asp Trp Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr  
                   35                                  40                                  45  
 Gly Ala Glu Phe Ser Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile  
                   50                                  55                                  60  
 Thr Glu Gln Gly Arg Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu  
                   65                                  70                                  75                                  80  
 Ala Val Ala Glu Lys Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr  
                                   85                                  90                                  95  
 Gly Leu Gly Pro Gln Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr  
                                   100                                  105                                  110  
 Pro Glu Met Trp Leu Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu  
                   115                                  120                                  125  
 Leu Gly Glu Arg Ala Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu  
                   130                                  135                                  140  
 Ala Val Asp His Pro Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu  
                   145                                  150                                  155                                  160  
 Ala Leu Val Lys Ala Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp  
                                   165                                  170                                  175  
 Leu Tyr His Ala Gln Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg  
                                   180                                  185                                  190  
 Glu Ala Gln Pro Phe Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly  
                   195                                  200                                  205  
 Arg Met Glu Pro Gly Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys  
                   210                                  215                                  220  
 Ala Leu Ala Ala Met Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp  
                   225                                  230                                  235                                  240  
 Ala Ser Gly Asp Ser Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe  
                                   245                                  250                                  255  
 Thr Val

<210> 601  
 <211> 1575  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXN03117

<400> 601



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	Met Ile Thr His Glu	
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gtg cgc acc cac cgt tct gcg gaa gag ttc ccg tac aag aag cac ctg	103	
Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro Tyr Lys Lys His Leu		
	10 15 20	
gct cac aag atg gct cgc gtt gca gcc gac cca gtt gag gtt gct gcg	151	
Ala His Lys Met Ala Arg Val Ala Ala Asp Pro Val Glu Val Ala Ala		
	25 30 35	
gac act cag gaa atg atc atc acc cgc atc atc gac aat gca tcg gtg	199	
Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile Asp Asn Ala Ser Val		
	40 45 50	
cag gca gct tcc gtg ttg cgt cga cca gtt agc tct gcc cgt gcg atg	247	
Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser Ser Ala Arg Ala Met		
	55 60 65	
gca cag gtc agg cca gtt acc gat ggt cgg ggt gca tct gtt ttc ggt	295	
Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly Ala Ser Val Phe Gly		
	70 75 80 85	
ctg cca gga cgt tat gcc gcg gaa tgg gct gcg ctt gct aac ggc act	343	
Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala Leu Ala Asn Gly Thr		
	90 95 100	
gcg gtg cgt gag ctt gat ttc cat gac acg ttc ctc gct gcg gaa tac	391	
Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr		
	105 110 115	
tcc cac cca gga gat aac att cct ccg att ttg gct gca gca cag cag	439	
Ser His Pro Gly Asp Asn Ile Pro Pro Ile Leu Ala Ala Ala Gln Gln		
	120 125 130	
gct gga aaa ggt ggc aag gat ctg atc cgt ggc atc gct act ggg tat	487	
Ala Gly Lys Gly Gly Lys Asp Leu Ile Arg Gly Ile Ala Thr Gly Tyr		
	135 140 145	
gag att cag gtt aac ttg gtg cgt gga atg tgc ctg cat gag cac aag	535	
Glu Ile Gln Val Asn Leu Val Arg Gly Met Cys Leu His Glu His Lys		
	150 155 160 165	
att gat cac gtt gct cat ctt gga cca tca gcg gct gct ggt atc gga	583	
Ile Asp His Val Ala His Leu Gly Pro Ser Ala Ala Ala Gly Ile Gly		
	170 175 180	
acc ttg cta gac cta gat gtg gac acc atc tac cag gca att ggt cag	631	
Thr Leu Leu Asp Leu Asp Val Asp Thr Ile Tyr Gln Ala Ile Gly Gln		
	185 190 195	
gca ttg cac acc acc acg gcg acg agg cag tcc cgt aaa ggt gcg att	679	
Ala Leu His Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Ala Ile		
	200 205 210	
tct tca tgg aag gca ttt gct cct gcg ttt gcg ggc aag atg tcc atc	727	
Ser Ser Trp Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ser Ile		
	215 220 225	
gag gca gta gat cgc gca atg cgt ggc gag ggc gca ccg tca cca atc	775	

Glu 230	Ala	Val	Asp	Arg	Ala 235	Met	Arg	Gly	Glu	Gly 240	Ala	Pro	Ser	Pro	Ile 245	
tg	g	g	g	g	g	g	g	g	g	g	g	g	g	g	g	823
Trp	Glu	Gly	Glu	Asp	Gly	Val	Ile	Ala	Trp	Leu	Leu	Ser	Gly	Leu	Asp	
				250					255					260		
cac	atc	tac	acc	att	cct	ttg	cct	gca	gaa	ggt	gaa	gcc	aaa	cga	gca	871
His	Ile	Tyr		Ile	Pro	Leu	Pro	Ala	Glu	Gly	Glu	Ala	Lys	Arg	Ala	
			265					270					275			
atc	ttg	gat	acc	tac	acc	aag	gaa	cac	tcg	gcg	gaa	tac	cag	tca	cag	919
Ile	Leu	Asp	Thr	Tyr	Thr	Lys	Glu	His	Ser	Ala	Glu	Tyr	Gln	Ser	Gln	
		280					285					290				
gca	ccg	atc	gac	ttg	gcg	cgc	agc	atg	ggg	gag	aag	ctg	gca	gca	cag	967
Ala	Pro	Ile	Asp	Leu	Ala	Arg	Ser	Met	Gly	Glu	Lys	Leu	Ala	Ala	Gln	
	295					300					305					
ggc	ttg	gac	ctg	cgt	gat	gtg	gac	tcc	atc	gtt	ttg	cac	acc	tcc	cac	1015
Gly	Leu	Asp	Leu	Arg	Asp	Val	Asp	Ser	Ile	Val	Leu	His	Thr	Ser	His	
310				315					320						325	
cac	act	cac	tac	gtg	atc	ggc	acc	gga	tct	aat	gat	cca	cag	aag	ttc	1063
His	Thr	His	Tyr	Val	Ile	Gly	Thr	Gly	Ser	Asn	Asp	Pro	Gln	Lys	Phe	
				330				335						340		
gat	cca	gat	gca	tcg	cga	gaa	acc	ctt	gat	cac	tcc	atc	atg	tac	att	1111
Asp	Pro	Asp	Ala	Ser	Arg	Glu	Thr	Leu	Asp	His	Ser	Ile	Met	Tyr	Ile	
			345					350					355			
ttc	gct	gtc	gcg	ctg	aag	gat	cgc	gcg	tg	cac	cac	gag	cgt	tcc	tat	1159
Phe	Ala	Val	Ala	Leu	Lys	Asp	Arg	Ala	Trp	His	His	Glu	Arg	Ser	Tyr	
		360					365					370				
gct	cct	gag	cga	gcc	cac	cgc	cga	gag	acc	atc	gag	ctg	tg	aac	aag	1207
Ala	Pro	Glu	Arg	Ala	His	Arg	Arg	Glu	Thr	Ile	Glu	Leu	Trp	Asn	Lys	
	375					380					385					
att	tcc	acg	gtg	gag	gat	cct	gaa	tg	acc	agg	cgt	tac	cac	tcc	gtt	1255
Ile	Ser	Thr	Val	Glu	Asp	Pro	Glu	Trp	Thr	Arg	Arg	Tyr	His	Ser	Val	
390					395				400						405	
gat	cct	gca	gaa	aag	gcc	ttc	ggc	gca	cgc	gca	gtg	atc	acc	ttc	aag	1303
Asp	Pro	Ala	Glu	Lys	Ala	Phe	Gly	Ala	Arg	Ala	Val	Ile	Thr	Phe	Lys	
			410					415						420		
gat	gga	acc	gtc	gtg	gaa	gat	gaa	ctg	gct	gtg	gcg	aat	gcg	cat	cct	1351
Asp	Gly	Thr	Val	Val	Glu	Asp	Glu	Leu	Ala	Val	Ala	Asn	Ala	His	Pro	
			425					430					435			
ctg	gga	gca	cgg	cct	ttc	gct	agg	gag	cag	tac	att	cag	aaa	ttc	cgc	1399
Leu	Gly	Ala	Arg	Pro	Phe	Ala	Arg	Glu	Gln	Tyr	Ile	Gln	Lys	Phe	Arg	
		440					445					450				
acc	ttg	gct	gaa	ggt	gtt	gtg	tcc	gaa	aag	gaa	cag	gat	cgc	ttc	ttg	1447
Thr	Leu	Ala	Glu	Gly	Val	Val	Ser	Glu	Lys	Glu	Gln	Asp	Arg	Phe	Leu	
	455					460					465					
gat	gcg	gca	cag	cgt	acg	cac	gag	ctt	gag	gat	ctt	tca	gaa	ctc	aac	1495
Asp	Ala	Ala	Gln	Arg	Thr	His	Glu	Leu	Glu	Asp	Leu	Ser	Glu	Leu	Asn	

gga ctg ttc tgatggcggg tttgttttcc tct 1575  
Gly Leu Phe

<400> 602															
Met 1	Ile	Thr	His	Glu 5	Val	Arg	Thr	His	Arg 10	Ser	Ala	Glu	Glu	Phe 15	Pro
Tyr	Lys	Lys	His 20	Leu	Ala	His	Lys	Met 25	Ala	Arg	Val	Ala	Ala 30	Asp	Pro
Val	Glu	Val 35	Ala	Ala	Asp	Thr	Gln 40	Glu	Met	Ile	Ile	Thr 45	Arg	Ile	Ile
Asp	Asn 50	Ala	Ser	Val	Gln	Ala 55	Ala	Ser	Val	Leu	Arg 60	Arg	Pro	Val	Ser
Ser 65	Ala	Arg	Ala	Met	Ala 70	Gln	Val	Arg	Pro	Val 75	Thr	Asp	Gly	Arg	Gly 80
Ala	Ser	Val	Phe	Gly 85	Leu	Pro	Gly	Arg	Tyr 90	Ala	Ala	Glu	Trp	Ala 95	Ala
Leu	Ala	Asn	Gly 100	Thr	Ala	Val	Arg	Glu 105	Leu	Asp	Phe	His	Asp 110	Thr	Phe
Leu	Ala 115	Ala	Glu	Tyr	Ser	His	Pro 120	Gly	Asp	Asn	Ile	Pro 125	Pro	Ile	Leu
Ala 130	Ala	Ala	Gln	Gln	Ala	Gly 135	Lys	Gly	Gly	Lys	Asp 140	Leu	Ile	Arg	Gly
Ile 145	Ala	Thr	Gly	Tyr	Glu 150	Ile	Gln	Val	Asn 155	Leu	Val	Arg	Gly	Met	Cys 160
Leu	His	Glu	His	Lys 165	Ile	Asp	His	Val	Ala 170	His	Leu	Gly	Pro	Ser 175	Ala
Ala	Ala	Gly	Ile 180	Gly	Thr	Leu	Leu	Asp 185	Leu	Asp	Val	Asp	Thr 190	Ile	Tyr
Gln	Ala 195	Ile	Gly	Gln	Ala	Leu	His 200	Thr	Thr	Thr	Ala	Thr 205	Arg	Gln	Ser
Arg	Lys 210	Gly	Ala	Ile	Ser	Ser 215	Trp	Lys	Ala	Phe	Ala 220	Pro	Ala	Phe	Ala
Gly 225	Lys	Met	Ser	Ile	Glu 230	Ala	Val	Asp	Arg	Ala 235	Met	Arg	Gly	Glu	Gly 240

Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu  
 245 250 255  
 Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly  
 260 265 270  
 Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala  
 275 280 285  
 Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu  
 290 295 300  
 Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val  
 305 310 315 320  
 Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly Ser Asn  
 325 330 335  
 Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His  
 340 345 350  
 Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His  
 355 360 365  
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile  
 370 375 380  
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg  
 385 390 395 400  
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala  
 405 410 415  
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val  
 420 425 430  
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr  
 435 440 445  
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu  
 450 455 460  
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp  
 465 470 475 480  
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala  
 485 490 495  
 Pro Val Ile Pro Glu Gly Leu Phe  
 500

&lt;210&gt; 603

&lt;211&gt; 975

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(975)

&lt;223&gt; FRXA00406

&lt;400&gt; 603

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Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg	
1 5 10 15	
atc atc gac aat gca tct gtg cag gca gct tcc gtg ttg cgt cga cca	96
Ile Ile Asp Asn Ala Ser Val Gln Ala Ser Val Leu Arg Arg Pro	
20 25 30	
gtt agc tct gcc cgt gcg atg gca cag gtc agg cca gtt acc gat ggt	144
Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly	
35 40 45	
cgg ggt gca tct gtt ttc ggt ctg cca gga cgt tat gcc gcg gaa tgg	192
Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp	
50 55 60	
gct gcg ctt gct aac ggc act gcg gtg cgt gag ctt gat ttc cat gac	240
Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp	
65 70 75 80	
acg ttc ctc gct gcg gaa tac tcc cac cca gga gat aac att cct ccg	288
Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro	
85 90 95	
att ttg gct gca gca cag cag gct gga aaa ggt ggc aag gat ctg atc	336
Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile	
100 105 110	
cgt ggc atc gct act ggg tat gag att cag gtt aac ttg gtg cgt gga	384
Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly	
115 120 125	
atg tgc ctg cat gag cac aag att gat cac gtt gct cat ctt gga cca	432
Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro	
130 135 140	
tca gcg gct gct ggt atc gga acc ttg cta gac cta gat gtg gac acc	480
Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr	
145 150 155 160	
atc tac cag gca att ggt cag gca ttg cac acc acc acg gcg acg agg	528
Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg	
165 170 175	
cag tcc cgt aaa ggt gcg att tct tca tgg aag gca ttt gct cct gcg	576
Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala	
180 185 190	
ttt gcg ggc aag atg tcc atc gag gca gta gat cgc gca atg cgt ggc	624
Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly	
195 200 205	
gag ggc gca ccg tca cca atc tgg gaa ggc gaa gac ggc gta atc gcg	672
Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala	
210 215 220	
tgg ctg ctg tcc ggt ctt gat cac atc tac acc att cct ttg cct gca	720
Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala	

225	230	235	240	
gaa ggt gaa gcc aaa cga gca atc ttg gat acc tac acc aag gaa cac				768
Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His				
	245	250	255	
tcg gcg gaa tac cag tca cag gca ccg atc gac ttg gcg cgc agc atg				816
Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met				
	260	265	270	
ggg gag aag ctg gca gca cag ggc ttg gac ctg cgt gat gtg gac tcc				864
Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser				
	275	280	285	
atc gtt ttg cac acc tcc cac cac act cac tac gtg atc ggc acc gga				912
Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly				
	290	295	300	
tct aat gat cca cag aag ttc gat cca gat gca tcg cga gaa acc ctt				960
Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu				
305	310	315	320	
gat cac tcc atc atg				975
Asp His Ser Ile Met				
	325			

&lt;210&gt; 604

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 604

Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg				
1	5	10	15	
Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro				
	20	25	30	
Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly				
	35	40	45	
Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp				
	50	55	60	
Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp				
	65	70	75	80
Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro				
	85	90	95	
Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile				
	100	105	110	
Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly				
	115	120	125	
Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro				
	130	135	140	
Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr				

145                      150                      155                      160  
 Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg  
                                  165                      170                      175  
 Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala  
                                  180                      185                      190  
 Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly  
                                  195                      200                      205  
 Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala  
                                  210                      215                      220  
 Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala  
 225                                   230                      235                      240  
 Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His  
                                  245                      250                      255  
 Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met  
                                  260                      265                      270  
 Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser  
                                  275                      280                      285  
 Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly  
                                  290                      295                      300  
 Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu  
 305                                   310                      315                      320  
 Asp His Ser Ile Met  
                                  325

<210> 605  
 <211> 431  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(408)  
 <223> FRXA00514

<400> 605  
 cac gag cgt tcc tat gct cct gag cga gcc ctc cgc cga gag acc atc    48  
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile  
   1                                  5                                  10                                  15  
 gag ctg tgg aac aag att tcc acg gtg gag gat cct gaa tgg acc agg    96  
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg  
                                   20                                  25                                  30  
 cgt tac cac tcc gtt gat cct gca gaa aag gcc ttc ggc gca cgc gca    144  
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala  
                                   35                                  40                                  45  
 gtg atc acc ttc aag gat gga acc gtc gtg gaa gat gaa ctg gct gtg    192  
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val

50	55	60	
gcg aat gcg cat cct ctg gga gca cgg cct ttc gct agg gag cag tac			240
Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr			
65	70	75	80
att cag aaa ttc cgc acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa			288
Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu			
	85	90	95
cag gat cgc ttc ttg gat gcg gca cag cgt acg cac gag ctt gag gat			336
Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp			
	100	105	110
ctt tca gaa ctc aac att gaa ttg gat gcc gat att ttg gcc aag gct			384
Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala			
	115	120	125
cct gtg att ccg gaa gga ctg ttc tgatggcggg tttgttttcc tct			431
Pro Val Ile Pro Glu Gly Leu Phe			
130	135		

<210> 606  
 <211> 136  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 606
His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile
1 5 10 15
Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg
20 25 30
Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
35 40 45
Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
50 55 60
Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
65 70 75 80
Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
85 90 95
Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
100 105 110
Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
115 120 125
Pro Val Ile Pro Glu Gly Leu Phe
130 135

<210> 607  
 <211> 718  
 <212> DNA  
 <213> Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(718)

&lt;223&gt; RXA00512

&lt;400&gt; 607

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cccatcttct aaccgccta tatataagga gtgaatcacc atg tcc agc gcc aca 115
                                         Met Ser Ser Ala Thr
                                         1 5
acc act gat gtt cgc aaa ggg ctc tac gga gtc atc gcc gat tac acg 163
Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val Ile Ala Asp Tyr Thr
                        10 15 20
gcc gtt tcc aaa gtc atg cca gag acc aat tca ctg acc tac cgt ggc 211
Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser Leu Thr Tyr Arg Gly
                        25 30 35
tac gcg gtg gaa gat ttg gtg gaa aac tgc agc ttc gag gag gtg ttt 259
Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Phe
                        40 45 50
tac ctc ctg tgg cac ggc gag ctg ccc act gcg caa caa ctt gcg gag 307
Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala Gln Gln Leu Ala Glu
                        55 60 65
ttc aat gag cgt ggc cgt tcc tac cgc tcc ctg gat gcc ggt ttg atc 355
Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile
                        70 75 80 85
tcc ctg atc cac tct ttg ccc aaa gaa gcc cac ccg atg gat gtt atg 403
Ser Leu Ile His Ser Leu Pro Lys Glu Ala His Pro Met Asp Val Met
                        90 95 100
cgc acc gcg gtg tcc tac atg ggc acc aag gat tcc gag tat ttc acc 451
Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp Ser Glu Tyr Phe Thr
                        105 110 115
acc gat tct gag cac atc cgc aaa gtt ggc cac acc ttg ttg gcg cag 499
Thr Asp Ser Glu His Ile Arg Lys Val Gly His Thr Leu Leu Ala Gln
                        120 125 130
ctt ccg atg gtg cta gcc atg gat att cgt cgc cgc aag ggc ctc gat 547
Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg Arg Lys Gly Leu Asp
                        135 140 145
atc atc gcc cct gac tcc agc aag tca gtc gcc gaa aac ctg ctg tct 595
Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala Glu Asn Leu Leu Ser
                        150 155 160 165
atg gtg ttt ggt act ggc ccg gaa tca cct gca tcc aac cca gct gac 643
Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala Ser Asn Pro Ala Asp
                        170 175 180
gtc cgc gat ttt gag aaa tca ctg atc ctc tac gcc gag cac tcc ttc 691
Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr Ala Glu His Ser Phe
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aac gcc tcc acc ttc acc gcc cgc gtg  
 Asn Ala Ser Thr Phe Thr Ala Arg Val  
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718

<210> 608  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser  
           20                    25                    30  
 Leu Thr Tyr Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser  
           35                    40                    45  
 Phe Glu Glu Val Phe Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala  
   50                    55                    60  
 Gln Gln Leu Ala Glu Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu  
   65                    70                    75                    80  
 Asp Ala Gly Leu Ile Ser Leu Ile His Ser Leu Pro Lys Glu Ala His  
           85                    90                    95  
 Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp  
          100                    105                    110  
 Ser Glu Tyr Phe Thr Thr Asp Ser Glu His Ile Arg Lys Val Gly His  
          115                    120                    125  
 Thr Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg  
  130                    135                    140  
 Arg Lys Gly Leu Asp Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala  
 145                    150                    155                    160  
 Glu Asn Leu Leu Ser Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala  
          165                    170                    175  
 Ser Asn Pro Ala Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr  
          180                    185                    190  
 Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ala Arg Val  
  195                    200                    205

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 <211> 320  
 <212> DNA  
 <213> Corynebacterium glutamicum  
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 <221> CDS  
 <222> (1)..(297)  
 <223> RXA00518

&lt;400&gt; 609

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Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala
  1             5             10             15

atg tat gaa aac atg cgc gac gcc atg gac gcc cgc acc ggc atc aag 96
Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys
             20             25             30

ccg aat ctc gat ttc cct gct ggc cct gcc tac cac ctg ctc ggt ttc 144
Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe
             35             40             45

ccg gtc gat ttc ttc acc ccg ctg ttc gtc atc gcc cgc gtc gcc ggc 192
Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly
             50             55             60

tgg acg gcc cac atc gtg gag cag tac gaa aac aac tcg ctc atc cgc 240
Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg
  65             70             75             80

cca ctg tcc gag tac aac ggc gag gag cag cgc gag gtc gcg ccc att 288
Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile
             85             90             95

gaa aag cgc taaaagattt tcgcttttcg acg 320
Glu Lys Arg

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&lt;210&gt; 610

&lt;211&gt; 99

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 610

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Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala
  1             5             10             15

Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys
             20             25             30

Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe
             35             40             45

Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly
             50             55             60

Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg
  65             70             75             80

Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile
             85             90             95

Glu Lys Arg

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&lt;210&gt; 611

&lt;211&gt; 1494

&lt;212&gt; DNA

aca gcc aat gtt gca ctt cgt gtc act cgc act gga aac ttg agc cac 691  
Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr Gly Asn Leu Ser His  
185 190 195

tgg	aaa	ggc	ctt	gcc	tac	cca	cac	gtg	tcc	aaa	gaa	gga	acc	tgg	gca	739
Trp	Lys	Gly	Leu	Ala	Tyr	Pro	His	Val	Ser	Lys	Glu	Gly	Thr	Trp	Ala	
		200					205					210				
gca	ctg	ctc	gca	agc	cga	ggg	att	acc	ggg	ccg	gaa	gaa	gtc	ttc	gaa	787
Ala	Leu	Leu	Ala	Ser	Arg	Gly	Ile	Thr	Gly	Pro	Glu	Glu	Val	Phe	Glu	
	215					220					225					
ggc	aac	aag	gga	ttc	aaa	gag	tcc	gtc	tcc	gga	ccg	ttc	gag	atc	gat	835
Gly	Asn	Lys	Gly	Phe	Lys	Glu	Ser	Val	Ser	Gly	Pro	Phe	Glu	Ile	Asp	
230					235					240					245	
tgg	tcc	aag	gaa	gac	ttg	gaa	agc	gtt	aag	cgc	acc	atc	atc	aag	aaa	883
Trp	Ser	Lys	Glu	Asp	Leu	Glu	Ser	Val	Lys	Arg	Thr	Ile	Ile	Lys	Lys	
				250					255					260		
cac	aac	gcg	gaa	att	cac	tcg	cag	tca	gcg	ctt	gat	gca	gcc	caa	gaa	931
His	Asn	Ala	Glu	Ile	His	Ser	Gln	Ser	Ala	Leu	Asp	Ala	Ala	Gln	Glu	
		265					270						275			
ata	cgc	gca	caa	gaa	ggc	ttc	aat	gtg	gac	aac	att	gaa	aag	att	cac	979
Ile	Arg	Ala	Gln	Glu	Gly	Phe	Asn	Val	Asp	Asn	Ile	Glu	Lys	Ile	His	
		280					285					290				
ctg	act	act	ttc	gac	gtt	gcc	tac	tcc	atc	att	ggc	ggc	ggc	gaa	gaa	1027
Leu	Thr	Thr	Phe	Asp	Val	Ala	Tyr	Ser	Ile	Ile	Gly	Gly	Gly	Glu	Glu	
	295					300					305					
ggc	gac	aaa	cag	ctt	att	cgc	acc	aaa	gaa	gaa	gcc	gat	cac	tca	ctg	1075
Gly	Asp	Lys	Gln	Leu	Ile	Arg	Thr	Lys	Glu	Glu	Ala	Asp	His	Ser	Leu	
310					315					320					325	
ccg	tgg	atg	ctc	gct	gta	gtt	ctg	ctg	gat	ggg	cag	ctc	aat	ccc	gaa	1123
Pro	Trp	Met	Leu	Ala	Val	Val	Leu	Leu	Asp	Gly	Gln	Leu	Asn	Pro	Glu	
				330					335					340		
cag	tac	gaa	cca	tca	cgc	atc	gtt	gct	gat	gat	gta	caa	acc	ttg	atg	1171
Gln	Tyr	Glu	Pro	Ser	Arg	Ile	Val	Ala	Asp	Asp	Val	Gln	Thr	Leu	Met	
			345					350					355			
aag	aaa	atc	gaa	atc	aca	ccg	tca	gat	gaa	ttc	tct	gat	cgc	ttc	cct	1219
Lys	Lys	Ile	Glu	Ile	Thr	Pro	Ser	Asp	Glu	Phe	Ser	Asp	Arg	Phe	Pro	
		360					365					370				
gac	cac	atg	cca	gct	gat	cta	gaa	gtc	aca	cta	aac	gat	ggc	tcg	gtg	1267
Asp	His	Met	Pro	Ala	Asp	Leu	Glu	Val	Thr	Leu	Asn	Asp	Gly	Ser	Val	
		375				380					385					
ttc	aaa	gct	tca	caa	gat	agc	tac	tta	ggc	ttc	cac	gac	aat	ccc	cta	1315
Phe	Lys	Ala	Ser	Gln	Asp	Ser	Tyr	Leu	Gly	Phe	His	Asp	Asn	Pro	Leu	
390					395					400					405	
gat	tgg	gac	aac	gcg	cgc	aag	aaa	ttc	gat	gcc	ctt	gtc	aca	cca	ttc	1363
Asp	Trp	Asp	Asn	Ala	Arg	Lys	Lys	Phe	Asp	Ala	Leu	Val	Thr	Pro	Phe	
				410					415					420		
acc	ggg	gaa	gaa	cta	cgt	gaa	gaa	atc	gcc	acg	atc	att	cac	gag	ctc	1411
Thr	Gly	Glu	Glu	Leu	Arg	Glu	Glu	Ile	Ala	Thr	Ile	Ile	His	Glu	Leu	
			425					430					435			

gat agc cga cag gtt tct gaa ctc aca gaa gcc ctg gcc aaa gtc tcc 1459  
 Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala Leu Ala Lys Val Ser  
           440                          445                          450

acc acc cgc agc taaaactttt tgaaaggagc tca 1494  
 Thr Thr Arg Ser  
           455

<210> 612  
 <211> 457  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 612  
 Met Thr Glu Ser Gln Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu  
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Asn Asp Ala Ser Pro Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu  
           20                          25                          30

Asp Thr Val Gly Val Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val  
           35                          40                          45

Ala Ile Arg Gly Leu Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr  
           50                          55                          60

Leu Ile Gly Gly Gly Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn  
       65                          70                          75                          80

Ser Ala Leu Ser Arg Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys  
           85                          90                          95

Gly Glu Thr Asn His Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala  
           100                          105                          110

Ala Glu Ser Val Gly Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala  
           115                          120                          125

Val Ala Tyr Gln Val His Thr Arg Leu Ser Asp Val Ala Pro Val Arg  
           130                          135                          140

Ala Lys Gly Phe Asp His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala  
       145                          150                          155                          160

Ser Ala Ala Lys Ala Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala  
           165                          170                          175

Leu Ala Ile Ala Gly Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr  
           180                          185                          190

Gly Asn Leu Ser His Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys  
           195                          200                          205

Glu Gly Thr Trp Ala Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro  
       210                          215                          220

Glu Glu Val Phe Glu Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly  
       225                          230                          235                          240

Pro Phe Glu Ile Asp Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg

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<210> 613
<211> 923
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1)..(900)  
<223> RXN03144
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<400> 613																
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Thr	Thr	Thr	Ala	Thr	Arg	Gln	Ser	Arg	Lys	Gly	Glu	Ile	Ser	Ser	Trp	
1				5					10					15		
aag	gcg	ttc	gcg	cca	gcg	ttt	gcg	gga	aag	atg	gcc	att	gag	gcg	atg	96
Lys	Ala	Phe	Ala	Pro	Ala	Phe	Ala	Gly	Lys	Met	Ala	Ile	Glu	Ala	Met	
			20					25					30			

gat	cgt	gcg	atg	cgt	ggg	gag	ggt	tcg	ccc	gca	ccg	att	tgg	gag	ggc	144
Asp	Arg	Ala	Met	Arg	Gly	Glu	Gly	Ser	Pro	Ala	Pro	Ile	Trp	Glu	Gly	
		35					40					45				
gaa	gac	ggg	gtc	atc	gcg	tgg	ctg	tta	tcg	ggc	aaa	gat	cat	gtt	tat	192
Glu	Asp	Gly	Val	Ile	Ala	Trp	Leu	Leu	Ser	Gly	Lys	Asp	His	Val	Tyr	
	50					55					60					
cat	gtg	cca	ttg	ccg	gaa	cac	ggc	gag	ccc	aag	ctg	ggg	att	cta	gag	240
His	Val	Pro	Leu	Pro	Glu	His	Gly	Glu	Pro	Lys	Leu	Gly	Ile	Leu	Glu	
	65				70					75					80	
act	tac	aca	aag	gaa	cat	tca	gcg	gaa	tat	caa	tcg	cag	gca	ccg	att	288
Thr	Tyr	Thr	Lys	Glu	His	Ser	Ala	Glu	Tyr	Gln	Ser	Gln	Ala	Pro	Ile	
			85						90					95		
gat	ctg	gcg	cgc	agg	atg	aag	cca	ctg	gtt	gac	gcg	gct	ggc	gga	acg	336
Asp	Leu	Ala	Arg	Arg	Met	Lys	Pro	Leu	Val	Asp	Ala	Ala	Gly	Gly	Thr	
			100					105					110			
gaa	cac	att	gca	gag	att	gtg	ctg	cgc	acc	agt	cac	cac	acg	cat	tat	384
Glu	His	Ile	Ala	Glu	Ile	Val	Leu	Arg	Thr	Ser	His	His	Thr	His	Tyr	
		115					120					125				
gtg	att	ggc	act	ggg	gcg	aac	gat	ccg	cag	aag	atg	gat	ccg	cag	gcc	432
Val	Ile	Gly	Thr	Gly	Ala	Asn	Asp	Pro	Gln	Lys	Met	Asp	Pro	Gln	Ala	
	130					135					140					
tcg	cgt	gaa	acc	ctg	gat	cat	tcc	atc	atg	tac	att	ttc	gcc	gtc	gcg	480
Ser	Arg	Glu	Thr	Leu	Asp	His	Ser	Ile	Met	Tyr	Ile	Phe	Ala	Val	Ala	
	145				150					155				160		
ctt	caa	gat	ggc	gtg	tgg	cac	cac	gag	ttt	tcc	tac	acc	cgc	aag	cgt	528
Leu	Gln	Asp	Gly	Val	Trp	His	His	Glu	Phe	Ser	Tyr	Thr	Arg	Lys	Arg	
			165					170						175		
tcc	acc	cgc	ccg	gaa	act	gtg	gag	ctg	tgg	cac	aag	att	cgc	acc	gtg	576
Ser	Thr	Arg	Pro	Glu	Thr	Val	Glu	Leu	Trp	His	Lys	Ile	Arg	Thr	Val	
			180					185					190			
gag	gat	cct	gaa	tgg	acg	cgc	cga	tac	cat	tct	gat	gat	cct	gca	aaa	624
Glu	Asp	Pro	Glu	Trp	Thr	Arg	Arg	Tyr	His	Ser	Asp	Asp	Pro	Ala	Lys	
		195					200					205				
aag	gcc	ttt	ggt	gcg	aaa	gca	gtg	atc	aca	atg	gct	gat	ggc	acc	gtg	672
Lys	Ala	Phe	Gly	Ala	Lys	Ala	Val	Ile	Thr	Met	Ala	Asp	Gly	Thr	Val	
	210					215					220					
att	gag	gat	gaa	ttg	gct	gtc	gcg	gat	gcc	cac	ccg	ctg	ggt	gct	cgg	720
Ile	Glu	Asp	Glu	Leu	Ala	Val	Ala	Asp	Ala	His	Pro	Leu	Gly	Ala	Arg	
	225				230					235				240		
ccg	ttt	gcg	cgg	gag	aat	tac	att	gaa	aaa	ttc	cgc	aca	ctc	gcg	cag	768
Pro	Phe	Ala	Arg	Glu	Asn	Tyr	Ile	Glu	Lys	Phe	Arg	Thr	Leu	Ala	Gln	
			245						250					255		
ggg	att	gtc	att	gat	tca	gaa	cag	gaa	cgc	ttc	ttg	cat	gcc	gtg	caa	816
Gly	Ile	Val	Ile	Asp	Ser	Glu	Gln	Glu	Arg	Phe	Leu	His	Ala	Val	Gln	
			260					265					270			
agc	ctg	cct	gac	ctg	gat	gat	ctt	gat	cag	ctc	aac	atc	gaa	gtc	gac	864



Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp  
 275 280 285

ata agc aac cag gcc gcg acg aaa gcg ggg ctg tta tgaatctctt 910  
 Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu  
 290 295 300

ttcgaatggt gtt 923

<210> 614

<211> 300

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 614

Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp  
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Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met  
 20 25 30

Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly  
 35 40 45

Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr  
 50 55 60

His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu  
 65 70 75 80

Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile  
 85 90 95

Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr  
 100 105 110

Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr  
 115 120 125

Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala  
 130 135 140

Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala  
 145 150 155 160

Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg  
 165 170 175

Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val  
 180 185 190

Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys  
 195 200 205

Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val  
 210 215 220

Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg  
 225 230 235 240

Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln  
 245 250 255

Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln  
 260 265 270

Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp  
 275 280 285

Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu  
 290 295 300

&lt;210&gt; 615

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(511)

&lt;223&gt; FRXA02322

&lt;400&gt; 615

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ctttaaggaa acagtgcaca aataaatctc aaggagcccc atg cgc atc cac gat 115  
 Met Arg Ile His Asp  
 1 5

gtt tat acc cac ctt tcg gcc gat aac ttt ccc aaa gca gag cac ctt 163  
 Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro Lys Ala Glu His Leu  
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gcg tgg aaa ttc tcc gag ctt gcc acc gac ccc gtg gag gtg aca ccg 211  
 Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro Val Glu Val Thr Pro  
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gat gtt tcg gag atg atc atc aac cgg atc atc gac aac gcg gcg gtg 259  
 Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile Asp Asn Ala Ala Val  
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 Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr Val Ala Arg Gln Gln  
 55 60 65

gcg cag tcc cat ccg cgg gaa aag ggc gga aaa gtt ttt gga att tca 355  
 Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys Val Phe Gly Ile Ser  
 70 75 80 85

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 Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala Asn Gly Val Ala Val  
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cgt gaa ttg gac ttc cac gat aca ttt tta gca gct gaa tac tcc cat 451  
 Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr Ser His  
 105 110 115

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Asp Asn Ala Ala Val Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr  
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Val Ala Arg Gln Gln Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys  
65 70 75 80  
Val Phe Gly Ile Ser Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala  
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Asn Gly Val Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala  
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Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg  
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Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp

35	40	45	
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Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val			
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Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr			
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Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu			
	85	90	95
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Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His			
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Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile			
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Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg			
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gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg ctt caa			480
Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln			
	145	150	155
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Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr			
	165	170	175
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Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp			
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Pro Glu Trp Thr Arg Arg Tyr His Ser			
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&lt;210&gt; 618

&lt;211&gt; 201

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 618

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Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr  
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Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu  
85 90 95

Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His  
100 105 110

Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile  
115 120 125

Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg  
130 135 140

Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln  
145 150 155 160

Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr  
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Pro Glu Trp Thr Arg Arg Tyr His Ser  
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Met Ser Asp Ser Gln  
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Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp Tyr Thr Ser Ile Ser  
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aaa gtg atg cca gag agc aac tcg ctg act tac cgt ggc tac gcc gtg 211  
Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr Arg Gly Tyr Ala Val  
25 30 35

gag gat ttg gtg gaa aac tgc agc ttt gaa gaa gtg atc tac ctc ctg 259  
Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Ile Tyr Leu Leu  
40 45 50

tgg ttt ggg gag ctg ccc acc act gaa caa ctc cgg acc ttc aac acg 307  
Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu Arg Thr Phe Asn Thr  
55 60 65

aca ggt cga agc tac cgc tca ctc gac gcc gga ctg att tcc ctc atc	355
Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile Ser Leu Ile	
70 75 80 85	
cac tcc tta ccc aac acc tgc cac ccc atg gac gtg ctg cgc acc gca	403
His Ser Leu Pro Asn Thr Cys His Pro Met Asp Val Leu Arg Thr Ala	
90 95 100	
gtg tcc tac atg ggt acc ttt gat ccc gat ccg ttt acc cgc gat gcc	451
Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro Phe Thr Arg Asp Ala	
105 110 115	
gat cat atc cga agc att gga cac aac ctg ctt gcg cag ctt ccc atg	499
Asp His Ile Arg Ser Ile Gly His Asn Leu Leu Ala Gln Leu Pro Met	
120 125 130	
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Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly Glu Glu Ile Ile Ala	
135 140 145	
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Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe Leu Ser Met Val Phe	
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Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala Asp Asp Ile Arg Asp	
170 175 180	
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Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His Ser Phe Asn Ala Ser	
185 190 195	
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Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg Ser Asp Thr Tyr Ser	
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Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Leu His Gly Gly	
215 220 225	
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Ala Asn Glu Phe Val Met His Thr Met Leu Asp Ile Asp Asp Pro Asn	
230 235 240 245	
aat gct gcc gac tgg atg ggc aag gcg ttg gat cgt aaa gaa cgc atc	883
Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp Arg Lys Glu Arg Ile	
250 255 260	
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Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly Asp Ser Arg Val Pro	
265 270 275	
tcc atg gag aaa tcc atg cgc tcc ctt gct gct cgt cac cgt ggt caa	979
Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala Arg His Arg Gly Gln	
280 285 290	
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Lys Trp Val His Met Tyr Glu Ser Met Gln Glu Val Met Glu Ala Arg	
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Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr Tyr  
 310 315 320 325

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Val Ile Tyr Leu Leu Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu  
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Arg Thr Phe Asn Thr Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly  
 65 70 75 80

Leu Ile Ser Leu Ile His Ser Leu Pro Asn Thr Cys His Pro Met Asp  
 85 90 95

Val Leu Arg Thr Ala Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro  
 100 105 110

Phe Thr Arg Asp Ala Asp His Ile Arg Ser Ile Gly His Asn Leu Leu  
 115 120 125

Ala Gln Leu Pro Met Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly  
 130 135 140

Glu Glu Ile Ile Ala Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe  
 145 150 155 160

Leu Ser Met Val Phe Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala  
 165 170 175

Asp Asp Ile Arg Asp Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His  
 180 185 190

Ser Phe Asn Ala Ser Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg  
 195 200 205  
 Ser Asp Thr Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly  
 210 215 220  
 Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr Met Leu Asp  
 225 230 235 240  
 Ile Asp Asp Pro Asn Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp  
 245 250 255  
 Arg Lys Glu Arg Ile Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly  
 260 265 270  
 Asp Ser Arg Val Pro Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala  
 275 280 285  
 Arg His Arg Gly Gln Lys Trp Val His Met Tyr Glu Ser Met Gln Glu  
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 Val Met Glu Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala  
 305 310 315 320  
 Gly Pro Ala Tyr Tyr Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro  
 325 330 335  
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 Met Asn Leu Phe Ser  
 1 5  
 aat ggt gtt gat gtg ggg agg cgt cga caa gca ttt aaa gcg gca ctc 163  
 Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala Phe Lys Ala Ala Leu  
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 Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala Phe Ser Pro Leu Ile



25				30				35								
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Ala	Arg	Ser	Ile	Glu	Glu	Ala	Gly	Phe	Glu	Gly	Val	Tyr	Val	Ser	Gly	
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gcc	gtc	ata	gct	gct	gac	ctg	gca	cta	ccc	gat	atc	ggc	ttg	acg	acg	307
Ala	Val	Ile	Ala	Ala	Asp	Leu	Ala	Leu	Pro	Asp	Ile	Gly	Leu	Thr	Thr	
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Leu	Thr	Glu	Val	Ala	His	Arg	Ala	Arg	Gln	Ile	Ala	Arg	Val	Thr	Asp	
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cta	gga	gtg	ctt	gtc	gac	gcc	gac	acc	ggc	ttt	ggc	gaa	ccc	atg	tcg	403
Leu	Gly	Val	Leu	Val	Asp	Ala	Asp	Thr	Gly	Phe	Gly	Glu	Pro	Met	Ser	
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Ala	Ala	Arg	Thr	Val	Ala	Glu	Leu	Glu	Asp	Ala	Gly	Val	Ala	Gly	Cys	
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cac	ctt	gaa	gac	caa	gtc	aac	ccc	aaa	cgt	tgc	ggg	cac	ttg	gac	ggc	499
His	Leu	Glu	Asp	Gln	Val	Asn	Pro	Lys	Arg	Cys	Gly	His	Leu	Asp	Gly	
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aaa	gaa	gtc	gtg	cgc	aca	gac	gtg	atg	gtt	cga	cgc	atc	gca	gcc	gcc	547
Lys	Glu	Val	Val	Arg	Thr	Asp	Val	Met	Val	Arg	Arg	Ile	Ala	Ala	Ala	
	135					140					145					
gtc	tcg	gcc	cgg	cgc	gac	ccg	aac	ttt	gtc	atc	tgc	gcc	cgc	acc	gac	595
Val	Ser	Ala	Arg	Arg	Asp	Pro	Asn	Phe	Val	Ile	Cys	Ala	Arg	Thr	Asp	
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gcc	gct	gga	gtg	gaa	gga	atc	gac	gcc	gcc	att	gag	cgc	gcg	aaa	gcc	643
Ala	Ala	Gly	Val	Glu	Gly	Ile	Asp	Ala	Ala	Ile	Glu	Arg	Ala	Lys	Ala	
				170					175					180		
tac	tta	gat	gcg	ggc	gcc	gac	atg	att	ttc	acc	gaa	gcc	ctc	cac	agc	691
Tyr	Leu	Asp	Ala	Gly	Ala	Asp	Met	Ile	Phe	Thr	Glu	Ala	Leu	His	Ser	
			185					190					195			
gaa	gcc	gac	ttc	cga	tac	ttc	cgg	cac	gcc	atc	cct	gat	gcc	ttg	ttg	739
Glu	Ala	Asp	Phe	Arg	Tyr	Phe	Arg	His	Ala	Ile	Pro	Asp	Ala	Leu	Leu	
		200					205					210				
ctg	gcg	aat	atg	acc	gaa	ttt	ggc	aaa	acg	acg	ctg	ctg	tca	gcc	gac	787
Leu	Ala	Asn	Met	Thr	Glu	Phe	Gly	Lys	Thr	Thr	Leu	Leu	Ser	Ala	Asp	
	215					220					225					
gtg	ttg	gaa	gag	att	ggc	tac	aac	gcc	gtg	atc	tac	ccc	gtg	acc	acg	835
Val	Leu	Glu	Glu	Ile	Gly	Tyr	Asn	Ala	Val	Ile	Tyr	Pro	Val	Thr	Thr	
	230				235				240					245		
ctg	cgt															

aga tta tat gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag 979  
 Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln  
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cac att ttc acc tac aga aaa gga gaa aac aat gag tgacagccaa 1025  
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Phe Ser Pro Leu Ile Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly  
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Val Tyr Val Ser Gly Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp  
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Ile Gly Leu Thr Thr Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile  
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Ala Arg Val Thr Asp Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe  
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Gly Glu Pro Met Ser Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala  
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Gly Val Ala Gly Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys  
           115                          120                          125

Gly His Leu Asp Gly Lys Glu Val Val Arg Thr Asp Val Met Val Arg  
           130                          135                          140

Arg Ile Ala Ala Ala Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile  
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Cys Ala Arg Thr Asp Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile  
           165                          170                          175

Glu Arg Ala Lys Ala Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr  
           180                          185                          190

Glu Ala Leu His Ser Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile  
           195                          200                          205

Pro Asp Ala Leu Leu Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr  
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Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser Arg Leu Tyr  
           35                  40                  45

Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln His Ile Phe  
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Thr Tyr Arg Lys Gly Glu Asn Asn Glu  
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   Met Arg Ile Glu Ile  
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aca agc gta ttt gtt gat gac cag gcc aaa gca ctc gat ttc tac acc 163  
 Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala Leu Asp Phe Tyr Thr  
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acg aag ctc gga ttt gag ctc aaa cac gat gta act gct ggt gac tac 211  
 Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val Thr Ala Gly Asp Tyr  
                   25                  30                  35

cgc tgg ttg act gtt gtt gat cca gaa aac cca gat ggt gtg cag ctt 259  
 Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro Asp Gly Val Gln Leu  
                   40                  45                  50

ttg ttg gaa cca aac cag cac cca gat gca gcg act tac caa gct gga 307  
 Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala Thr Tyr Gln Ala Gly  
                   55                  60                  65

att aaa cga gac ggt att ccc gct aca cag ttt tat gtt gat gat gtg 355  
 Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe Tyr Val Asp Asp Val  
                   70                  75                  80                  85

cag gaa gaa tat gac agc ctc aag gat aaa ggc gtg gat ttc atc atg 403  
 Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly Val Asp Phe Ile Met  
                   90                  95                  100

gaa cca acc gat gtg ggc cct tca gtg att gcc att ctc gat gac acc 451  
 Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala Ile Leu Asp Asp Thr  
                   105                  110                  115

gta gga aac cta att cag att gtt caa ttg aag cag aac taaccccgtg 500  
 Val Gly Asn Leu Ile Gln Ile Val Gln Leu Lys Gln Asn  
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513

&lt;210&gt; 626

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 626

Met	Arg	Ile	Glu	Ile	Thr	Ser	Val	Phe	Val	Asp	Asp	Gln	Ala	Lys	Ala
1				5					10					15	

Leu	Asp	Phe	Tyr	Thr	Thr	Lys	Leu	Gly	Phe	Glu	Leu	Lys	His	Asp	Val
			20					25					30		

Thr	Ala	Gly	Asp	Tyr	Arg	Trp	Leu	Thr	Val	Val	Asp	Pro	Glu	Asn	Pro
		35					40					45			

Asp	Gly	Val	Gln	Leu	Leu	Leu	Glu	Pro	Asn	Gln	His	Pro	Asp	Ala	Ala
	50					55					60				

Thr	Tyr	Gln	Ala	Gly	Ile	Lys	Arg	Asp	Gly	Ile	Pro	Ala	Thr	Gln	Phe
65					70					75					80

Tyr	Val	Asp	Asp	Val	Gln	Glu	Glu	Tyr	Asp	Ser	Leu	Lys	Asp	Lys	Gly
				85					90					95	

Val	Asp	Phe	Ile	Met	Glu	Pro	Thr	Asp	Val	Gly	Pro	Ser	Val	Ile	Ala
			100					105					110		

Ile	Leu	Asp	Asp	Thr	Val	Gly	Asn	Leu	Ile	Gln	Ile	Val	Gln	Leu	Lys
		115					120					125			

Gln	Asn
	130

&lt;210&gt; 627

&lt;211&gt; 2334

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2311)

&lt;223&gt; RXN00148

&lt;400&gt; 627

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gacgctggct	gacctgctag	atgctttggg	agcttaaate	atg	acg	tcg	atc	cct	115
				Met	Thr	Ser	Ile	Pro	
				1				5	

aat	ttt	tca	gac	atc	cca	ttg	act	gct	gag	aca	cgt	gca	tcg	gag	tca	163
Asn	Phe	Ser	Asp	Ile	Pro	Leu	Thr	Ala	Glu	Thr	Arg	Ala	Ser	Glu	Ser	
				10				15						20		

cac	aac	gtt	gac	gcc	ggc	aag	gtg	tgg	aac	act	ccc	gaa	ggc	att	gat	211
His	Asn	Val	Asp	Ala	Gly	Lys	Val	Trp	Asn	Thr	Pro	Glu	Gly	Ile	Asp	

				25				30				35							
gtc	aag	cgc	gta	ttc	acg	cag	gct	gac	cgc	gac	gag	gcg	caa	gcg	gcg	259			
Val	Lys	Arg	Val	Phe	Thr	Gln	Ala	Asp	Arg	Asp	Glu	Ala	Gln	Ala	Ala				
40				45				50											
gga	cat	ccg	gtg	gat	tct	ttg	cca	ggt	caa	aag	cca	ttt	atg	cgc	ggg	307			
Gly	His	Pro	Val	Asp	Ser	Leu	Pro	Gly	Gln	Lys	Pro	Phe	Met	Arg	Gly				
55				60				65											
ccg	tac	cca	act	atg	tac	acc	aat	cag	ccg	tgg	acg	att	cgc	cag	tac	355			
Pro	Tyr	Pro	Thr	Met	Tyr	Thr	Asn	Gln	Pro	Trp	Thr	Ile	Arg	Gln	Tyr				
70				75				80											
gca	ggc	ttt	tca	acc	gcc	gcg	gaa	tcc	aat	gcg	ttt	tat	cgg	agg	aac	403			
Ala	Gly	Phe	Ser	Thr	Ala	Ala	Glu	Ser	Asn	Ala	Phe	Tyr	Arg	Arg	Asn				
90				95				100											
ctt	gct	gcg	ggg	caa	aaa	ggg	ttg	tcg	gtt	gcg	ttc	gat	cta	gcg	acc	451			
Leu	Ala	Ala	Gly	Gln	Lys	Gly	Leu	Ser	Val	Ala	Phe	Asp	Leu	Ala	Thr				
105				110				115											
cac	cgc	ggg	tat	gac	tcg	gat	aat	gag	cgc	gtg	gtc	ggc	gat	gtg	ggg	499			
His	Arg	Gly	Tyr	Asp	Ser	Asp	Asn	Glu	Arg	Val	Val	Gly	Asp	Val	Gly				
120				125				130											
atg	gcc	ggc	gtg	gcg	att	gat	tcg	att	ttg	gat	atg	cgt	cag	ctg	ttt	547			
Met	Ala	Gly	Val	Ala	Ile	Asp	Ser	Ile	Leu	Asp	Met	Arg	Gln	Leu	Phe				
135				140				145											
gat	ggc	att	gat	ttg	tcc	agc	gtg	tcg	gtg	tcg	atg	acc	atg	aat	ggc	595			
Asp	Gly	Ile	Asp	Leu	Ser	Ser	Val	Ser	Val	Ser	Met	Thr	Met	Asn	Gly				
150				155				160				165							
gct	gtg	ctg	ccg	att	ctt	gcg	ttc	tat	atc	gtg	gcg	gct	gag	gaa	caa	643			
Ala	Val	Leu	Pro	Ile	Leu	Ala	Phe	Tyr	Ile	Val	Ala	Ala	Glu	Glu	Gln				
170				175				180											
ggg	gtg	ggg	ccg	gag	cag	ctt	gcg	ggc	acg	atc	cag	aat	gac	atc	ttg	691			
Gly	Val	Gly	Pro	Glu	Gln	Leu	Ala	Gly	Thr	Ile	Gln	Asn	Asp	Ile	Leu				
185				190				195											
aaa	gaa	ttt	atg	gtg	cgc	aac	acc	tat	att	tat	ccg	ccg	aag	ccg	tcg	739			
Lys	Glu	Phe	Met	Val	Arg	Asn	Thr	Tyr	Ile	Tyr	Pro	Pro	Lys	Pro	Ser				
200				205				210											
atg	cgc	atc	att	tcc	aac	atc	ttt	gag	tac	acc	tcc	ttg	aag	atg	cca	787			
Met	Arg	Ile	Ile	Ser	Asn	Ile	Phe	Glu	Tyr	Thr	Ser	Leu	Lys	Met	Pro				
215				220				225											
cgt	ttt	aac	tcc	att	tcg	att	tct	ggc	tat	cac	atc	cag	gaa	gcg	gga	835			
Arg	Phe	Asn	Ser	Ile	Ser	Ile	Ser	Gly	Tyr	His	Ile	Gln	Glu	Ala	Gly				
230				235				240				245							
gcg	act	gcc	gat	ttg	gag	ctg	gcc	tac	act	ctg	gcg	gat	ggg	att	gaa	883			
Ala	Thr	Ala	Asp	Leu	Glu	Leu	Ala	Tyr	Thr	Leu	Ala	Asp	Gly	Ile	Glu				
250				255				260											
tac	atc	cgt	gca	ggg	aaa	gag	gta	ggc	ctt	gac	gtg	gat	aag	ttc	gcg				

cct cgt ctg tcc ttc ttc tgg ggt att tct atg tac acc ttc atg gag	979
Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu	
280 285 290	
atc gca aag ctg cgt gcg gga cga ctg ctg tgg agc gag ttg gtg gca	1027
Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp Ser Glu Leu Val Ala	
295 300 305	
aaa ttc gat ccg aaa aac gcc aag tcc cag tgc ctg cgc acg cac tcg	1075
Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser	
310 315 320 325	
cag acc tct ggt tgg tgc ttg acc gcg cag gat gtg tac aac aac gtc	1123
Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val	
330 335 340	
gcc cgc acc gcg att gag gcg atg gct gca acc cag ggc cac acc cag	1171
Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln	
345 350 355	
tcg ctg cac acc aat gca ctt gat gag gcg ttg gcg ctg ccc acc gat	1219
Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp	
360 365 370	
ttc tct gct cgt atc gcc cga aac acc cag ctg ttg ctg cag cag gaa	1267
Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Gln Gln Glu	
375 380 385	
tct ggc acg gtg cgt cca gtt gat cca tgg gcg ggc tcc tat tac gtg	1315
Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala Gly Ser Tyr Tyr Val	
390 395 400 405	
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Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala Arg Lys His Ile Asp	
410 415 420	
gag gtg gag gaa gcc gcc gga atg gcg cag gcc acc gcg cag gga att	1411
Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala Thr Ala Gln Gly Ile	
425 430 435	
cct aag ctg cgc att gag gaa tca gcg gca cgc acc cag gct cgc att	1459
Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg Thr Gln Ala Arg Ile	
440 445 450	
gat tcc ggc cgc cag gcg ctg atc gcc gtg aat cgc tac gtg gcg gaa	1507
Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn Arg Tyr Val Ala Glu	
455 460 465	
gaa gat gag gaa att gaa gtc ctc aag gtt gac aac acc aag gtt cgc	1555
Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg	
470 475 480 485	
gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat	1603
Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp	
490 495 500	
gcg gaa gtc aag gct gcg ctg gat gcg ttg aca gct gct gcc cgc aac	1651
Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Ala Arg Asn	
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gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc 1699  
 Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala  
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gtc gat gct gcg cgc gca aaa gct acc att gga gag atc tcc gat gct 1747  
 Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly Glu Ile Ser Asp Ala  
 535 540 545

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 Leu Glu Val Val Phe 555 Arg His Glu Ala Glu Ile Arg Thr Leu Ser  
 550 560 565

ggc gtg tac aag gat gag gtt gga aag gaa ggc aca gtg agc aac gtc 1843  
 Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly Thr Val Ser Asn Val  
 570 575 580

gaa cgc gcg atc gcc ctg gct gac gcc ttt gag gct gag gaa ggc cgc 1891  
 Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu Ala Glu Glu Gly Arg  
 585 590 595

cgc cca cgt atc ttt att gcc aag atg ggc cag gat gga cat gac cgt 1939  
 Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg  
 600 605 610

gga cag aag gtt gtc gcg tct gcc tat gct gac ctg ggc atg gac gtg 1987  
 Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val  
 615 620 625

gat gtt gga ccg ctg ttt caa act cca gcc gaa gct gcc cgc gcc gcc 2035  
 Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala  
 630 635 640 645

gtg gac gcc gat gtt cac gtg gtg ggt atg tct tcg ctg gca gca ggc 2083  
 Val Asp Ala Asp Val His Val Val Gly Met Ser Ser Leu Ala Ala Gly  
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cac ctc acc ttg ctg ccc gag ctg aag aaa gaa ctt gca gct ctt ggc 2131  
 His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu Leu Ala Ala Leu Gly  
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cgc gat gac att ctg gtc acc gtg ggc ggc gtc att ccg ccg ggc gat 2179  
 Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val Ile Pro Pro Gly Asp  
 680 685 690

ttc cag gat ctc tac gat atg ggt gcc gcc gcg att tac cct tca gga 2227  
 Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala Ile Tyr Pro Ser Gly  
 695 700 705

acc gtc atc gcg gag tcg gcg atc gat ctg atc acc cga ctc gcc gca 2275  
 Thr Val Ile Ala Glu Ser Ala Ile Asp Leu Ile Thr Arg Leu Ala Ala  
 710 715 720 725

cac ctg ggc ttt gac ctg gat gtg gat gtg aat gaa tgatcacggt 2321  
 His Leu Gly Phe Asp Leu Asp Val Asp Val Asn Glu  
 730 735

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&lt;210&gt; 628

&lt;211&gt; 737



&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 628

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Arg Ala Ser Glu Ser His Asn Val Asp Ala Gly Lys Val Trp Asn Thr
          20           25           30

Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp
          35           40           45

Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
          50           55           60

Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
          65           70           75           80

Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
          85           90           95

Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
          100          105          110

Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
          115          120          125

Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
          130          135          140

Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser
          145          150          155          160

Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
          165          170          175

Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile
          180          185          190

Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr
          195          200          205

Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr
          210          215          220

Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His
          225          230          235          240

Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
          245          250          255

Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
          260          265          270

Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met
          275          280          285

Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
          290          295          300

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Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser  
 305 310 315 320  
 Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp  
 325 330 335  
 Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr  
 340 345 350  
 Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu  
 355 360 365  
 Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu  
 370 375 380  
 Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala  
 385 390 395 400  
 Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala  
 405 410 415  
 Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala  
 420 425 430  
 Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg  
 435 440 445  
 Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn  
 450 455 460  
 Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp  
 465 470 475 480  
 Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys  
 485 490 495  
 Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr  
 500 505 510  
 Ala Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn  
 515 520 525  
 Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly  
 530 535 540  
 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu  
 545 550 555 560  
 Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly  
 565 570 575  
 Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu  
 580 585 590  
 Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln  
 595 600 605  
 Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp  
 610 615 620  
 Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu

625		630		635		640
Ala Ala Arg Ala	Ala Val Asp Ala Asp	Val His Val Val	Gly Met Ser			
	645	650	655			
Ser Leu Ala Ala	Gly His Leu Thr	Leu Leu Pro Glu	Leu Lys Lys Glu			
	660	665	670			
Leu Ala Ala Leu	Gly Arg Asp Asp	Ile Leu Val Thr	Val Gly Gly Val			
	675	680	685			
Ile Pro Pro Gly	Asp Phe Gln Asp	Leu Tyr Asp Met	Gly Ala Ala Ala			
	690	695	700			
Ile Tyr Pro Ser	Gly Thr Val Ile	Ala Glu Ser Ala	Ile Asp Leu Ile			
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Thr Arg Leu Ala	Ala His Leu Gly	Phe Asp Leu Asp	Val Asp Val Asn			
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Glu

<210> 629  
 <211> 2098  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2098)  
 <223> FRXA00148

<400> 629  
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 Met Thr Ser Ile Pro  
 1 5  
 aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca 163  
 Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser  
 10 15 20  
 cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat 211  
 His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp  
 25 30 35  
 gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg 259  
 Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala  
 40 45 50  
 gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg 307  
 Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly  
 55 60 65  
 ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac 355  
 Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr  
 70 75 80 85

gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat cgg agg aac	403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn	
90 95 100	
ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc	451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr	
105 110 115	
cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt	499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly	
120 125 130	
atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt	547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe	
135 140 145	
gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc	595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly	
150 155 160 165	
gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa	643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln	
170 175 180	
ggt gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg	691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu	
185 190 195	
aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg	739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser	
200 205 210	
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Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr Ser Leu Lys Met Pro	
215 220 225	
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Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His Ile Gln Glu Ala Gly	
230 235 240 245	
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Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Ile Glu	
250 255 260	
tac atc cgt gca ggt aaa gag gta ggc ctt gac gtg gat aag ttc gcg	931
Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala	
265 270 275	
cct cgt ctg tcc ttc ttc tgg ggt att tct atg tac acc ttc atg gag	979
Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu	
280 285 290	
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Ile Ala Lys Leu Arg Ala Glu Arg Leu Leu Trp Ser Glu Leu Val Ala	
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Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser	
310 315 320 325	
cag acc tct ggt tgg tcg ttg acc gcg cag gat gtg tac aac aac gtc	1123

Gln	Thr	Ser	Gly	Trp	Ser	Leu	Thr	Ala	Gln	Asp	Val	Tyr	Asn	Asn	Val		
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Ala	Arg	Thr	Ala	Ile	Glu	Ala	Met	Ala	Ala	Thr	Gln	Gly	His	Thr	Gln		
			345					350					355				
tcg	ctg	cac	acc	aat	gca	ctt	gat	gag	gcg	ttg	gcg	ctg	ccc	acc	gat	1219	
Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Leu	Pro	Thr	Asp		
			360					365					370				
ttc	tct	gct	cgt	atc	gcc	cga	aac	acc	cag	ctg	ttg	ctg	cag	cag	gaa	1267	
Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu	Leu	Leu	Gln	Gln	Glu		
			375					380					385				
tct	ggc	acg	gtg	cgt	cca	gtt	gat	cca	tgg	gcg	ggc	tcc	tat	tac	gtg	1315	
Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala	Gly	Ser	Tyr	Tyr	Val		
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gag	tgg	ttg	acc	aat	gag	ctg	gct	aac	cgc	gcg	cgc	aag	cac	atc	gat	1363	
Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala	Arg	Lys	His	Ile	Asp		
				410					415					420			
gag	gtg	gag	gaa	gcc	ggc	gga	atg	gcg	cag	gcc	acc	gcg	cag	gga	att	1411	
Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala	Thr	Ala	Gln	Gly	Ile		
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cct	aag	ctg	cgc	att	gag	gaa	tca	gcg	gca	cgc	acc	cag	gct	cgc	att	1459	
Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg	Thr	Gln	Ala	Arg	Ile		
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Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn	Arg	Tyr	Val	Ala	Glu		
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gaa	gat	gag	gaa	att	gaa	gtc	ctc	aag	gtt	gac	aac	acc	aag	gtt	cgc	1555	
Glu	Asp	Glu	Glu	Ile	Glu	Val	Leu	Lys	Val	Asp	Asn	Thr	Lys	Val	Arg		
						475				480					485		
gca	gaa	cag	ttg	gct	aaa	ctc	gcg	caa	ctg	aaa	gca	gag	cgc	aac	gat	1603	
Ala	Glu	Gln	Leu	Ala	Lys	Leu	Ala	Gln	Leu	Lys	Ala	Glu	Arg	Asn	Asp		
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Ala	Glu	Val	Lys	Ala	Ala	Leu	Asp	Ala	Leu	Thr	Ala	Ala	Ala	Arg	Asn		
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Glu	His	Lys	Glu	Pro	Gly	Asp	Leu	Asp	Gln	Asn	Leu	Leu	Lys	Leu	Ala		
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gtc	gat	gct	gcg	cgc	gca	aaa	gct	acc	att	gga	gag	atc	tcc	gat	gct	1747	
Val	Asp	Ala	Ala	Arg	Ala	Lys	Ala	Thr	Ile	Gly	Glu	Ile	Ser	Asp	Ala		
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Leu	Glu	Val	Val	Phe	Gly	Arg	His	Glu	Ala	Glu	Ile	Arg	Thr	Leu	Ser		
						555				560					565		
ggc	gtg	tac	aag	gat	gag	gtt	gga	aag	gaa	ggc	aca	gtg	agc	aac	gtc	1843	
Gly	Val	Tyr	Lys	Asp	Glu	Val	Gly	Lys	Glu	Gly	Thr	Val	Ser	Asn	Val		

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gaa	cgc	gcg	atc	gcc	ctg	gct	gac	gcc	ttt	gag	gct	gag	gaa	ggc	cgc	1891				
Glu	Arg	Ala	Ile	Ala	Leu	Ala	Asp	Ala	Phe	Glu	Ala	Glu	Glu	Gly	Arg					
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cgc	cca	cgt	atc	ttt	att	gcc	aag	atg	ggc	cag	gat	gga	cat	gac	cgt	1939				
Arg	Pro	Arg	Ile	Phe	Ile	Ala	Lys	Met	Gly	Gln	Asp	Gly	His	Asp	Arg					
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gga	cag	aag	gtt	gtc	gcg	tct	gcc	tat	gct	gac	ctg	ggc	atg	gac	gtg	1987				
Gly	Gln	Lys	Val	Val	Ala	Ser	Ala	Tyr	Ala	Asp	Leu	Gly	Met	Asp	Val					
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gat	gtt	gga	ccg	ctg	ttt	caa	act	cca	gcc	gaa	gct	gcc	cgc	gcc	gcc	2035				
Asp	Val	Gly	Pro	Leu	Phe	Gln	Thr	Pro	Ala	Glu	Ala	Ala	Arg	Ala	Ala					
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gtg	gac	gcc	gat	gtt	cac	gtg	gtg	ggt	atg	tct	tcg	ctg	gca	gca	ggc	2083				
Val	Asp	Ala	Asp	Val	His	Val	Val	Gly	Met	Ser	Ser	Leu	Ala	Ala	Gly					
			650				655				660									
cac	ctc	acc	ttg	ctg											2098					
His	Leu	Thr	Leu	Leu																
			665																	

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&lt;211&gt; 666

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 630

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Pro	Glu	Gly	Ile	Asp	Val	Lys	Arg	Val	Phe	Thr	Gln	Ala	Asp	Arg	Asp
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Glu	Ala	Gln	Ala	Ala	Gly	His	Pro	Val	Asp	Ser	Leu	Pro	Gly	Gln	Lys
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Pro	Phe	Met	Arg	Gly	Pro	Tyr	Pro	Thr	Met	Tyr	Thr	Asn	Gln	Pro	Trp
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Thr	Ile	Arg	Gln	Tyr	Ala	Gly	Phe	Ser	Thr	Ala	Ala	Glu	Ser	Asn	Ala
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Phe	Tyr	Arg	Arg	Asn	Leu	Ala	Ala	Gly	Gln	Lys	Gly	Leu	Ser	Val	Ala
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Phe	Asp	Leu	Ala	Thr	His	Arg	Gly	Tyr	Asp	Ser	Asp	Asn	Glu	Arg	Val
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Val	Gly	Asp	Val	Gly	Met	Ala	Gly	Val	Ala	Ile	Asp	Ser	Ile	Leu	Asp
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Met	Arg	Gln	Leu	Phe	Asp	Gly	Ile	Asp	Leu	Ser	Ser	Val	Ser	Val	Ser
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Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val						
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Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile						
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Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr						
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Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr						
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Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His						
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Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu						
		245		250		255
Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp						
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Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met						
		275		280		285
Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp						
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Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser						
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Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp						
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Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr						
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Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu						
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Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu						
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Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala						
		385		390		395
Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala						
		405		410		415
Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala						
		420		425		430
Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg						
		435		440		445
Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn						
		450		455		460
Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp						
		465		470		475
						480

Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys  
 485 490 495  
 Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr  
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 530 535 540  
 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu  
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 Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln  
 595 600 605  
 Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp  
 610 615 620  
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 Leu Thr Asp Leu Thr 5  
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 Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn Leu Glu Thr Trp Tyr 20  
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 Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln Lys Lys Asp Ile Gly



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Lys	Phe	Thr	Glu	Val	Pro	Gly	Glu	Phe	Pro	Phe	Thr	Arg	Gly	Thr	Thr															
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Ser	Arg	Pro	Leu	Thr	Ala	Gln	Val	Asp	Gly	Ser	His	Ser	Asp	Thr	Ile															
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gaa	gaa	gca	ggt	cag	ttg	gca	gtg	aat	gct	tcc	aag	cgt	gcg	aat	gtg	739														
Glu	Glu	Ala	Val	Gln	Leu	Ala	Val	Asn	Ala	Ser	Lys	Arg	Ala	Asn	Val															
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Arg	Arg	Leu	Val	Asp	Ala	Gly	Leu	Ser	Thr	Glu	Ala	Ala	Leu	Lys	Gln															
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Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His Ala Val Thr Ala Arg	
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Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn Met Leu Arg Ser Thr	
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Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala Thr Asp Val Glu Val	
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Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val Pro Gly Val Ser Arg	
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Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn Leu Leu Leu Leu Glu	
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gag tca cat ctt ggt cac gtg gtt gat cct gct ggt gga tca tat ttc	1267
Glu Ser His Leu Gly His Val Val Asp Pro Ala Gly Gly Ser Tyr Phe	
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Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys Ala Trp Ala Val Phe	
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Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala Ala Cys Ala Ser Gly	
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Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu Gln Thr Arg Ala Asp	
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Leu Ala Glu Ser Pro Leu Pro Ala Asp Arg Arg Val Glu Pro Ala Gly	
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Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu Arg Asn Arg Ser Asp	
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Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln Ile Thr Met Ile Pro	
490 495 500	
ctg gga ccg ttg tcc aag cac aat att cgc act ggt ttt act tcc aac	1651
Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr Gly Phe Thr Ser Asn	
505 510 515	

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ccc ggc act gac gct ttt gca gaa gct gca cag gcc gca ggc att gta 1747  
 Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln Ala Ala Gly Ile Val  
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gcg ccg aag agc ttt gag ggc agc gcg cat gcg ccc gat ggt tat ttg 1891  
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aac atg aca att gat gcc gcg gcg acg ctg gct gac ctg cta gat gct 1939  
 Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala Asp Leu Leu Asp Ala  
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           20                                  25                                  30

Lys Lys Asp Ile Gly Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile  
           35                                  40                                  45

Val Thr Thr Pro Asp Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala  
           50                                  55                                  60

Asp Glu Ser Gln Arg Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe  
           65                                  70                                  75                                  80

Thr Arg Gly Thr Thr Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr  
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Glu Thr Phe Gly His Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu  
           100                                  105                                  110

Asn Ala Leu Asn Ser Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu  
           115                                  120                                  125

Glu Phe Thr Ala Ala Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu  
           130                                  135                                  140

Asn Met Ala Pro Leu Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val  
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 Ala Leu Thr Leu Gly Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser  
 180 185 190  
 His Ser Asp Thr Ile Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser  
 195 200 205  
 Lys Arg Ala Asn Val Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser  
 210 215 220  
 Asn Gln Gly Ala Ser Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala  
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 Gly Val Asp Tyr Val Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu  
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 Ala Ala Leu Lys Gln Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln  
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Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln  
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Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr  
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Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn  
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Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln  
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 Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Arg Leu Lys Tyr  
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 Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys Gly Glu Phe Phe Ala  
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 gag aag gta ctt cgc aaa ttc gag atg ttc gat ctc ttc gaa ttc atg 499  
 Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp Leu Phe Glu Phe Met  
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 aaa cat gtc ctc gac agc gtt ggg ttg gac gaa cca aat gat att ttg 595  
 Lys His Val Leu Asp Ser Val Gly Leu Asp Glu Pro Asn Asp Ile Leu  
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 Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly Ser Ser Glu Phe Gly  
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 Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly Ser Lys Thr Glu Trp  
 185 190 195  
 gac gct gcc cgc tac acc gtg agc acc gca gaa gaa tta gaa agg atc 739  
 Asp Ala Ala Arg Tyr Thr Val Ser Thr Ala Glu Glu Leu Glu Arg Ile  
 200 205 210  
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 Ile His Asp Trp Ala  
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&lt;210&gt; 634

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 634

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 Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu  
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 His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val  
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 Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro  
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Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln  
 65 70 75 80  
 Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu  
 85 90 95  
 Ile Arg Leu Lys Tyr Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys  
 100 105 110  
 Gly Glu Phe Phe Ala Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp  
 115 120 125  
 Leu Phe Glu Phe Met Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser  
 130 135 140  
 Lys Ser Ala Val Ile Lys His Val Leu Asp Ser Val Gly Leu Asp Glu  
 145 150 155 160  
 Pro Asn Asp Ile Leu Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly  
 165 170 175  
 Ser Ser Glu Phe Gly Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly  
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 <212> DNA  
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 Val Thr Thr Pro Ser  
 1 5  
 aag aaa act ctg ctc ttt gat ctc gac gga acc ctc gtc gat tct ttc 163  
 Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe  
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 Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp  
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 gaa atc ccc tct gag gaa cgc atc tcg caa gtt cca gga cct ccc atg 259  
 Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met  
 40 45 50

gaa tgg acg ttc cag gat ttg ggc atg act cca gag cag gca caa gac 307  
 Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro Glu Gln Ala Gln Asp  
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gct ctg cag acc tac ctt gag cat tac ggc cag gtg ggt tgg gat ctt 355  
 Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln Val Gly Trp Asp Leu  
     70                    75                    80                    85

tcc gaa gca ttc ccc ggc atg cga gat ttg ctg atc ccc ttg ata tac 403  
 Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Pro Leu Ile Tyr  
                     90                    95                    100

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<211> 113

<212> PRT

<213> Corynebacterium glutamicum

<400> 636

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Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu  
             20                    25                    30

His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val  
             35                    40                    45

Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro  
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Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln  
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Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu  
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Ile Pro Leu Ile Tyr Glu Gly Phe Arg Leu Cys Thr Ala Thr Phe Gln  
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Gly

<210> 637

<211> 816

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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<400> 637

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Met Ile Lys Ala Ile
1 5

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Phe Trp Asp Met Asp Gly Thr Met Val Asp Ser Glu Pro Gln Trp Gly
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Ile Ala Thr Tyr Glu Leu Ser Glu Ala Met Gly Arg Arg Leu Thr Pro
25 30 35

gag ctc cgg gaa ctc acc gtc ggc tcg agc ctg ccg cgc acc atg cgc 259
Glu Leu Arg Glu Leu Thr Val Gly Ser Ser Leu Pro Arg Thr Met Arg
40 45 50

tta tgc gca gag cac gca ggc att aca ttg agc gac gcg gac tac gag 307
Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser Asp Ala Asp Tyr Glu
55 60 65

cgc tac cgg gct ggc atg ttc gcc cgg gtc cat gag ctt ttc gac gaa 355
Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His Glu Leu Phe Asp Glu
70 75 80 85

tcc ctc gtc cca aat cca ggc gtc acc gaa ctc ctg aca gag ttg aag 403
Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu Leu Thr Glu Leu Lys
90 95 100

gcc ctc gag atc ccc atg ttg gtc acc acc aac aca gag cgc gat ctc 451
Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn Thr Glu Arg Asp Leu
105 110 115

gcg acc cgt tca gtc gca gcc gtg gga aat gag ttc ttc atc ggt tct 499
Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu Phe Phe Ile Gly Ser
120 125 130

atc gct ggt gat gaa gtc cca aca gca aag cca gcc ccc gac atg tac 547
Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro Ala Pro Asp Met Tyr
135 140 145

ctc gaa gca gca cga cgt gtg ggc ttt gac cca tca gag tgc ctc gtg 595
Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro Ser Glu Cys Leu Val
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ttc gaa gat tcc tac aac ggc atg ctg ggc gct gtt act gca ggt tgc 643
Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala Val Thr Ala Gly Cys
170 175 180

cgc gtc att ggt ctg cac cca gaa gaa gtc caa gcg cca gaa ggt gta 691
Arg Val Ile Gly Leu His Pro Glu Glu Val Gln Ala Pro Glu Gly Val
185 190 195

gtg cct ttg cgt tcc ctc cac ggt aaa aac tct ttc gaa ggt gtc acc 739
Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser Phe Glu Gly Val Thr
200 205 210

gct gag atg gtc act gcc tgg tac cac cag atc gag ccg gca ggt gtc 787
Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile Glu Pro Ala Gly Val
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Ala Lys  
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<212> PRT  
<213> Corynebacterium glutamicum

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Arg Arg Leu Thr Pro Glu Leu Arg Glu Leu Thr Val Gly Ser Ser Leu  
35 40 45  
Pro Arg Thr Met Arg Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser  
50 55 60  
Asp Ala Asp Tyr Glu Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His  
65 70 75 80  
Glu Leu Phe Asp Glu Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu  
85 90 95  
Leu Thr Glu Leu Lys Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn  
100 105 110  
Thr Glu Arg Asp Leu Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu  
115 120 125  
Phe Phe Ile Gly Ser Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro  
130 135 140  
Ala Pro Asp Met Tyr Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro  
145 150 155 160  
Ser Glu Cys Leu Val Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala  
165 170 175  
Val Thr Ala Gly Cys Arg Val Ile Gly Leu His Pro Glu Glu Val Gln  
180 185 190  
Ala Pro Glu Gly Val Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser  
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Phe Glu Gly Val Thr Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile  
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<210> 639  
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<212> DNA  
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&lt;221&gt; CDS

&lt;222&gt; (101)..(508)

&lt;223&gt; RXN02461

&lt;400&gt; 639

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                                         Met Arg Gly Leu Ile
                                         1 5
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Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg
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Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val
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atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa 259
Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu
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ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt 307
Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu
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ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc 355
Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala
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Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val Asp Asp Ser Ile Leu
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Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val Gly Val Tyr Tyr Gln
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Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly Leu Phe Gly Leu Glu
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Gly Glu Phe
135

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&lt;210&gt; 640

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 640

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Glu Asp Gln Arg Arg Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn
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Gly Val Gly Thr Val Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala  
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 Ala Ala Ala Asp Ala Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val  
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 Asp Asp Ser Ile Leu Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val  
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 Gly Val Tyr Tyr Gln Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly  
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<220>  
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 <223> RXN01744

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   Val Asp Val Val Asp  
   1                          5  
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 Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe  
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 Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr  
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 Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr Arg Ala Thr Arg Phe  
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 Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val Gly Val Ala Thr Gly  
          55                         60                         65  
 att gtg cag gag ttc cag ttc ggt atg aac tgg tcg gaa tat tcg cgt 355  
 Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp Ser Glu Tyr Ser Arg  
      70                         75                         80                         85  
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Ala	Phe	Phe	Leu	Glu	Ser	Val	Phe	Leu	Gly	Leu	Trp	Ile	Phe	Gly	Trp		
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ggg	aag	att	cct	ggg	tgg	ttg	cac	act	gca	tcc	att	tgg	atc	gtt	gct	499	
Gly	Lys	Ile	Pro	Gly	Trp	Leu	His	Thr	Ala	Ser	Ile	Trp	Ile	Val	Ala		
120								125				130					
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Ile	Ala	Thr	Asn	Ile	Ser	Ala	Tyr	Phe	Ile	Ile	Val	Ala	Asn	Ser	Phe		
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Met	Gln	His	Pro	Val	Gly	Ala	Glu	Tyr	Asn	Pro	Glu	Thr	Gly	Arg	Ala		
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Ala	Phe	Pro	His	Ala	Val	Ala	Gly	Gly	Phe	Leu	Thr	Ala	Gly	Thr	Phe		
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Val	Leu	Gly	Ile	Ser	Gly	Trp	Trp	Ile	Ile	Arg	Ala	His	Arg	Gln	Ala		
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Lys	Lys	Ala	Glu	Ser	Glu	Ile	Glu	Ser	Lys	His	Ser	Met	His	Arg	Pro		
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Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu	Met	Phe	Val	Gln	Gln	Pro		
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Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys	Glu	Thr	Ala	Thr	Asp	Pro		
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Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His	Asn	Asn	Cys	Asp	Thr	Val		
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Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val	Asn	Gln	Leu	Gln	Ala	Ala		
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 Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg Lys Lys Arg Thr Pro  
 360 365 370  
  
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 Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly Ser Leu Ile Ala Ile  
 375 380 385  
  
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 Gly Arg Gln Pro Trp Val Val His Pro Asn Pro Glu Ser Ala Gly Asp  
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 Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp Met Gly Val Ser Asp  
 425 430 435  
  
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 His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile Gly Phe Thr Ile Leu  
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 Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu Ile Arg Arg Ala Val  
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 Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser Val Glu Ala Lys Thr  
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 Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro Met Thr Pro Leu Gln  
 490 495 500  
  
 ttt act gcc gct gcc cca acc aca ggt gaa aag gaa taaccatgga 1649  
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&lt;210&gt; 642

&lt;211&gt; 513

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 642

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Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val  
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Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr

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Ser	Glu	Tyr	Ser	Arg	Phe	Val	Gly	Asp	Val	Phe	Gly	Gly	Pro	Leu	Ala
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Leu	Glu	Gly	Leu	Ile	Ala	Phe	Phe	Leu	Glu	Ser	Val	Phe	Leu	Gly	Leu
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Trp	Ile	Phe	Gly	Trp	Gly	Lys	Ile	Pro	Gly	Trp	Leu	His	Thr	Ala	Ser
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Ile	Trp	Ile	Val	Ala	Ile	Ala	Thr	Asn	Ile	Ser	Ala	Tyr	Phe	Ile	Ile
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Val	Ala	Asn	Ser	Phe	Met	Gln	His	Pro	Val	Gly	Ala	Glu	Tyr	Asn	Pro
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Glu	Thr	Gly	Arg	Ala	Glu	Leu	Thr	Asp	Phe	Trp	Ala	Leu	Leu	Thr	Asn
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Ser	Thr	Ala	Leu	Ala	Ala	Phe	Pro	His	Ala	Val	Ala	Gly	Gly	Phe	Leu
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210						215					220				
Ser	Met	His	Arg	Pro	Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val	Val
225					230					235					240
Ser	Ser	Val	Ala	Leu	Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu	Met
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Phe	Val	Gln	Gln	Pro	Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys	Glu
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Thr	Ala	Thr	Asp	Pro	Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His	Asn
		275					280					285			
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290						295					300				
Phe	Leu	Ala	Glu	Gly	Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val	Asn
305					310					315					320
Gln	Leu	Gln	Ala	Ala	Ala	Glu	Gln	Ala	Tyr	Gly	Pro	Gly	Asn	Tyr	Ser
				325					330					335	
Pro	Asn	Leu	Phe	Val	Thr	Tyr	Trp	Ser	Phe	Arg	Ala	Met	Ile	Gly	Leu
				340				345					350		
Met	Leu	Gly	Ser	Leu	Ala	Ile	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Leu	Arg
		355					360					365			

Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly  
 370 375 380  
 Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp  
 385 390 395 400  
 Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn Pro  
 405 410 415  
 Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp  
 420 425 430  
 Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile  
 435 440 445  
 Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu  
 450 455 460  
 Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser  
 465 470 475 480  
 Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro  
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 Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys  
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Glu

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 <213> Corynebacterium glutamicum

<220>  
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 <223> FRXA00055

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 Val Asp Val Val Asp  
 1 5  
 atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt 163  
 Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe  
 10 15 20  
 gtc cca ctg acc att ggc tta gca ccg ctg gtc gcg atc atg caa acg 211  
 Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr  
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 Phe Trp Gln Val Thr Gly Lys Glu His  
 40 45



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 <212> PRT  
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 Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val  
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 Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His  
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<220>  
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 Trp Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu  
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 gct ttg gag ggt ctt atc gcg ttc ttc ctt gag tct gta ttc ctg gga 96  
 Ala Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly  
           20                    25                    30  
 ctg tgg att ttc gga tgg ggg aag att cct ggt tgg ttg cac act gca 144  
 Leu Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala  
           35                    40                    45  
 tcc att tgg atc gtt gct att gcg acg aat att tct gcc tat ttc atc 192  
 Ser Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile  
           50                    55                    60  
 atc gtg gcc aac tcg ttt atg cag cat ccg gtg ggt gct gag tat aac 240  
 Ile Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn  
           65                    70                    75                    80  
 cct gag act ggt cgt gcg gag ctt act gat ttt tgg gct ctt ctg aca 288  
 Pro Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr  
           85                    90                    95  
 aac tcc acc gcg ctg gct gcg ttc ccg cat gct gtt gcc ggt ggt ttt 336  
 Asn Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe  
           100                    105                    110  
 tta aca gct gga act ttc gtt ctg gga att tcg ggt tgg tgg att att 384  
 Leu Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile  
           115                    120                    125  
 cgt gcg cac cgt cag gcc aag aag gct gag tcg gaa atc gag tcg aag 432

Arg	Ala	His	Arg	Gln	Ala	Lys	Lys	Ala	Glu	Ser	Glu	Ile	Glu	Ser	Lys	
130						135					140					
cat	tcg	atg	cac	agg	ccc	gcg	ttg	tgg	gtt	ggt	tgg	tgg	acc	aca	gtt	480
His	Ser	Met	His	Arg	Pro	Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val	
145					150					155					160	
gtc	tct	tcc	gtg	gcg	ctg	ttc	atc	act	ggc	gat	atc	cag	gcg	aag	ctc	528
Val	Ser	Ser	Val	Ala	Leu	Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu	
				165					170					175		
atg	ttc	gtg	caa	cag	cca	atg	aag	atg	gcg	tcg	gcg	gaa	tcc	ttg	tgt	576
Met	Phe	Val	Gln	Gln	Pro	Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys	
			180					185					190			
gaa	acc	gcc	aca	gat	cca	aac	ttc	tcc	att	ctg	aca	att	ggt	acg	cac	624
Glu	Thr	Ala	Thr	Asp	Pro	Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His	
		195					200					205				
aac	aac	tgc	gat	acg	gta	acc	cac	ctg	atc	gat	gtt	ccg	ttt	gtg	ctt	672
Asn	Asn	Cys	Asp	Thr	Val	Thr	His	Leu	Ile	Asp	Val	Pro	Phe	Val	Leu	
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cca	ttc	ttg	gct	gaa	gga	aaa	ttc	acc	ggt	gtg	act	ttg	cag	ggt	gta	720
Pro	Phe	Leu	Ala	Glu	Gly	Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val	
225					230				235						240	
aac	cag	ctc	caa	gct	gca	gcg	gag	caa	gca	tac	ggt	cct	ggc	aac	tac	768
Asn	Gln	Leu	Gln	Ala	Ala	Ala	Glu	Gln	Ala	Tyr	Gly	Pro	Gly	Asn	Tyr	
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tcc	cct	aac	ttg	ttt	gtc	acc	tac	tgg	tca	ttc	cgc	gca	atg	atc	ggc	816
Ser	Pro	Asn	Leu	Phe	Val	Thr	Tyr	Trp	Ser	Phe	Arg	Ala	Met	Ile	Gly	
			260					265					270			
ctg	atg	ctt	ggt	tct	ttg	gct	atc	gct	gcg	att	gcg	tgg	ctg	ttg	ctg	864
Leu	Met	Leu	Gly	Ser	Leu	Ala	Ile	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Leu	
		275					280					285				
cgt	aag	aag	cgc	aca	cca	act	gga	aag	att	gct	cgt	ctg	ttc	cag	atc	912
Arg	Lys	Lys	Arg	Thr	Pro	Thr	Gly	Lys	Ile	Ala	Arg	Leu	Phe	Gln	Ile	
	290					295					300					
ggc	agc	ctc	att	gct	atc	ccg	ttc	cca	ttc	ttg	gcc	aac	tct	gct	ggt	960
Gly	Ser	Leu	Ile	Ala	Ile	Pro	Phe	Pro	Phe	Leu	Ala	Asn	Ser	Ala	Gly	
305					310					315					320	
tgg	atc	ttc	acc	gag	atg	ggc	cgc	cag	cct	tgg	gtg	gtg	cac	ccg	aac	1008
Trp	Ile	Phe	Thr	Glu	Met	Gly	Arg	Gln	Pro	Trp	Val	Val	His	Pro	Asn	
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cct	gaa	tct	gcc	ggc	gat	gcc	cga	aca	gag	atg	atc	cgg	atg	act	gtt	1056
Pro	Glu	Ser	Ala	Gly	Asp	Ala	Arg	Thr	Glu	Met	Ile	Arg	Met	Thr	Val	
			340					345					350			
gat	atg	ggt	gta	tct	gat	cat	gcg	cca	tgg	caa	gtc	tgg	ctg	act	ctc	1104
Asp	Met	Gly	Val	Ser	Asp	His	Ala	Pro	Trp	Gln	Val	Trp	Leu	Thr	Leu	
		355					360					365				
att	ggc	ttc	acg	att	ctc	tat	ctc	att	ttg	ttc	gtg	gtg	tgg	gtg	tgg	1152
Ile	Gly	Phe	Thr	Ile	Leu	Tyr	Leu	Ile	Leu	Phe	Val	Val	Trp	Val	Trp	

370	375	380	
ctg att cgc cgc gca gtt	ctg atc gga cca cca	gag gaa ggc gct cca	1200
Leu Ile Arg Arg Ala Val	Leu Ile Gly Pro Pro	Glu Glu Gly Ala Pro	
385	390	395 400	
tcc gtg gag gca aag act	gga ccg gca acc ccg	att ggt tca gat atg	1248
Ser Val Glu Ala Lys Thr	Gly Pro Ala Thr Pro	Ile Gly Ser Asp Met	
	405 410	415	
ccc atg aca ccg ctg caa ttt	act gcc gct gcc cca acc	aca ggt gaa	1296
Pro Met Thr Pro Leu Gln	Phe Thr Ala Ala Ala	Pro Thr Thr Gly Glu	
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Lys Glu			

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 646  
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 Leu Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala  
 35 40 45  
 Ser Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile  
 50 55 60  
 Ile Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn  
 65 70 75 80  
 Pro Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr  
 85 90 95  
 Asn Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe  
 100 105 110  
 Leu Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile  
 115 120 125  
 Arg Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys  
 130 135 140  
 His Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val  
 145 150 155 160  
 Val Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu  
 165 170 175  
 Met Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys  
 180 185 190

Glu Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His  
 195 200 205  
 Asn Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu  
 210 215 220  
 Pro Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val  
 225 230 235 240  
 Asn Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr  
 245 250 255  
 Ser Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly  
 260 265 270  
 Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu  
 275 280 285  
 Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile  
 290 295 300  
 Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly  
 305 310 315 320  
 Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn  
 325 330 335  
 Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val  
 340 345 350  
 Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu  
 355 360 365  
 Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp  
 370 375 380  
 Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro  
 385 390 395 400  
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 Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu  
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Lys Glu

<210> 647  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA00379

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Met Ser Glu Ile Val
1 5

gta gcc caa agc atc ggc cag cag ttt gct gac gtc gca gct tcc ggg 163
Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp Val Ala Ala Ser Gly
10 15 20

cca ctg ttc ctt ggc atc ctt gcc gca gcg ctc gca ggt ctg gtg tct 211
Pro Leu Phe Leu Gly Ile Leu Ala Ala Leu Ala Gly Leu Val Ser
25 30 35

ttt gcc agc ccg tgt gtt gtg ccg ttg gtg cca gga tat att tcc tac 259
Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro Gly Tyr Ile Ser Tyr
40 45 50

ctc gcc ggc gtg gtc ggt ggg gaa gtg gaa tac agc gct cat gcc acc 307
Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr Ser Ala His Ala Thr
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 <212> PRT  
 <213> Corynebacterium glutamicum

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Val Ala Ala Ser Gly Pro Leu Phe Leu Gly Ile Leu Ala Ala Ala Leu
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Ala Gly Leu Val Ser Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro
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Gly Tyr Ile Ser Tyr Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr
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Ser Ala His Ala Thr
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(339)  
 <223> RXA00385

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ctg gct gcg atc atc tcc att tct gca ggt act gaa ggc atg acc gct 96
Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala

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20										25										30										
gcg	cgt	ggc	gtg	atc	tta	att	gtg	ggg	tac	tgc	ctc	gga	ctg	ggg	ctg		144													
Ala	Arg	Gly	Val	Ile	Leu	Ile	Val	Gly	Tyr	Cys	Leu	Gly	Leu	Gly	Leu															
		35						40					45																	
ccg	ttc	ctg	ctg	atc	gcg	ttg	ggc	tcc	agc	aag	gca	ctc	acc	gga	gtc		192													
Pro	Phe	Leu	Leu	Ile	Ala	Leu	Gly	Ser	Ser	Lys	Ala	Leu	Thr	Gly	Val															
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gag	tgg	ttg	cgc	aag	cat	tcc	cgc	acc	ctg	caa	att	atc	ggc	ggg	gtg		240													
Glu	Trp	Leu	Arg	Lys	His	Ser	Arg	Thr	Leu	Gln	Ile	Ile	Gly	Gly	Val															
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Phe	Leu	Ile	Leu	Val	Gly	Val	Ala	Leu	Leu	Ser	Gly	Ser	Trp	Ala	Ile															
				85					90					95																
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Phe	Ile	Asn	Trp	Val	Arg	Gln	Trp	Thr	Val	Glu	Tyr	Gly	Ala	Thr	Leu															
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ctc	tagaaaaaga	cttttagtag	gaa														362													
Leu																														

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 650															
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Ala	Arg	Gly	Val	Ile	Leu	Ile	Val	Gly	Tyr	Cys	Leu	Gly	Leu	Gly	Leu
		35					40					45			
Pro	Phe	Leu	Leu	Ile	Ala	Leu	Gly	Ser	Ser	Lys	Ala	Leu	Thr	Gly	Val
		50				55					60				
Glu	Trp	Leu	Arg	Lys	His	Ser	Arg	Thr	Leu	Gln	Ile	Ile	Gly	Gly	Val
		65				70				75					80
Phe	Leu	Ile	Leu	Val	Gly	Val	Ala	Leu	Leu	Ser	Gly	Ser	Trp	Ala	Ile
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Leu															

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 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(901)

&lt;223&gt; RXA01743

&lt;400&gt; 651

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                                         Met Asp Leu Asn Thr
                                         1 5

ttt tgg ttt att ctc atc gca ttt ttg ttt gcg gga tac ttt ctc ctc 163
Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala Gly Tyr Phe Leu Leu
          10          15          20

gaa gga ttc gac ttc ggc gtc gga att ttg gca ccc atc atc ggt aaa 211
Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala Pro Ile Ile Gly Lys
          25          30          35

gat tca gcg gct agg aac aca gtg atc cgt acg att ggc cct gtc tgg 259
Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr Ile Gly Pro Val Trp
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gac gga aat gaa gtg tgg ctg atc gtg gca ggt ggc gct ttg ttt gct 307
Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly Gly Ala Leu Phe Ala
          55          60          65

gcc ttc cct gag tgg tac gca acg atg ttc tcc gga atg tat ctg ccg 355
Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser Gly Met Tyr Leu Pro
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ctg ttc ctc gtg ctt gtg tcg ttg atc atg cgc gtg gtg ggc ctt gaa 403
Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg Val Val Gly Leu Glu
          90          95          100

tgg cgc aag aaa gtc gat gat cct cgt tgg caa aag tgg tct gac cgg 451
Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln Lys Trp Ser Asp Arg
          105          110          115

gcc atc ttt att ggt tct tgg act cca ccg ctg atg tgg gga ttc atc 499
Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu Met Trp Gly Phe Ile
          120          125          130

ttc gcc aat att ttg cgt ggc atg ccc ctc aag gcg gat cac acc atc 547
Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys Ala Asp His Thr Ile
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gat gct gcg gca gcc ctt cct ggc atg gtc aac gtc ttc gcc att ctg 595
Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn Val Phe Ala Ile Leu
          150          155          160          165

ggg gca ctt gcg ttc acc gca ctg ttc gcc ctt cat ggt ctc gca ttc 643
Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu His Gly Leu Ala Phe
          170          175          180

atc cgc ctg aaa act gct ggt cgg gtg cgc acc gat gcg gcg aag gca 691
Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr Asp Ala Ala Lys Ala
          185          190          195

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gct cca gta gtc gca ctt ctt gct gcg gtg act ggt gga cct ttc gtg 739  
 Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr Gly Gly Pro Phe Val  
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 Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp Ser Trp Ile Leu Ala  
 215 220 225  
 gtg ctg atc atc gca gcg gtt ctc ggt gga gct ttc gca ctg atc aaa 835  
 Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala Phe Ala Leu Ile Lys  
 230 235 240 245  
 gac cgc gat gga tta agc ttc ctg tcc act tcc gtc gct gtc atc ggt 883  
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 gtc gtt gca ctg ctg ttt 901  
 Val Val Ala Leu Leu Phe  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Pro Ile Ile Gly Lys Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr  
 35 40 45  
 Ile Gly Pro Val Trp Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly  
 50 55 60  
 Gly Ala Leu Phe Ala Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser  
 65 70 75 80  
 Gly Met Tyr Leu Pro Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg  
 85 90 95  
 Val Val Gly Leu Glu Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln  
 100 105 110  
 Lys Trp Ser Asp Arg Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu  
 115 120 125  
 Met Trp Gly Phe Ile Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys  
 130 135 140  
 Ala Asp His Thr Ile Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn  
 145 150 155 160  
 Val Phe Ala Ile Leu Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu  
 165 170 175



His Gly Leu Ala Phe Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr  
 180 185 190  
 Asp Ala Ala Lys Ala Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr  
 195 200 205  
 Gly Gly Pro Phe Val Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp  
 210 215 220  
 Ser Trp Ile Leu Ala Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala  
 225 230 235 240  
 Phe Ala Leu Ile Lys Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser  
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 <212> DNA  
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 Met Thr Thr Thr Asp 5  
 1  
 cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttc 163  
 His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe 20  
 10 15  
 ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211  
 Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr 35  
 25 30  
 cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259  
 Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr 50  
 40 45  
 atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg 307  
 Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp 65  
 55 60  
 ggt ttt gct aac tac gtc ctg cca ctt cag atc ggt gcg cct gac gta 355  
 Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile Gly Ala Pro Asp Val 85  
 70 75 80  
 gct ttc cca cgt ttg aat gct ttc ggc ttc tgg atc acc acc gtc ggt 403  
 Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp Ile Thr Thr Val Gly 100  
 90 95  
 ggt gtc gcg atg ctg acc ggc ttc ctg acc ccg ggt ggt gct gcc gac 451

Gly	Val	Ala	Met	Leu	Thr	Gly	Phe	Leu	Thr	Pro	Gly	Gly	Ala	Ala	Asp		
			105					110					115				
ttc	ggt	tgg	acc	atg	tac	tcc	cca	ctg	tct	gac	gca	att	cac	tcc	cca	499	
Phe	Gly	Trp	Thr	Met	Tyr	Ser	Pro	Leu	Ser	Asp	Ala	Ile	His	Ser	Pro		
		120					125					130					
ggc	ctt	ggc	tct	gac	atg	tgg	att	gtc	ggt	gtc	ggt	gca	act	ggt	att	547	
Gly	Leu	Gly	Ser	Asp	Met	Trp	Ile	Val	Gly	Val	Gly	Ala	Thr	Gly	Ile		
	135					140					145						
ggc	tcc	gtt	gct	tcc	gca	att	aac	atg	ctc	acc	acc	atc	ctc	tgc	ctc	595	
Gly	Ser	Val	Ala	Ser	Ala	Ile	Asn	Met	Leu	Thr	Thr	Ile	Leu	Cys	Leu		
150					155				160						165		
cgc	gca	cct	ggt	atg	acc	atg	ttc	cgt	atg	cct	att	ttc	acc	tgg	aat	643	
Arg	Ala	Pro	Gly	Met	Thr	Met	Phe	Arg	Met	Pro	Ile	Phe	Thr	Trp	Asn		
			170					175						180			
atc	ttc	gtt	gtt	tcc	gtt	ctt	gct	ctg	ctg	atc	ttc	cca	ctg	ctg	ctc	691	
Ile	Phe	Val	Val	Ser	Val	Leu	Ala	Leu	Leu	Ile	Phe	Pro	Leu	Leu	Leu		
		185						190					195				
gct	gct	gca	ctg	ggt	gtt	ctg	tat	gac	cgc	aag	ctt	ggt	gga	cac	ctg	739	
Ala	Ala	Ala	Leu	Gly	Val	Leu	Tyr	Asp	Arg	Lys	Leu	Gly	Gly	His	Leu		
		200					205					210					
tac	gat	cca	gct	aac	ggc	ggc	tcc	ctc	ctg	tgg	cag	cac	ctg	ttc	tgg	787	
Tyr	Asp	Pro	Ala	Asn	Gly	Gly	Ser	Leu	Leu	Trp	Gln	His	Leu	Phe	Trp		
	215					220					225						
ttc	ttc	gga	cac	cct	gag	gtt	tac	gtt	ctg	gcg	ctg	ccg	ttc	ttc	ggc	835	
Phe	Phe	Gly	His	Pro	Glu	Val	Tyr	Val	Leu	Ala	Leu	Pro	Phe	Phe	Gly		
230					235				240						245		
att	gtt	tct	gag	atc	att	cct	gtg	ttc	tcc	cgt	aag	cca	atg	ttc	ggt	883	
Ile	Val	Ser	Glu	Ile	Ile	Pro	Val	Phe	Ser	Arg	Lys	Pro	Met	Phe	Gly		
			250					255						260			
tac	gtc	ggc	ctg	atc	ttc	gca	acc	ttg	tcc	att	ggt	gca	ctg	tcc	atg	931	
Tyr	Val	Gly	Leu	Ile	Phe	Ala	Thr	Leu	Ser	Ile	Gly	Ala	Leu	Ser	Met		
			265					270					275				
gct	gtg	tgg	gct	cac	cac	atg	ttc	gtt	act	ggc	gca	gtt	ttg	ctt	ccg	979	
Ala	Val	Trp	Ala	His	His	Met	Phe	Val	Thr	Gly	Ala	Val	Leu	Leu	Pro		
		280					285					290					
ttc	ttc	tcc	ttc	atg	acg	ttc	ctg	att	tgc	gtt	cct	acc	ggc	gtt	aag	1027	
Phe	Phe	Ser	Phe	Met	Thr	Phe	Leu	Ile	Ser	Val	Pro	Thr	Gly	Val	Lys		
		295				300					305						
ttc	ttc	aac	tgg	gtt	gga	acc	atg	tgg	aag	ggt	cac	atc	act	tgg	gaa	1075	
Phe	Phe	Asn	Trp	Val	Gly	Thr	Met	Trp	Lys	Gly	His	Ile	Thr	Trp	Glu		
310					315				320						325		
acc	cca	atg	atc	tgg	tct	gtt	ggc	ttc	atg	gct	acc	ttc	ctc	ttc	ggt	1123	
Thr	Pro	Met	Ile	Trp	Ser	Val	Gly	Phe	Met	Ala	Thr	Phe	Leu	Phe	Gly		
			330					335						340			
ggt	ctg	acc	ggc	att	atg	ctg	gcg	tcc	cca	cca	ctg	gac	ttc	cac	ttg	1171	
Gly	Leu	Thr	Gly	Ile	Met	Leu	Ala	Ser	Pro	Pro	Leu	Asp	Phe	His	Leu		

345								350				355								
gct	gac	tcc	tac	ttc	ctg	atc	gcg	cac	ttc	cac	tac	acc	ctc	ttc	ggt	1219				
Ala	Asp	Ser	Tyr	Phe	Leu	Ile	Ala	His	Phe	His	Tyr	Thr	Leu	Phe	Gly					
360								365				370								
acc	gtg	gtg	ttc	gca	tcg	tgt	gca	ggc	gtt	tac	ttc	tgg	ttc	ccg	aag	1267				
Thr	Val	Val	Phe	Ala	Ser	Cys	Ala	Gly	Val	Tyr	Phe	Trp	Phe	Pro	Lys					
375								380				385								
atg	act	ggc	cgc	atg	atg	gac	gag	cgt	ctt	ggc	aag	atc	cac	ttc	tgg	1315				
Met	Thr	Gly	Arg	Met	Met	Asp	Glu	Arg	Leu	Gly	Lys	Ile	His	Phe	Trp					
390								395				400				405				
ttg	acc	ttc	gtc	ggg	ttc	cac	gga	acc	ttc	ctc	atc	cag	cac	tgg	gtg	1363				
Leu	Thr	Phe	Val	Gly	Phe	His	Gly	Thr	Phe	Leu	Ile	Gln	His	Trp	Val					
410								415				420								
ggc	aac	atg	ggg	atg	cca	cgt	cgt	tac	gct	gac	tac	ctg	gat	tct	gat	1411				
Gly	Asn	Met	Gly	Met	Pro	Arg	Arg	Tyr	Ala	Asp	Tyr	Leu	Asp	Ser	Asp					
425								430				435								
ggg	ttc	acc	atc	tac	aac	cag	atc	tcc	acc	gtg	ttc	tac	ttc	ctg	ctt	1459				
Gly	Phe	Thr	Ile	Tyr	Asn	Gln	Ile	Ser	Thr	Val	Phe	Tyr	Phe	Leu	Leu					
440								445				450								
ggc	ctg	tct	gtc	att	cca	ttc	atc	tgg	aac	gtc	ttc	aag	tcc	tgg	cgc	1507				
Gly	Leu	Ser	Val	Ile	Pro	Phe	Ile	Trp	Asn	Val	Phe	Lys	Ser	Trp	Arg					
455								460				465								
tac	ggg	gag	ctc	gtt	acc	gtt	gat	gat	cct	tgg	ggg	tac	ggc	aac	tcc	1555				
Tyr	Gly	Glu	Leu	Val	Thr	Val	Asp	Asp	Pro	Trp	Gly	Tyr	Gly	Asn	Ser					
470								475				480				485				
ctg	gag	tgg	gca	acc	tcc	tgc	cct	cct	cct	cgc	cac	aac	ttc	gca	tcc	1603				
Leu	Glu	Trp	Ala	Thr	Ser	Cys	Pro	Pro	Pro	Arg	His	Asn	Phe	Ala	Ser					
490								495				500								
ttg	cct	cgt	atc	cgc	tcc	gag	cgc	cct	gcg	ttc	gag	ctg	cac	tac	ccg	1651				
Leu	Pro	Arg	Ile	Arg	Ser	Glu	Arg	Pro	Ala	Phe	Glu	Leu	His	Tyr	Pro					
505								510				515								
cac	atg	att	gaa	cgc	atg	cgc	gca	gag	gca	cac	act	gga	cat	cac	gat	1699				
His	Met	Ile	Glu	Arg	Met	Arg	Ala	Glu	Ala	His	Thr	Gly	His	His	Asp					
520								525				530								
gat	att	aat	gct	cca	gaa	ttg	ggg	acc	gcc	cca	gcc	ctt	gca	tct	gac	1747				
Asp	Ile	Asn	Ala	Pro	Glu	Leu	Gly	Thr	Ala	Pro	Ala	Leu	Ala	Ser	Asp					
535								540				545								
tcc	agc	cgc	taaaagcgtc	tgattttaagt	cgg											1779				
Ser	Ser	Arg																		
550																				

&lt;210&gt; 654

&lt;211&gt; 552

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 654

Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met  
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 Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg  
 20 25 30  
 Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe  
 35 40 45  
 Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly  
 50 55 60  
 Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile  
 65 70 75 80  
 Gly Ala Pro Asp Val Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp  
 85 90 95  
 Ile Thr Thr Val Gly Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro  
 100 105 110  
 Gly Gly Ala Ala Asp Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp  
 115 120 125  
 Ala Ile His Ser Pro Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val  
 130 135 140  
 Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr  
 145 150 155 160  
 Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro  
 165 170 175  
 Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile  
 180 185 190  
 Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys  
 195 200 205  
 Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp  
 210 215 220  
 Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala  
 225 230 235 240  
 Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg  
 245 250 255  
 Lys Pro Met Phe Gly Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile  
 260 265 270  
 Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly  
 275 280 285  
 Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val  
 290 295 300  
 Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly  
 305 310 315 320  
 His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala

325										330					335				
Thr	Phe	Leu	Phe	Gly	Gly	Leu	Thr	Gly	Ile	Met	Leu	Ala	Ser	Pro	Pro				
			340					345					350						
Leu	Asp	Phe	His	Leu	Ala	Asp	Ser	Tyr	Phe	Leu	Ile	Ala	His	Phe	His				
		355					360					365							
Tyr	Thr	Leu	Phe	Gly	Thr	Val	Val	Phe	Ala	Ser	Cys	Ala	Gly	Val	Tyr				
	370					375					380								
Phe	Trp	Phe	Pro	Lys	Met	Thr	Gly	Arg	Met	Met	Asp	Glu	Arg	Leu	Gly				
385					390				395						400				
Lys	Ile	His	Phe	Trp	Leu	Thr	Phe	Val	Gly	Phe	His	Gly	Thr	Phe	Leu				
			405						410					415					
Ile	Gln	His	Trp	Val	Gly	Asn	Met	Gly	Met	Pro	Arg	Arg	Tyr	Ala	Asp				
			420					425					430						
Tyr	Leu	Asp	Ser	Asp	Gly	Phe	Thr	Ile	Tyr	Asn	Gln	Ile	Ser	Thr	Val				
	435						440					445							
Phe	Tyr	Phe	Leu	Leu	Gly	Leu	Ser	Val	Ile	Pro	Phe	Ile	Trp	Asn	Val				
450						455					460								
Phe	Lys	Ser	Trp	Arg	Tyr	Gly	Glu	Leu	Val	Thr	Val	Asp	Asp	Pro	Trp				
465					470				475						480				
Gly	Tyr	Gly	Asn	Ser	Leu	Glu	Trp	Ala	Thr	Ser	Cys	Pro	Pro	Pro	Arg				
			485					490						495					
His	Asn	Phe	Ala	Ser	Leu	Pro	Arg	Ile	Arg	Ser	Glu	Arg	Pro	Ala	Phe				
		500						505					510						
Glu	Leu	His	Tyr	Pro	His	Met	Ile	Glu	Arg	Met	Arg	Ala	Glu	Ala	His				
	515					520						525							
Thr	Gly	His	His	Asp	Asp	Ile	Asn	Ala	Pro	Glu	Leu	Gly	Thr	Ala	Pro				
	530					535					540								
Ala	Leu	Ala	Ser	Asp	Ser	Ser	Arg												
545					550														

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 <213> Corynebacterium glutamicum

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 <223> FRXA01919

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<220>

&lt;221&gt; VARIANT

&lt;222&gt; 82

&lt;223&gt; Xaa = any amino acid

&lt;400&gt; 655

acctatgacc gctgtggcgc ctagggtcga cgggcacgtc gcccctcaga ggcccagacc 60

gacaggccat gcacgcaagg gcagcaaagc atggttaatg atg acc acc acc gac 115  
 Met Thr Thr Thr Asp  
 1 5

cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttt 163  
 His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe  
 10 15 20

ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211  
 Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr  
 25 30 35

cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259  
 Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr  
 40 45 50

atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg 307  
 Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp  
 55 60 65

ggt ttt gct aac tac gtc ctg cca ctt cca acc acc ang caa gcc ttc 355  
 Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr Thr Xaa Gln Ala Phe  
 70 75 80 85

tct aaa acc cgg gtg aac tct ccc agg gag 385  
 Ser Lys Thr Arg Val Asn Ser Pro Arg Glu  
 90 95

&lt;210&gt; 656

&lt;211&gt; 95

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 82

&lt;223&gt; Xaa = any amino acid

&lt;400&gt; 656

Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met  
 1 5 10 15

Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg  
 20 25 30

Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe  
 35 40 45

Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly  
 50 55 60

Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr  
 65 70 75 80

Thr Xaa Gln Ala Phe Ser Lys Thr Arg Val Asn Ser Pro Arg Glu  
                   85                                  90                                  95

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 <213> Corynebacterium glutamicum

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 <223> FRXA02480

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 aagccaatgt tcgggttacg tcggcctgat cttcgcaacc ttg tcc att ggt gca 115  
   Leu Ser Ile Gly Ala  
   1                                  5  
 ctg tcc atg gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt 163  
 Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val  
                                   10                                  15                                  20  
 ttg ctt ccg ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc 211  
 Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr  
                                   25                                  30                                  35  
 ggc gtt aag ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc 259  
 Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile  
                                   40                                  45                                  50  
 act tgg gaa acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc 307  
 Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe  
                                   55                                  60                                  65  
 ctc ttc ggt ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac 355  
 Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp  
                                   70                                  75                                  80                                  85  
 ttc cac ttg gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc 403  
 Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr  
                                   90                                  95                                  100  
 ctc ttc ggt acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg 451  
 Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp  
                                   105                                  110                                  115  
 ttc ccg aag atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc 499  
 Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile  
                                   120                                  125                                  130  
 cac ttc tgg ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag 547  
 His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln  
                                   135                                  140                                  145  
 cac tgg gtg ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg 595  
 His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu  
                                   150                                  155                                  160                                  165

gat tct gat ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac 643  
Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr  
170 175 180  
  
ttc ctg ctt ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag 691  
Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys  
185 190 195  
  
tcc tgg cgc tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac 739  
Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr  
200 205 210  
  
ggc aac tcc ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac 787  
Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn  
215 220 225  
  
ttc gca tcc ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg 835  
Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu  
230 235 240 245  
  
cac tac ccg cac atg att gaa cgc atg cgc gca gag gca cac act gga 883  
His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly  
250 255 260  
  
cat cac gat gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt 931  
His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu  
265 270 275  
  
gca tct gac tcc agc cgc taaaagcgtc tgatttaagt cgg 972  
Ala Ser Asp Ser Ser Arg  
280

&lt;210&gt; 658

&lt;211&gt; 283

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 658

Leu Ser Ile Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe  
1 5 10 15  
  
Val Thr Gly Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu  
20 25 30  
  
Ile Ser Val Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met  
35 40 45  
  
Trp Lys Gly His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly  
50 55 60  
  
Phe Met Ala Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala  
65 70 75 80  
  
Ser Pro Pro Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala  
85 90 95  
  
His Phe His Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala  
100 105 110



Gly Val Tyr Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu  
 115 120 125  
 Arg Leu Gly Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly  
 130 135 140  
 Thr Phe Leu Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg  
 145 150 155 160  
 Tyr Ala Asp Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile  
 165 170 175  
 Ser Thr Val Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile  
 180 185 190  
 Trp Asn Val Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp  
 195 200 205  
 Asp Pro Trp Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro  
 210 215 220  
 Pro Pro Arg His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg  
 225 230 235 240  
 Pro Ala Phe Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala  
 245 250 255  
 Glu Ala His Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly  
 260 265 270  
 Thr Ala Pro Ala Leu Ala Ser Asp Ser Ser Arg  
 275 280

<210> 659  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(712)  
 <223> FRXA02481

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 tgctttcggc ttctgaatca ccaccgtcgg tgggtgtcgcg atg ctg acc ggc ttc 115  
 Met Leu Thr Gly Phe  
 1 5  
 cta acc ccg ggt ggt gct gcc gac ttg ggt gga cca tgt act ccc cac 163  
 Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly Pro Cys Thr Pro His  
 10 15 20  
 tgt ctg acg caa ttc act ccc cag gcc ttg gtt cta aca tgt gga ttg 211  
 Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val Leu Thr Cys Gly Leu  
 25 30 35  
 tcg ggt gtc ggt gca act ggt att ggc tcc gtt gct tcc gca att aac 259  
 Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn

40					45					50						
atg	ctc	acc	acc	atc	ctc	tgc	ctc	cgc	gca	cct	ggt	atg	acc	atg	ttc	307
Met	Leu	Thr	Thr	Ile	Leu	Cys	Leu	Arg	Ala	Pro	Gly	Met	Thr	Met	Phe	
	55					60					65					
cgt	atg	cct	att	ttc	acc	tgg	aat	atc	ttc	ggt	ggt	tcc	ggt	ctt	gct	355
Arg	Met	Pro	Ile	Phe	Thr	Trp	Asn	Ile	Phe	Val	Val	Ser	Val	Leu	Ala	
	70				75					80					85	
ctg	ctg	atc	ttc	cca	ctg	ctg	ctc	gct	gct	gca	ctg	ggt	ggt	ctg	tat	403
Leu	Leu	Ile	Phe	Pro	Leu	Leu	Leu	Ala	Ala	Ala	Leu	Gly	Val	Leu	Tyr	
				90					95					100		
gac	cgc	aag	ctt	ggt	gga	cac	ctg	tac	gat	cca	gct	aac	ggc	ggc	tcc	451
Asp	Arg	Lys	Leu	Gly	Gly	His	Leu	Tyr	Asp	Pro	Ala	Asn	Gly	Gly	Ser	
			105					110					115			
ctc	ctg	tgg	cag	cac	ctg	ttc	tgg	ttc	ttc	gga	cac	cct	gag	ggt	tac	499
Leu	Leu	Trp	Gln	His	Leu	Phe	Trp	Phe	Phe	Gly	His	Pro	Glu	Val	Tyr	
		120					125					130				
ggt	ctg	gcg	ctg	ccg	ttc	ttc	ggc	att	ggt	tct	gag	atc	att	cct	gtg	547
Val	Leu	Ala	Leu	Pro	Phe	Phe	Gly	Ile	Val	Ser	Glu	Ile	Ile	Pro	Val	
	135					140					145					
ttc	tcc	cgt	aag	cca	atg	ttc	ggg	tta	cgt	cgg	cct	gat	ctt	cgc	aac	595
Phe	Ser	Arg	Lys	Pro	Met	Phe	Gly	Leu	Arg	Arg	Pro	Asp	Leu	Arg	Asn	
	150				155				160						165	
ctt	gtc	cat	tgg	tgc	act	gtc	cat	ggc	tgt	gtg	ggc	tca	cca	cat	ggt	643
Leu	Val	His	Trp	Cys	Thr	Val	His	Gly	Cys	Val	Gly	Ser	Pro	His	Val	
				170					175					180		
cgt	tac	tgg	cgc	agt	ttt	gct	tcc	ggt	ctt	ctc	ctt	cat	gac	ggt	cct	691
Arg	Tyr	Trp	Arg	Ser	Phe	Ala	Ser	Val	Leu	Leu	Leu	His	Asp	Val	Pro	
			185					190					195			
gat	ttc	ggt	tcc	tac	cgg	cgt	taagttcttc	aactggggttg	gaa							735
Asp	Phe	Gly	Ser	Tyr	Arg	Arg										
		200														

&lt;210&gt; 660

&lt;211&gt; 204

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 660

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Leu	Thr	Cys	Gly	Leu	Ser	Gly	Val	Gly	Ala	Thr	Gly	Ile	Gly	Ser	Val
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Ala	Ser	Ala	Ile	Asn	Met	Leu	Thr	Thr	Ile	Leu	Cys	Leu	Arg	Ala	Pro
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Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val  
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 Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala  
 85 90 95  
 Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro  
 100 105 110  
 Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly  
 115 120 125  
 His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser  
 130 135 140  
 Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg  
 145 150 155 160  
 Pro Asp Leu Arg Asn Leu Val His Trp Cys Thr Val His Gly Cys Val  
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 Gly Ser Pro His Val Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu  
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 Leu His Asp Val Pro Asp Phe Gly Ser Tyr Arg Arg  
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 Val Glu Gln Gln Asn  
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 Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly Gly Val Leu Gly Leu  
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 Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala Pro Pro Gly Gly Val  
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 ctt gga gat ttc cta cgt atg ggt tgg cct gat ggc att acc cct gaa 259  
 Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp Gly Ile Thr Pro Glu  
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 Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val Trp Val Ala Ala Trp  
 55 60 65

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Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu Thr Ala Ile Phe Ala	
70 75 80 85	
tgg ggc gca aag agg gct gaa aag cgc ggc gag ggt gaa ttc cct aag	403
Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu Gly Glu Phe Pro Lys	
90 95 100	
cag ctc cag tac aac gtt cca ctt gag ctc gtt ctg acg atc gtt ccg	451
Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val Leu Thr Ile Val Pro	
105 110 115	
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Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr Val Gln Thr Gln Asp	
120 125 130	
aag gtc acc gct ctg gat aag aac cca gag gtt acc gtg gac gtc acc	547
Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val Thr Val Asp Val Thr	
135 140 145	
gct tac cag tgg aac tgg aag ttc gga tac tcc gaa att gat ggc tca	595
Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser Glu Ile Asp Gly Ser	
150 155 160 165	
ctg gca cct ggt gga cag gat tac caa gga agc gac ccg gag cgt cag	643
Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser Asp Pro Glu Arg Gln	
170 175 180	
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Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser Gly Asp Asn Pro Ile	
185 190 195	
cac ggc aac tca aag tct gac gtt tct tac ctt gag ttc aac cga att	739
His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu Glu Phe Asn Arg Ile	
200 205 210	
gaa acc ctc gga acc act gat gaa atc cca gtg atg gtt ctt cct gtg	787
Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val Met Val Leu Pro Val	
215 220 225	
aac acc cca atc gag ttc aac ctc gca tct gct gac gtt gca cac tcc	835
Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala Asp Val Ala His Ser	
230 235 240 245	
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Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp Ala Tyr Ala His Pro	
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Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile Glu Glu Ile Thr Glu	
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Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met Cys Gly Thr Tyr His	
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Ala Met Met Asn Phe Glu Leu Arg Val Val Asp Arg Asp Ser Phe Ala	
295 300 305	
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Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp Ala Thr Asn Ala Gln  
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 Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala Thr Ser Thr Ser Pro  
 330 335 340  
 ttc gtt tcc gat cgc acc gca acc cgc gac ggc gaa aac act cag agc 1171  
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 Asn Ala

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 35 40 45  
 Gly Ile Thr Pro Glu Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val  
 50 55 60  
 Trp Val Ala Ala Trp Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu  
 65 70 75 80  
 Thr Ala Ile Phe Ala Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu  
 85 90 95  
 Gly Glu Phe Pro Lys Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val  
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 Leu Thr Ile Val Pro Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr  
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 Val Gln Thr Gln Asp Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val  
 130 135 140  
 Thr Val Asp Val Thr Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser  
 145 150 155 160  
 Glu Ile Asp Gly Ser Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser  
 165 170 175  
 Asp Pro Glu Arg Gln Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser  
 180 185 190  
 Gly Asp Asn Pro Ile His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu  
 195 200 205

Glu Phe Asn Arg Ile Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val  
 210 215 220  
 Met Val Leu Pro Val Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala  
 225 230 235 240  
 Asp Val Ala His Ser Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp  
 245 250 255  
 Ala Tyr Ala His Pro Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile  
 260 265 270  
 Glu Glu Ile Thr Glu Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met  
 275 280 285  
 Cys Gly Thr Tyr His Ala Met Met Asn Phe Glu Leu Arg Val Val Asp  
 290 295 300  
 Arg Asp Ser Phe Ala Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp  
 305 310 315 320  
 Ala Thr Asn Ala Gln Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala  
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 Glu Asn Thr Gln Ser Asn Ala  
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 Val Thr Leu Ala Asn  
 1 5  
 caa aca gcc ata cta gat agc gtg acg agc gca gtt gga aat aca ggt 163  
 Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala Val Gly Asn Thr Gly  
 10 15 20  
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 Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn Arg Pro Asn Met Val  
 25 30 35  
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 Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu Leu Met Phe Phe Ala  
 40 45 50  
 ggg cta ttc gcg atg tac ttc gtg tcc cgt gcg aac gga ctg gca aat 307

Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala Asn Gly Leu Ala Asn  
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 gga tca tgg gga gag cag aca gat cac ctc aac gtg ccc tac gca ctg 355  
 Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn Val Pro Tyr Ala Leu 85  
 70 75 80  
 ttg att acg gtc att ctg gtg tct tcc tca gtg act tgc cag ttc gga 403  
 Leu Ile Thr Val Ile Leu Val Ser Ser Val Thr Cys Gln Phe Gly 100  
 90 95  
 gtt ttt gcg gct gaa agg ggt gac gtt tac ggc ctc cgc aag tgg ttc 451  
 Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly Leu Arg Lys Trp Phe 115  
 105 110  
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 Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val Ile Gly Gln Gly Tyr 130  
 120 125  
 gag tac atc act ctc gta ggt cac gga ctt aca atc cag agc agt gtc 547  
 Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr Ile Gln Ser Ser Val 145  
 135 140  
 tac gga tcg gca ttc ttt att aca acc ggt ttc cac gca ctg cac gtg 595  
 Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe His Ala Leu His Val 165  
 150 155 160  
 atc gcg ggt gtt atg gcc ttc gtt gtg gtt ctt atg aga atc cat aag 643  
 Ile Ala Gly Val Met Ala Phe Val Val Val Leu Met Arg Ile His Lys 180  
 170 175  
 tcg aag ttc act ccg gca cag gca acc gca gca atg gtt gtg tct tat 691  
 Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala Met Val Val Ser Tyr 195  
 185 190  
 tac tgg cac ttc gtt gac gtg gtc tgg atc ggc ctc ttc atc act att 739  
 Tyr Trp His Phe Val Asp Val Val Trp Ile Gly Leu Phe Ile Thr Ile 210  
 200 205  
 tac ttc att cag taggcagtaa ggaatcctca acg 774  
 Tyr Phe Ile Gln  
 215

&lt;210&gt; 664

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 664

Val Thr Leu Ala Asn Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala  
 1 5 10 15  
 Val Gly Asn Thr Gly Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn  
 20 25 30  
 Arg Pro Asn Met Val Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu  
 35 40 45  
 Leu Met Phe Phe Ala Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala  
 50 55 60

Asn Gly Leu Ala Asn Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn  
 65 70 75 80  
 Val Pro Tyr Ala Leu Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val  
 85 90 95  
 Thr Cys Gln Phe Gly Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly  
 100 105 110  
 Leu Arg Lys Trp Phe Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val  
 115 120 125  
 Ile Gly Gln Gly Tyr Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr  
 130 135 140  
 Ile Gln Ser Ser Val Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe  
 145 150 155 160  
 His Ala Leu His Val Ile Ala Gly Val Met Ala Phe Val Val Val Leu  
 165 170 175  
 Met Arg Ile His Lys Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala  
 180 185 190  
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 <223> RXA02144

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 Met Ser Asn Asn Asn  
 1 5  
 gac aaa cag tac aca acc caa gaa ctc aac gcg atg agc aat gag gat 163  
 Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala Met Ser Asn Glu Asp  
 10 15 20  
 ctt gca cga ctt ggt aca gag ctg gac gac gtt acc att gca tac cgc 211  
 Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val Thr Ile Ala Tyr Arg  
 25 30 35  
 aag gaa cgt ttc cca atc gct aat gac cca gct gag aag cgc gct gca 259  
 Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala Glu Lys Arg Ala Ala  
 40 45 50



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Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile Ile Gly Gly Leu Gly	
55 60 65	
ttc ctg gct acc tac att ttc tgg cct tgg gag tac aag gca cac gga	355
Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu Tyr Lys Ala His Gly	
70 75 80 85	
gat gaa ggt ctc ctg gcg tac acc ttg tac acc cca atg ctg ggt att	403
Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr Pro Met Leu Gly Ile	
90 95 100	
act tcc ggt ctt tgc atc ctg tcc ctg gga ttt gca gtt gtc ctt tat	451
Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe Ala Val Val Leu Tyr	
105 110 115	
gtc aag aag ttc att cca gag gaa atc gca gta cag cgt cgc cac gac	499
Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val Gln Arg Arg His Asp	
120 125 130	
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Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile Val Ala Leu Leu Asn	
135 140 145	
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Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg Lys Leu Ile Met Gly	
150 155 160 165	
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Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu Thr Ile Ile Ala Pro	
170 175 180	
atg ggc ggt atg atc aag aac cct tgg aat cct aag gaa ggc cca atg	691
Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro Lys Glu Gly Pro Met	
185 190 195	
gac gtt cag ggt gac ggc acc ctg tgg act tcc ggt tgg act ctc gtt	739
Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser Gly Trp Thr Leu Val	
200 205 210	
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Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp Thr Ala Ala Ile Ala	
215 220 225	
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Glu Ser His Thr Asp Ala Thr Gly Glu His Trp Ser Thr Thr Gly Val	
230 235 240 245	
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Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu Ala Ala Ala Ser Met	
250 255 260	
gaa act gtc ttc cca ctt cca gct gaa atg gtg aac gac ggt gct gaa	931
Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val Asn Asp Gly Ala Glu	
265 270 275	
tac gat cct gcg aag gac gtc tac gag cac caa atg cac tcg gtg cac	979
Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln Met His Ser Val His	
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Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu Arg Thr Ala Asp Ala  
 295 300 305  
 gaa aag gtt atc gaa cgc gaa ggc cag gag tcc ttc cac tac ggt gac 1075  
 Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser Phe His Tyr Gly Asp 325  
 310 315 320  
 tac tac gct tac tcc aag att tgt aca cac att ggt tgc cca acc tca 1123  
 Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile Gly Cys Pro Thr Ser 340  
 330 335  
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 Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys Pro Cys His Gln Ser 355  
 345 350  
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 Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val Phe Gly Pro Ala Ala 370  
 360 365  
 cgt gca ctg cca cag ctg cca att acc gtt gat gaa gag ggc tac ctc 1267  
 Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp Glu Glu Gly Tyr Leu 385  
 375 380  
 atc gcc gct ggt aac ttc att gag cca ctc ggc cct gca ttc tgg gag 1315  
 Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly Pro Ala Phe Trp Glu 405  
 390 395 400  
 cgt aag tca tgagtctagc taccgtggga aac 1347  
 Arg Lys Ser

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 666  
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 Thr Ile Ala Tyr Arg Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala  
 35 40 45  
 Glu Lys Arg Ala Ala Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile  
 50 55 60  
 Ile Gly Gly Leu Gly Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu  
 65 70 75 80  
 Tyr Lys Ala His Gly Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr  
 85 90 95  
 Pro Met Leu Gly Ile Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe  
 100 105 110  
 Ala Val Val Leu Tyr Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val  
 115 120 125

Gln Arg Arg His Asp Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile  
 130 135 140  
 Val Ala Leu Leu Asn Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg  
 145 150 155 160  
 Lys Leu Ile Met Gly Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu  
 165 170 175  
 Thr Ile Ile Ala Pro Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro  
 180 185 190  
 Lys Glu Gly Pro Met Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser  
 195 200 205  
 Gly Trp Thr Leu Val Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp  
 210 215 220  
 Thr Ala Ala Ile Ala Glu Ser His Thr Asp Ala Thr Gly Glu His Trp  
 225 230 235 240  
 Ser Thr Thr Gly Val Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu  
 245 250 255  
 Ala Ala Ala Ser Met Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val  
 260 265 270  
 Asn Asp Gly Ala Glu Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln  
 275 280 285  
 Met His Ser Val His Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu  
 290 295 300  
 Arg Thr Ala Asp Ala Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser  
 305 310 315 320  
 Phe His Tyr Gly Asp Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile  
 325 330 335  
 Gly Cys Pro Thr Ser Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys  
 340 345 350  
 Pro Cys His Gln Ser Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val  
 355 360 365  
 Phe Gly Pro Ala Ala Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp  
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 Glu Glu Gly Tyr Leu Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly  
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&lt;210&gt; 667

&lt;211&gt; 1053

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1030)

&lt;223&gt; RXA02740

&lt;400&gt; 667

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Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile Glu Leu Leu Leu Val
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gcc aca atc ccc aca atg ctt cag gct gaa cgc ggt gag aac aac att 211
Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg Gly Glu Asn Asn Ile
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gtg ctc atc ttg ctg act gtg ttc ggt ggc tgg atg ggt gcg gcc gcc 259
Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp Met Gly Ala Ala Ala
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gcc aac acc ttc aac atg gtg gca gac tcc gat att gat cag cgc atg 307
Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp Ile Asp Gln Arg Met
              55              60              65

gga cgc act agg gct cgc cct ttg gtg cgc cac acc gtg agt aat cgc 355
Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His Thr Val Ser Asn Arg
              70              75              80              85

gac gcc tcc att ttt gcg tgg gtc ctg aca gtg gcc agc ttc ttg tgg 403
Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val Ala Ser Phe Leu Trp
              90              95              100

ctg tgg ctg ctg tgc gat tgc atg ctc gcc ggc atc ttc gtg ttg atc 451
Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly Ile Phe Val Leu Ile
              105              110              115

acg att ttc ttc tac att ttt gtc tac acc aag tgg ctg aag cgc cgc 499
Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys Trp Leu Lys Arg Arg
              120              125              130

acg cac atg aat atc gtg tgg ggc gga gcc gca ggt tgt atg cca gtg 547
Thr His Met Asn Ile Val Trp Gly Gly Ala Ala Gly Cys Met Pro Val
              135              140              145

ctc gtc ggc tgg gca gtg atc gtt gat cag ttt gag cca ggc gtt cca 595
Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe Glu Pro Gly Val Pro
              150              155              160              165

cag cag tgg tgg cag gca att gtc ctg ttc atg gtg att ttc ttc tgg 643
Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met Val Ile Phe Phe Trp
              170              175              180

acc cca cct cac acc tgg gct ctg gcc atg aag tac cgc gaa gac tac 691
Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys Tyr Arg Glu Asp Tyr
              185              190              195

aag gcg gct ggc gtc cca atg ctt cct gtc gtg cgc acc cca gtc cag 739

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Lys Ala Ala Gly Val Pro Met Leu Pro Val Val Arg Thr Pro Val Gln  
 200 205 210  
 gtc acc gca caa atc gtg tgg tac tcc gtg gca act gtg ctg acc acc 787  
 Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala Thr Val Leu Thr Thr  
 215 220 225  
 ttc ttg ctc atc cca gca act ggt tgg atc tac gca gcg atc gcc gtc 835  
 Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr Ala Ala Ile Ala Val  
 230 235 240 245  
 att tcc ggc gtc acc ttc ttg ttc atg gcc atc aag ctg cac ctc ggc 883  
 Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile Lys Leu His Leu Gly  
 250 255 260  
 atc aaa aac ggt ggc aag gtc aag cct ctg aag ctg ttt att ttg tcc 931  
 Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys Leu Phe Ile Leu Ser  
 265 270 275  
 aac aac tac ttg gca gtc ctc ttc gtg gca ttg tcc gtc gac gcg gtc 979  
 Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu Ser Val Asp Ala Val  
 280 285 290  
 ctc ggc ctt gag acc atc ggc gag atg ctc ggc tgg acc acc acc ttc 1027  
 Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly Trp Thr Thr Thr Phe  
 295 300 305  
 ttc taaaagcttg cttttcgacg aaa 1053  
 Phe  
 310

&lt;210&gt; 668

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 668

Leu Asp Thr Ile Lys Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile  
 1 5 10 15  
 Glu Leu Leu Leu Val Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg  
 20 25 30  
 Gly Glu Asn Asn Ile Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp  
 35 40 45  
 Met Gly Ala Ala Ala Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp  
 50 55 60  
 Ile Asp Gln Arg Met Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His  
 65 70 75 80  
 Thr Val Ser Asn Arg Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val  
 85 90 95  
 Ala Ser Phe Leu Trp Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly  
 100 105 110  
 Ile Phe Val Leu Ile Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys  
 115 120 125

Trp Leu Lys Arg Arg Thr His Met Asn Ile Val Trp Gly Gly Ala Ala  
 130 135 140  
 Gly Cys Met Pro Val Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe  
 145 150 155 160  
 Glu Pro Gly Val Pro Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met  
 165 170 175  
 Val Ile Phe Phe Trp Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys  
 180 185 190  
 Tyr Arg Glu Asp Tyr Lys Ala Ala Gly Val Pro Met Leu Pro Val Val  
 195 200 205  
 Arg Thr Pro Val Gln Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala  
 210 215 220  
 Thr Val Leu Thr Thr Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr  
 225 230 235 240  
 Ala Ala Ile Ala Val Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile  
 245 250 255  
 Lys Leu His Leu Gly Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys  
 260 265 270  
 Leu Phe Ile Leu Ser Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu  
 275 280 285  
 Ser Val Asp Ala Val Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly  
 290 295 300  
 Trp Thr Thr Thr Phe Phe  
 305 310

<210> 669  
 <211> 1161  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1138)  
 <223> RXA02743

<400> 669  
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 aattgtataa aactagccat gacctgctag gatcagcgac gtg tct act tca gat 115  
 Val Ser Thr Ser Asp  
 1 5  
 gct ccc tca aat aat cca gtt gag ttg aag ccc att act ttc tgg gca 163  
 Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro Ile Thr Phe Trp Ala  
 10 15 20  
 ccg acc atc aaa gtg cag cgc att ctc gcg ctc cta ctg ttg att ttc 211  
 Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu Leu Leu Ile Phe

25							30					35					
cag	gga	ggc	atc	acc	gtt	acg	ggc	tct	atc	gtc	cgt	gtc	aca	ggc	tcc	259	
Gln	Gly	Gly	Ile	Thr	Val	Thr	Gly	Ser	Ile	Val	Arg	Val	Thr	Gly	Ser		
	40						45					50					
ggc	ctc	ggg	tgt	gat	acc	tgg	cca	cta	tgc	cac	gaa	ggg	tca	cta	gtc	307	
Gly	Leu	Gly	Cys	Asp	Thr	Trp	Pro	Leu	Cys	His	Glu	Gly	Ser	Leu	Val		
	55					60					65						
cca	gtc	gca	ggc	gca	gca	cca	tgg	atc	cac	cag	gca	gtg	gaa	ttt	ggg	355	
Pro	Val	Ala	Gly	Ala	Ala	Pro	Trp	Ile	His	Gln	Ala	Val	Glu	Phe	Gly		
	70				75					80					85		
aac	cgc	atg	ctc	act	ttc	gtg	ctt	gct	gcc	gca	gcg	ctt	gcg	ttg	ttc	403	
Asn	Arg	Met	Leu	Thr	Phe	Val	Leu	Ala	Ala	Ala	Ala	Leu	Ala	Leu	Phe		
				90				95						100			
att	gca	gtt	ctt	ggc	gca	aaa	cgc	cgc	cgc	gag	atc	ctg	gtc	cat	tcc	451	
Ile	Ala	Val	Leu	Gly	Ala	Lys	Arg	Arg	Arg	Glu	Ile	Leu	Val	His	Ser		
			105					110					115				
ttc	atc	cag	ggg	ttg	ggc	atc	atc	ttg	cag	gct	gtc	atc	ggg	ggc	atc	499	
Phe	Ile	Gln	Gly	Leu	Gly	Ile	Ile	Leu	Gln	Ala	Val	Ile	Gly	Gly	Ile		
		120					125					130					
acc	gtg	ctg	gtt	gat	ttg	cac	tgg	tac	gcc	gtt	gct	ttg	cac	ttc	ctg	547	
Thr	Val	Leu	Val	Asp	Leu	His	Trp	Tyr	Ala	Val	Ala	Leu	His	Phe	Leu		
	135					140					145						
cca	tcc	atg	atc	ctt	gtt	ttc	atg	gcc	gcg	att	ttg	tac	acc	cgc	atc	595	
Pro	Ser	Met	Ile	Leu	Val	Phe	Met	Ala	Ala	Ile	Leu	Tyr	Thr	Arg	Ile		
	150				155					160					165		
ggc	gag	ccc	gat	gac	ggc	gag	att	acc	acc	aca	ttc	ccc	acg	tgg	atc	643	
Gly	Glu	Pro	Asp	Asp	Gly	Glu	Ile	Thr	Thr	Thr	Phe	Pro	Thr	Trp	Ile		
				170					175					180			
cgc	aat	gta	gct	gtc	att	ggg	gca	gta	gcg	ctc	tcc	gta	gta	ctg	atc	691	
Arg	Asn	Val	Ala	Val	Ile	Gly	Ala	Val	Ala	Leu	Ser	Val	Val	Leu	Ile		
			185					190					195				
acc	ggc	acc	atg	acc	acc	ggc	gct	ggc	gtt	cac	tct	ggc	gat	gca	tca	739	
Thr	Gly	Thr	Met	Thr	Thr	Gly	Ala	Gly	Val	His	Ser	Gly	Asp	Ala	Ser		
		200					205					210					
atc	acc	atg	gat	gat	cgc	ctc	gat	gtc	agc	atc	gac	ttg	atg	gcc	cac	787	
Ile	Thr	Met	Asp	Asp	Arg	Leu	Asp	Val	Ser	Ile	Asp	Leu	Met	Ala	His		
	215					220					225						
atc	cac	ggc	tac	agc	atg	tac	atc	tac	ctc	ttc	ttc	acc	ctc	atc	gtg	835	
Ile	His	Gly	Tyr	Ser	Met	Tyr	Ile	Tyr	Leu	Phe	Phe	Thr	Leu	Ile	Val		
	230				235					240					245		
gtc	gcc	ggg	ctg	tac	aag	gca	aaa	acc	acc	aag	cac	aac	aag	cag	ctt	883	
Val	Ala	Gly	Leu	Tyr	Lys	Ala	Lys	Thr	Thr	Lys	His	Asn	Lys	Gln	Leu		
				250					255					260			
ggc	ctc	atg	ctg	att	ctg	ttc	att	ctg	att	cag	gca	ggg	atc	ggc	atc	931	
Gly	Leu	Met	Leu	Ile	Leu	Phe	Ile	Leu	Ile	Gln	Ala	Gly	Ile	Gly	Ile		
			265					270					275				

ttg cag tac cgc atg ggt gtg cca cgc tgg agc atc cca ttc cac atc 979  
 Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser Ile Pro Phe His Ile  
 280 285 290  
  
 gca atg tct tct gtc gtt gtt gcc ttc act tcc ctt ctg tgg gcg cag 1027  
 Ala Met Ser Ser Val Val Val Ala Phe Thr Ser Leu Leu Trp Ala Gln  
 295 300 305  
  
 ggt cgt ata cgc gtc ggc ggt aaa gcc acc gtt act ggt tct gtt gat 1075  
 Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val Thr Gly Ser Val Asp  
 310 315 320 325  
  
 ggc gat att aag aac gag atc att acg aac ccc ttt gag aag aaa tca 1123  
 Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro Phe Glu Lys Lys Ser  
 330 335 340  
  
 aag cag cct gtt aaa taacacgcaa ctgtatcggg aaa 1161  
 Lys Gln Pro Val Lys  
 345

&lt;210&gt; 670

&lt;211&gt; 346

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 670

Val Ser Thr Ser Asp Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro  
 1 5 10 15  
  
 Ile Thr Phe Trp Ala Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu  
 20 25 30  
  
 Leu Leu Leu Ile Phe Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val  
 35 40 45  
  
 Arg Val Thr Gly Ser Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His  
 50 55 60  
  
 Glu Gly Ser Leu Val Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln  
 65 70 75 80  
  
 Ala Val Glu Phe Gly Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala  
 85 90 95  
  
 Ala Leu Ala Leu Phe Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu  
 100 105 110  
  
 Ile Leu Val His Ser Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala  
 115 120 125  
  
 Val Ile Gly Gly Ile Thr Val Leu Val Asp Leu His Trp Tyr Ala Val  
 130 135 140  
  
 Ala Leu His Phe Leu Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile  
 145 150 155 160  
  
 Leu Tyr Thr Arg Ile Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr  
 165 170 175



Phe Pro Thr Trp Ile Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu  
 180 185 190  
 Ser Val Val Leu Ile Thr Gly Thr Met Thr Thr Gly Ala Gly Val His  
 195 200 205  
 Ser Gly Asp Ala Ser Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile  
 210 215 220  
 Asp Leu Met Ala His Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe  
 225 230 235 240  
 Phe Thr Leu Ile Val Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys  
 245 250 255  
 His Asn Lys Gln Leu Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln  
 260 265 270  
 Ala Gly Ile Gly Ile Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser  
 275 280 285  
 Ile Pro Phe His Ile Ala Met Ser Ser Val Val Val Ala Phe Thr Ser  
 290 295 300  
 Leu Leu Trp Ala Gln Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val  
 305 310 315 320  
 Thr Gly Ser Val Asp Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro  
 325 330 335  
 Phe Glu Lys Lys Ser Lys Gln Pro Val Lys  
 340 345

<210> 671  
 <211> 444  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(421)  
 <223> RXA01227

<400> 671  
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 acctatatttc cacgtcttta tccgtagtat tggagatccg atg acc tac aca atc 115  
 Met Thr Tyr Thr Ile  
 1 5  
 gcc cag ccc tgc gtt gat gtc ctg gat cga gcc tgc gtc gag gaa tgt 163  
 Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys  
 10 15 20  
 ccc gtg gac tgc atc tac gag ggc aaa cgg atg ctc tac atc cac ccc 211  
 Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro  
 25 30 35  
 gat gag tgc gtc gac tgc ggt gcc tgc gag ccc gtc tgc ccg gtt gaa 259  
 Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Val Cys Pro Val Glu

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          40          45          50
gcc atc ttc tac gaa gat gat gtt ccc cac gaa tgg tgg gac tac acc 307
Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu Trp Trp Asp Tyr Thr
   55          60          65

ggc gct aac gcc gcc ttt ttc gac gac ctc ggt tcg cca ggc ggt gcc 355
Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala
   70          75          80          85

gcc agc ctg ggt ccg cag gac ttc gac gcc cag ctc gtc gcg gtg ctg 403
Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln Leu Val Ala Val Leu
          90          95          100

ccg cca cag aac cag aac taggacctga tatcggccct aaa 444
Pro Pro Gln Asn Gln Asn
          105

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<210> 672
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

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<400> 672
Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala
   1           5           10           15

Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met
          20          25          30

Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro
   35          40          45

Val Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu
   50          55          60

Trp Trp Asp Tyr Thr Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly
   65          70          75          80

Ser Pro Gly Gly Ala Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln
          85          90          95

Leu Val Ala Val Leu Pro Pro Gln Asn Gln Asn
          100          105

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<210> 673
<211> 438
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(415)
<223> RXA01865

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<400> 673
ggtggaattt ggccctgcggt caagggaag tagcataata agcctaaagc tttcccatat 60
ttattagcct cttagagttc tcaggagaaa acgaaatccc atg aca tac aca atc 115

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	Met	Thr	Tyr	Thr	Ile	
	1				5	
gca cag ccc tgc gtt gac gtc ttg gat cgt gcc tgc gtt gaa gaa tgc						163
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys						
cca gta gat tgc atc tac gaa ggt aag cgc atg ctg tac atc cac ccg						211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro						
gat gag tgc gtt gac tgt ggt gca tgt gag cct gct tgc cca gtt gag						259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Ala Cys Pro Val Glu						
gca atc ttc tac gag gac gat gtc cca gac gaa tgg ctt gac tac aac						307
Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu Trp Leu Asp Tyr Asn						
gat gcc aac gct gca ttc ttc gat gat ctg ggc tcc cca ggt ggt gcg						355
Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala						
gct aag ctt gga cca caa gat ttt gat cac cca atg atc gct gcg ctg						403
Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro Met Ile Ala Ala Leu						
ccg cct cag gca taatctaacg catgacctct cgc						438
Pro Pro Gln Ala						

&lt;210&gt; 674

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 674

Met	Thr	Tyr	Thr	Ile	Ala	Gln	Pro	Cys	Val	Asp	Val	Leu	Asp	Arg	Ala
1				5					10					15	
Cys	Val	Glu	Glu	Cys	Pro	Val	Asp	Cys	Ile	Tyr	Glu	Gly	Lys	Arg	Met
		20						25					30		
Leu	Tyr	Ile	His	Pro	Asp	Glu	Cys	Val	Asp	Cys	Gly	Ala	Cys	Glu	Pro
		35					40					45			
Ala	Cys	Pro	Val	Glu	Ala	Ile	Phe	Tyr	Glu	Asp	Asp	Val	Pro	Asp	Glu
		50				55					60				
Trp	Leu	Asp	Tyr	Asn	Asp	Ala	Asn	Ala	Ala	Phe	Phe	Asp	Asp	Leu	Gly
		65			70					75				80	
Ser	Pro	Gly	Gly	Ala	Ala	Lys	Leu	Gly	Pro	Gln	Asp	Phe	Asp	His	Pro
				85					90					95	
Met	Ile	Ala	Ala	Leu	Pro	Pro	Gln	Ala							
		100					105								

&lt;210&gt; 675

<211> 441  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(418)  
 <223> RXA00680

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 Met Ser Thr Ile His  
 1 5  
 ttc att gat cat gct ggc aaa acc cgc acc atc gag gcg act gtt ggt 163  
 Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile Glu Ala Thr Val Gly  
 10 15 20  
 gat tca gta atg gag acc gca gtc cga aac gga gtg cct gga att gtt 211  
 Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly Val Pro Gly Ile Val  
 25 30 35  
 gct gaa tgc ggc ggt tcc tta tcg tgt gca acc tgc cat gtg ttt gtt 259  
 Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr Cys His Val Phe Val  
 40 45 50  
 gac cct gca cag tat gat gcg ctt ccc cca atg gag gag atg gaa gat 307  
 Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met Glu Glu Met Glu Asp  
 55 60 65  
 gaa atg ctg tgg ggt gct gcc gtg gac cgt gag gat tgc tcc cgt ttg 355  
 Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu Asp Cys Ser Arg Leu  
 70 75 80 85  
 tct tgc caa atc aag gtc acc gaa ggc atg gat ctt tcg ttg acc acg 403  
 Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp Leu Ser Leu Thr Thr  
 90 95 100  
 cca gaa acg caa gtg tgaggttgaa tcatgaatac ttc 441  
 Pro Glu Thr Gln Val  
 105

<210> 676  
 <211> 106  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 676  
 Met Ser Thr Ile His Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile  
 1 5 10 15  
 Glu Ala Thr Val Gly Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly  
 20 25 30  
 Val Pro Gly Ile Val Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr  
 35 40 45  
 Cys His Val Phe Val Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met

<400> 677																
ggaccgtgag gattgctccc gtttgtcttg ccaaatcaag gtcaccgaag gcatggatct																60
ttcgttgacc acgccagaaa cgcaagtgtg aggttgaatc atg aat act tca gct																115
Met Asn Thr Ser Ala																5
1																
gaa act gga atc ttg atc atc ggt gca aac caa tcg ggt gtg cag ctg																163
Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln Ser Gly Val Gln Leu																20
10 15																
gcg att tcc ctg cgg gcc acg ggt ttc acc gaa tcg atc acg ctt cta																211
Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu Ser Ile Thr Leu Leu																35
25 30																
ggc gag gag gat cac cgc ccc tac cag cgt ccc gcc ttg tcc aag gag																259
Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro Ala Leu Ser Lys Glu																50
40 45																
ttc ctc cag gac aag atc gac aaa gag cgt ctg att ttc cgt tcc aat																307
Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu Ile Phe Arg Ser Asn																65
55 60																
gag tat tgg gaa gaa aat aat att cgc ctg gtc aag ggc gtg cgc atc																355
Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val Lys Gly Val Arg Ile																85
70 75 80																
gaa cgc att gaa aag aac gac gac gga tca ggg gtc gcc tac ggc gcc																403
Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly Val Ala Tyr Gly Ala																100
90 95																
gga caa gaa ttc gct ttt cga cgt ctc gct cta gcg gtt ggt gcc cgc																451
Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu Ala Val Gly Ala Arg																115
105 110																
cct cgc cac ctc gac ctc ccg ggc gcc acc ttg gag ggt gtc acc tac																499
Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu Glu Gly Val Thr Tyr																125
120 125 130																

ctg	cgc	aac	gcg	gac	gac	gcc	ttg	gcg	ctc	aaa	gcg	atg	att	ggc	tct	547
Leu	Arg	Asn	Ala	Asp	Asp	Ala	Leu	Ala	Leu	Lys	Ala	Met	Ile	Gly	Ser	
135						140					145					
gtc	acc	gat	gcc	gtt	gta	gtc	ggc	ggc	ggg	ttc	atc	gga	ttg	gaa	gct	595
Val	Thr	Asp	Ala	Val	Val	Val	Gly	Gly	Gly	Phe	Ile	Gly	Leu	Glu	Ala	
150					155					160					165	
gcg	tgt	tcg	ctt	cat	gac	ctc	ggc	aaa	aat	gtc	acc	gtc	ctg	gaa	tat	643
Ala	Cys	Ser	Leu	His	Asp	Leu	Gly	Lys	Asn	Val	Thr	Val	Leu	Glu	Tyr	
				170					175					180		
ggc	ccg	cgt	ctg	att	ggc	cga	gcg	gtg	ggc	gaa	gaa	acc	gca	gca	ttc	691
Gly	Pro	Arg	Leu	Ile	Gly	Arg	Ala	Val	Gly	Glu	Glu	Thr	Ala	Ala	Phe	
			185					190					195			
ttc	ctc	gaa	caa	cac	cgt	tcc	cgt	ggc	gta	aat	atc	gtg	ctt	gat	gcc	739
Phe	Leu	Glu	Gln	His	Arg	Ser	Arg	Gly	Val	Asn	Ile	Val	Leu	Asp	Ala	
		200					205					210				
cgc	atg	aaa	cag	ttt	gtg	ggc	aag	gat	gga	aag	ctc	agc	ggc	att	gag	787
Arg	Met	Lys	Gln	Phe	Val	Gly	Lys	Asp	Gly	Lys	Leu	Ser	Gly	Ile	Glu	
	215					220					225					
cta	gaa	gat	ggc	aca	gta	att	cct	gcc	caa	cta	gtc	att	gtg	ggc	atc	835
Leu	Glu	Asp	Gly	Thr	Val	Ile	Pro	Ala	Gln	Leu	Val	Ile	Val	Gly	Ile	
230					235					240					245	
ggc	gtc	att	ccg	aac	aca	gaa	ctt	gcc	gct	gtt	ctg	ggc	tta	gac	atc	883
Gly	Val	Ile	Pro	Asn	Thr	Glu	Leu	Ala	Ala	Val	Leu	Gly	Leu	Asp	Ile	
				250					255					260		
aac	aac	ggc	atc	gtg	gtg	gat	aaa	cat	gcc	gtc	gcg	tca	gat	ggc	acc	931
Asn	Asn	Gly	Ile	Val	Val	Asp	Lys	His	Ala	Val	Ala	Ser	Asp	Gly	Thr	
			265					270					275			
acc	att	gcg	att	ggc	gat	gtc	gcc	aac	att	ccc	aat	cca	atc	cct	ggc	979
Thr	Ile	Ala	Ile	Gly	Asp	Val	Ala	Asn	Ile	Pro	Asn	Pro	Ile	Pro	Gly	
		280					285					290				
tcc	ccc	gct	gat	gaa	cgc	atc	cga	cta	gaa	agc	gtc	aat	aac	gcc	atc	1027
Ser	Pro	Ala	Asp	Glu	Arg	Ile	Arg	Leu	Glu	Ser	Val	Asn	Asn	Ala	Ile	
		295				300					305					
gag	cac	gca	aag	atc	gct	gca	tac	tca	ctc	gtc	ggc	cag	ccc	gaa	gcc	1075
Glu	His	Ala	Lys	Ile	Ala	Ala	Tyr	Ser	Leu	Val	Gly	Gln	Pro	Glu	Ala	
310					315					320					325	
tac	gcc	gga	atc	ccc	tgg	ttc	tgg	tcc	aac	caa	ggc	gat	ctc	aaa	cta	1123
Tyr	Ala	Gly	Ile	Pro	Trp	Phe	Trp	Ser	Asn	Gln	Gly	Asp	Leu	Lys	Leu	
				330					335					340		
caa	att	gca	gga	ctt	acc	ctt	ggc	tat	gac	agc	aca	gta	atc	cga	cag	1171
Gln	Ile	Ala	Gly	Leu	Thr	Leu	Gly	Tyr	Asp	Ser	Thr	Val	Ile	Arg	Gln	
			345					350					355			
gat	ccc	gag	aaa	aag	aag	ttc	tct	gtc	ctt	tat	tac	cgt	ggc	gac	aac	1219
Asp	Pro	Glu	Lys	Lys	Lys	Phe	Ser	Val	Leu	Tyr	Tyr	Arg	Gly	Asp	Asn	
		360				365						370				
atc	atc	gcc	gcc	gat	tgt	gtc	aac	gct	cca	ctg	gat	ttc	atg	gct	gtg	1267

Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu Asp Phe Met Ala Val  
 375 380 385

cgc agt gca ctt tcc agg aac caa aat atc ccc gcc gac ctt gct gca 1315  
 Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro Ala Asp Leu Ala Ala  
 390 395 400 405

gat att tcg cag ccg ctg aaa aaa cta gcc gtt gac ctg gag gtt acc 1363  
 Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val Asp Leu Glu Val Thr  
 410 415 420

cga tgactcgcag taattttaccc gct 1389  
 Arg

<210> 678  
 <211> 422  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 678  
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Ser Ile Thr Leu Leu Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro  
 35 40 45

Ala Leu Ser Lys Glu Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu  
 50 55 60

Ile Phe Arg Ser Asn Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val  
 65 70 75 80

Lys Gly Val Arg Ile Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly  
 85 90 95

Val Ala Tyr Gly Ala Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu  
 100 105 110

Ala Val Gly Ala Arg Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu  
 115 120 125

Glu Gly Val Thr Tyr Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys  
 130 135 140

Ala Met Ile Gly Ser Val Thr Asp Ala Val Val Val Gly Gly Gly Phe  
 145 150 155 160

Ile Gly Leu Glu Ala Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val  
 165 170 175

Thr Val Leu Glu Tyr Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu  
 180 185 190

Glu Thr Ala Ala Phe Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn  
 195 200 205

Ile Val Leu Asp Ala Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys  
 210 215 220  
 Leu Ser Gly Ile Glu Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu  
 225 230 235 240  
 Val Ile Val Gly Ile Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val  
 245 250 255  
 Leu Gly Leu Asp Ile Asn Asn Gly Ile Val Val Asp Lys His Ala Val  
 260 265 270  
 Ala Ser Asp Gly Thr Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro  
 275 280 285  
 Asn Pro Ile Pro Gly Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser  
 290 295 300  
 Val Asn Asn Ala Ile Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val  
 305 310 315 320  
 Gly Gln Pro Glu Ala Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln  
 325 330 335  
 Gly Asp Leu Lys Leu Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser  
 340 345 350  
 Thr Val Ile Arg Gln Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr  
 355 360 365  
 Tyr Arg Gly Asp Asn Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu  
 370 375 380  
 Asp Phe Met Ala Val Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro  
 385 390 395 400  
 Ala Asp Leu Ala Ala Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val  
 405 410 415  
 Asp Leu Glu Val Thr Arg  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1051)  
 <223> RXA00224

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 Met Ser Ile Ser Tyr  
 1 5  
 gtg ctg gtt gag cag cta gat ggc cgc cca gaa cca gtt acc ctt gaa 163



Val	Leu.	Val	Glu	Gln	Leu	Asp	Gly	Arg	Pro	Glu	Pro	Val	Thr	Leu	Glu	
				10					15					20		
ttg	atc	act	gct	gct	cgc	gca	ctc	ggc	gac	gtc	gtt	gcc	gtt	gtc	gtt	211
Leu	Ile	Thr	Ala	Ala	Arg	Ala	Leu	Gly	Asp	Val	Val	Ala	Val	Val	Val	
			25					30					35			
ggc	gag	cca	ggc	gcc	ggc	gta	aac	ctt	gct	gct	gag	ctc	ggc	aat	tgg	259
Gly	Glu	Pro	Gly	Ala	Gly	Val	Asn	Leu	Ala	Ala	Glu	Leu	Gly	Asn	Trp	
		40					45					50				
ggc	gca	gca	cag	gtt	gtt	tcc	gct	gaa	atc	tct	ggc	gct	tcc	aac	cgt	307
Gly	Ala	Ala	Gln	Val	Val	Ser	Ala	Glu	Ile	Ser	Gly	Ala	Ser	Asn	Arg	
	55					60					65					
ttg	atc	ttg	cct	gct	gtt	gat	gcg	ctg	cac	att	ttg	gct	gcg	aac	aac	355
Leu	Ile	Leu	Pro	Ala	Val	Asp	Ala	Leu	His	Ile	Leu	Ala	Ala	Asn	Asn	
	70				75				80						85	
cca	ggc	cca	att	gtt	atc	gct	gca	act	gca	agc	ggc	aat	gag	atc	gct	403
Pro	Gly	Pro	Ile	Val	Ile	Ala	Ala	Thr	Ala	Ser	Gly	Asn	Glu	Ile	Ala	
				90					95					100		
ggc	cgt	ttg	gct	gcc	cgt	ttg	gct	tct	ggc	gtg	ctc	acc	gat	gtc	gtc	451
Gly	Arg	Leu	Ala	Ala	Arg	Leu	Ala	Ser	Gly	Val	Leu	Thr	Asp	Val	Val	
			105				110					115				
gga	atc	aat	gcc	gac	cgc	acc	gca	cag	cag	tcc	att	ttc	ggc	gac	acc	499
Gly	Ile	Asn	Ala	Asp	Arg	Thr	Ala	Gln	Gln	Ser	Ile	Phe	Gly	Asp	Thr	
		120					125					130				
att	cag	gtg	tcc	gct	gca	gtt	ggc	gct	tca	ccg	ctg	tac	acc	ctg		547
Ile	Gln	Val	Ser	Ala	Ala	Val	Gly	Gly	Ala	Ser	Pro	Leu	Tyr	Thr	Leu	
			135			140					145					
cgt	cca	ggc	gcc	ctt	gat	ggc	gtg	gcc	gtt	cct	gca	acc	ggc	gaa	ttg	595
Arg	Pro	Gly	Ala	Leu	Asp	Gly	Val	Ala	Val	Pro	Ala	Thr	Gly	Glu	Leu	
				155						160				165		
gca	acc	att	gag	atc	cca	ggc	gca	acc	gcc	aag	gat	gtc	acc	atc	acc	643
Ala	Thr	Ile	Glu	Ile	Pro	Gly	Ala	Thr	Ala	Lys	Asp	Val	Thr	Ile	Thr	
				170					175					180		
tcc	ttc	acg	cca	agc	acc	cag	agc	gat	cgc	cct	gag	ctg	cca	cag	gca	691
Ser	Phe	Thr	Pro	Ser	Thr	Gln	Ser	Asp	Arg	Pro	Glu	Leu	Pro	Gln	Ala	
			185					190					195			
aag	gtc	gtt	atc	gca	ggc	gga	cgt	ggc	gtc	gga	agc	gaa	gaa	aac	ttc	739
Lys	Val	Val	Ile	Ala	Gly	Gly	Arg	Gly	Val	Gly	Ser	Glu	Glu	Asn	Phe	
		200					205					210				
cgc	agc	atc	gtt	gaa	cca	ctg	gca	gat	gca	ttg	ggc	ggc	gcc	gtt	ggc	787
Arg	Ser	Ile	Val	Glu	Pro	Leu	Ala	Asp	Ala	Leu	Gly	Gly	Ala	Val	Gly	
		215				220					225					
gca	acc	cgc	gac	gcc	gtt	gat	ctg	ggc	tac	tac	cca	ggc	gag	tac	cag	835
Ala	Thr	Arg	Asp	Ala	Val	Asp	Leu	Gly	Tyr	Tyr	Pro	Gly	Glu	Tyr	Gln	
				235					240						245	
gtt	ggc	cag	acc	ggc	gtc	acc	gtg	tcc	cca	gac	ctc	tac	atc	ggc	ctc	883
Val	Gly	Gln	Thr	Gly	Val	Thr	Val	Ser	Pro	Asp	Leu	Tyr	Ile	Gly	Leu	

	250		255		260	
ggc att tcc ggt gca att cag cac act tct ggt atg cag acc gca aag						931
Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly Met Gln Thr Ala Lys						
	265		270		275	
aag gtt att gtg atc aac aac gat gag gac gcg ccg atc ttc cag att						979
Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala Pro Ile Phe Gln Ile						
	280		285		290	
gcg gac ctc ggt gtc gtt ggc gac ctc ttt gac atc gcc cct gcg ctc						1027
Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp Ile Ala Pro Ala Leu						
	295		300		305	
atc gaa gag atc aac aag cgc aag taggagtttt gaacactttt tat						1074
Ile Glu Glu Ile Asn Lys Arg Lys						
	310		315			

&lt;210&gt; 680

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 680

Met Ser Ile Ser Tyr Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu															
1		5					10						15		
Pro Val Thr Leu Glu Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val															
	20						25						30		
Val Ala Val Val Val Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala															
	35						40						45		
Glu Leu Gly Asn Trp Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser															
	50					55					60				
Gly Ala Ser Asn Arg Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile															
	65				70					75					80
Leu Ala Ala Asn Asn Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser															
			85						90					95	
Gly Asn Glu Ile Ala Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val															
	100						105						110		
Leu Thr Asp Val Val Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser															
	115						120					125			
Ile Phe Gly Asp Thr Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser															
	130					135				140					
Pro Leu Tyr Thr Leu Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro															
	145				150				155						160
Ala Thr Gly Glu Leu Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys															
		165					170						175		
Asp Val Thr Ile Thr Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro															
	180						185						190		

Glu Leu Pro Gln Ala Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly  
 195 200 205  
 Ser Glu Glu Asn Phe Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu  
 210 215 220  
 Gly Gly Ala Val Gly Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr  
 225 230 235 240  
 Pro Gly Glu Tyr Gln Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp  
 245 250 255  
 Leu Tyr Ile Gly Leu Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly  
 260 265 270  
 Met Gln Thr Ala Lys Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala  
 275 280 285  
 Pro Ile Phe Gln Ile Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp  
 290 295 300  
 Ile Ala Pro Ala Leu Ile Glu Glu Ile Asn Lys Arg Lys  
 305 310 315

<210> 681  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA00225

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 Met Ser Thr Ile Val 5  
 gtt ctg gtt aaa aat gtt cca gac acc tgg tct aag agg act ctg gaa 163  
 Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser Lys Arg Thr Leu Glu 20  
 gct gat ttc acc ctt gac cgt gag ggt gta gat cga gtc ttg gat gag 211  
 Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp Arg Val Leu Asp Glu 35  
 atc aat gag ttt gct ctg gag cag gca ctg cgc ttg cgg gag tcc aac 259  
 Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg Leu Arg Glu Ser Asn 50  
 ccg gat gct ggt tac cgc gtt gtt gcg ctg agc gcc ggc cct gcc ggt 307  
 Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser Ala Gly Pro Ala Gly 65  
 ggg gaa gag gcg ctg cgt aag gcg ctg tcc atg ggt gct gat gaa gca 355  
 Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met Gly Ala Asp Glu Ala 80

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atc cag ctc agt gat gat gcc ttg gct ggt tct gat ctt ttg gga acc 403
Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser Asp Leu Leu Gly Thr
          90                      95                      100

gct tgg gcg ctg aac aac gct atc aac acc atc gcg ggt gtt gct ctc 451
Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile Ala Gly Val Ala Leu
          105                      110                      115

atc gtg acg ggt tcg gct tct tcc gat ggt tcc atg ggt gcg ctt cct 499
Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser Met Gly Ala Leu Pro
          120                      125                      130

ggc gtg tta gct gag tac cgc cag gtc cca gcg ttg act aac ttg tct 547
Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala Leu Thr Asn Leu Ser
          135                      140                      145

gcg ctg aag gtc gag ggt gca tct att act gcc act cgc att gat aac 595
Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala Thr Arg Ile Asp Asn
150                      155                      160                      165

cac ggc acc tat gag ttg cag gct gca ctt cct gcg gtt gtg tcg att 643
His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro Ala Val Val Ser Ile
          170                      175                      180

tcc gat aag gct gac aag cca cgt ttc cct aac ttc aag ggc atc atg 691
Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn Phe Lys Gly Ile Met
          185                      190                      195

gct gct aag aag gct gag atc aag aag ctt tcc ttg gct gaa atc ggc 739
Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser Leu Ala Glu Ile Gly
          200                      205                      210

gtg gct cca gag cag gtt ggt ctg tct cac gcg gca act gct gtt act 787
Val Ala Pro Glu Gln Val Gly Leu Ser His Ala Ala Thr Ala Val Thr
          215                      220                      225

gct gca gct gat cgt cct gag cgc tcc caa ggt gat gtc att ggt gca 835
Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly Asp Val Ile Gly Ala
230                      235                      240                      245

tcg ggt gct gct gaa aag att gct gag tac ctc gct tca gag aac ctc 883
Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu Ala Ser Glu Asn Leu
          250                      255                      260

atc tagccactat cttcacaaag gag 909
Ile

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&lt;210&gt; 682

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 682

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Met Ser Thr Ile Val Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser
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Lys Arg Thr Leu Glu Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp
  20           25           30

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Arg Val Leu Asp Glu Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg  
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 Leu Arg Glu Ser Asn Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser  
           50                          55                          60  
 Ala Gly Pro Ala Gly Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met  
           65                          70                          75                          80  
 Gly Ala Asp Glu Ala Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser  
                           85                          90                          95  
 Asp Leu Leu Gly Thr Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile  
                           100                          105                          110  
 Ala Gly Val Ala Leu Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser  
           115                          120                          125  
 Met Gly Ala Leu Pro Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala  
           130                          135                          140  
 Leu Thr Asn Leu Ser Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala  
           145                          150                          155                          160  
 Thr Arg Ile Asp Asn His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro  
                           165                          170                          175  
 Ala Val Val Ser Ile Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn  
                           180                          185                          190  
 Phe Lys Gly Ile Met Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser  
           195                          200                          205  
 Leu Ala Glu Ile Gly Val Ala Pro Glu Gln Val Gly Leu Ser His Ala  
           210                          215                          220  
 Ala Thr Ala Val Thr Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly  
           225                          230                          235                          240  
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 Ala Ser Glu Asn Leu Ile  
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<211> 2378

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (82)..(2355)

<223> RXN00606

<400> 683

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ctg Leu	cct Pro	gag Glu 30	gcg Ala	atg Met	gct Ala	gcg Ala	gcc Ala	acc Thr 35	cca Pro	gtg Val	tgc Ser	gcg Ala	ttc Phe 40	ctg Leu	cac His	207
gct Ala	gcg Ala	gcc Ala 45	gtg Val	gtc Val	aag Lys	gcg Ala	ggt Gly 50	att Ile	tac Tyr	ctg Leu	ttg Leu	ctg Leu	cgc Arg 55	ttt Phe	agc Ser	255
att Ile	gtg Val 60	ttc Phe	cat His	gat Asp	gtt Val	gcg Ala 65	gtc Val	tgg Trp	aat Asn	tgg Trp 70	ttg Leu	ctg Leu	att Ile	atc Ile	gtc Val	303
ggc Gly 75	atg Met	ggt Gly	acg Thr	gcc Ala	atc Ile 80	atg Met	tgc Ser	gcg Ala	tat Tyr	ttc Phe 85	gcg Ala	gtg Val	cag Gln	aag Lys	acc Thr 90	351
gat Asp	ctg Leu	aag Lys	aag Lys 95	ctc Leu	acg Thr	gca Ala	tat Tyr	tcc Ser 100	acg Thr	gtg Val	tgc Ser	cat His	ttg Leu 105	ggt Gly	tgg Trp	399
atc Ile	gta Val	gcg Ala	acc Thr 110	atc Ile	ggc Gly	gtg Val	ggc Gly	act Thr 115	cct Pro	ttc Phe	gcg Ala	ctc Leu	ggc Gly 120	gct Ala	gcc Ala	447
att Ile	gtg Val 125	cac His	acg Thr	ctc Leu	agc Ser	cac His	gcg Ala 130	ctg Leu	ttt Phe	aag Lys	tcc Ser 135	tgc Ser	ttg Leu	ttc Phe	atg Met	495
ctc Leu 140	att Ile	ggc Gly	gtg Val	att Ile	gat Asp	cac His 145	cag Gln	act Thr	ggc Gly	acg Thr 150	cgc Arg	gat Asp	att Ile	cgt Arg	cgc Arg	543
ctc Leu 155	ggt Gly	ttc Phe	ctg Leu	gtc Val 160	aag Lys	aag Lys	atg Met	cgc Pro	ttc Phe 165	acg Thr	ttt Phe	gtg Val	tct Ser	gta Val 170	tta Leu	591
ata Ile	ggt Gly	gcg Ala	ttg Leu 175	tgc Ser	atg Met	gca Ala	tgc Ser	gtt Val	cgc Pro 180	cgc Pro	ttg Leu	ctc Leu	ggc Gly 185	ttc Phe	gtg Val	639
tcc Ser	aaa Lys	gaa Glu 190	ggc Gly	atg Met	atc Ile	aca Thr	gcg Ala 195	ttc Phe	atg Met	gac Asp	gcc Ala	ccc Pro	atc Ile 200	ggc Gly	aac Asn	687
tcc Ser	tat Tyr 205	gtt Val	gta Val	tta Leu	ctg Leu	ctg Leu	gtc Val 210	ggc Gly	gca Ala	gca Ala	atc Ile	ggc Gly 215	gcg Ala	gtc Val	cta Leu	735
acc Thr 220	ttc Phe	aca Thr	tac Tyr	tcc Ser	gcg Ala	aaa Lys 225	ctc Leu	gtg Val	ctc Leu	ggc Gly 230	gca Ala	ttc Phe	gtc Val	gac Asp	ggc Gly	783
cca Pro	cgc Arg	gac Asp	atg Met	tca Ser	cac His	gtc Val	aag Lys	gaa Glu	gcc Ala	ccc Pro	gtc Val	tcc Ser	ctc Leu	tgg Trp	ctt Leu	831

235	240	245	250	
ccg gcc gcc ctg cct gga ctt atg tct ctg cca cta gtc cta gta ctt	879			
Pro Ala Ala Leu Pro Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu				
255	260	265		
tcg ctt ttc gac gcc ccc gtc tcc gcc gca gcc acc tcc gcc gcg ggg	927			
Ser Leu Phe Asp Ala Pro Val Ser Ala Ala Thr Ser Ala Ala Gly				
270	275	280		
gaa gcg gcg cac atg cac ctg gca ttg tgg cac ggc atc aac acc cca	975			
Glu Ala Ala His Met His Leu Ala Leu Trp His Gly Ile Asn Thr Pro				
285	290	295		
ctg ttg att tcc ttg ggt gtg ctg gtg gcc gga atc ctt ggt gtg ctg	1023			
Leu Leu Ile Ser Leu Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu				
300	305	310		
ttc cgc aaa gag ctg tgg aaa atc gcc gag acc agc cct ttc ccc atc	1071			
Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile				
315	320	325		
gcc aca ggc aac gac atc cta tcg atg ctg gtt tac cga gcc aac ttg	1119			
Ala Thr Gly Asn Asp Ile Leu Ser Met Leu Val Tyr Arg Ala Asn Leu				
335	340	345		
ctg ggt aaa ttc ttc ggt cgc atg gct gat tcg atg agc cca cgc agg	1167			
Leu Gly Lys Phe Phe Gly Arg Met Ala Asp Ser Met Ser Pro Arg Arg				
350	355	360		
cac ttg gtc agc ctc atc gtg ctg ctc tgg gcg ctg gct gct ttt gcc	1215			
His Leu Val Ser Leu Ile Val Leu Leu Trp Ala Leu Ala Ala Phe Ala				
365	370	375		
acc att cac ccc tcg gtt cag ctt gca cca aag caa ccg gga att gat	1263			
Thr Ile His Pro Ser Val Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp				
380	385	390		
cgt tgg atc gac ctc att ccg ctt gcc atc atc gcg cta tct gtc ttc	1311			
Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile Ile Ala Leu Ser Val Phe				
395	400	405		
ggc ctg ctc acc acc cga aac cgc ctc agc gca gcc gtg ctt gtg ggt	1359			
Gly Leu Leu Thr Thr Arg Asn Arg Leu Ser Ala Ala Val Leu Val Gly				
415	420	425		
acc gtt ggt gtg ggt gtt tcc ttc cag atg cta ctt ctg ggc gct ccc	1407			
Thr Val Gly Val Gly Val Ser Phe Gln Met Leu Leu Leu Gly Ala Pro				
430	435	440		
gat gtt gca ctt acc cag ttc ctg gta gaa ggc ctc gtc gtg gta atc	1455			
Asp Val Ala Leu Thr Gln Phe Leu Val Glu Gly Leu Val Val Val Ile				
445	450	455		
atc atg atg gtt gtc cgg cac cag cct gcc aac ttc aag cgc atc aag	1503			
Ile Met Met Val Val Arg His Gln Pro Ala Asn Phe Lys Arg Ile Lys				
460	465	470		
ccc agc aga agg cgc agc acc gtt ctt gtc gcc gtc ctt gct gcc ttc	1551			
Pro Ser Arg Arg Arg Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe				
475	480	485		
				490

gcc gca ttc atg gcg gtg tgg gga ttg ctt ggc cgt cac gaa cgt tct	1599
Ala Ala Phe Met Ala Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser	
495 500 505	
gag ctg gcc atg tgg tac ctc aac caa ggt cca gag atc acc tct ggc	1647
Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly	
510 515 520	
gcc aac gtg gtg aac acc atc ctc gtg gaa ttc cgt gca ctg gat acg	1695
Ala Asn Val Val Asn Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr	
525 530 535	
ttg ggc gag ctc tcc gtg ctt ggc atg gca gct gtc gtc atc ggt gcg	1743
Leu Gly Glu Leu Ser Val Leu Gly Met Ala Ala Val Val Ile Gly Ala	
540 545 550	
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Met Val Ala Ser Met Pro Arg His Pro Phe Ala Lys Gly Thr His Pro	
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cgc ccc ttt ggc caa tca cag ttg aac tcc att ccg ctg cgc atg ctg	1839
Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu	
575 580 585	
ctt aag gtg ctg gtt cca gcg cta tgc ttc ttg agc ttc atg gtg ttc	1887
Leu Lys Val Leu Val Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe	
590 595 600	
atg cgt gga cac aat gat ccg gga ggc ggt ttc atc gca gcc cta att	1935
Met Arg Gly His Asn Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile	
605 610 615	
gcc ggt ggc gcg ctg atg ctc ctg tac ctg tcc aag gcc aaa gat ggc	1983
Ala Gly Gly Ala Leu Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly	
620 625 630	
cgc att ttc cgc ccg aat gtt cct ttc att ctc act ggt gcg ggc atc	2031
Arg Ile Phe Arg Pro Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile	
635 640 645 650	
ttg atg gca gtg ttc tcg ggc gta ctg gga ctc acc cac ggt tct ttc	2079
Leu Met Ala Val Phe Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe	
655 660 665	
ctg tac gcc atc cac ttc aac ttc gta ggc cag cac tgg acc acc tcg	2127
Leu Tyr Ala Ile His Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser	
670 675 680	
atg atc ttc gac ctc ggc gtg tac ctg gcc gtg ttg ggc atg gtg tcc	2175
Met Ile Phe Asp Leu Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser	
685 690 695	
atg gca atc aac ggc ctg ggc gga tac ctg cgc cca ggt acc gac aat	2223
Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn	
700 705 710	
gca gat ctg gac tac gcc gcg cga agt ggc cca ctg cca gca acg cca	2271
Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro	
715 720 725 730	



acg gtt gaa ccc gaa cca gaa ggc gat gaa gac tgg ccc gaa ccc atc 2319  
 Thr Val Glu Pro Glu Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile  
                     735                    740                    745

aac ccc gca ggc gat aac aaa gag gag gca aac cga tgattctcgc 2365  
 Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala Asn Arg  
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                     20                    25                    30  
 Ala Ala Thr Pro Val Ser Ala Phe Leu His Ala Ala Ala Val Val Lys  
                     35                    40                    45  
 Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser Ile Val Phe His Asp Val  
                     50                    55                    60  
 Ala Val Trp Asn Trp Leu Leu Ile Ile Val Gly Met Gly Thr Ala Ile  
                     65                    70                    75                    80  
 Met Ser Ala Tyr Phe Ala Val Gln Lys Thr Asp Leu Lys Lys Leu Thr  
                     85                    90                    95  
 Ala Tyr Ser Thr Val Ser His Leu Gly Trp Ile Val Ala Thr Ile Gly  
                     100                    105                    110  
 Val Gly Thr Pro Phe Ala Leu Gly Ala Ala Ile Val His Thr Leu Ser  
                     115                    120                    125  
 His Ala Leu Phe Lys Ser Ser Leu Phe Met Leu Ile Gly Val Ile Asp  
                     130                    135                    140  
 His Gln Thr Gly Thr Arg Asp Ile Arg Arg Leu Gly Phe Leu Val Lys  
                     145                    150                    155                    160  
 Lys Met Pro Phe Thr Phe Val Ser Val Leu Ile Gly Ala Leu Ser Met  
                     165                    170                    175  
 Ala Ser Val Pro Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile  
                     180                    185                    190  
 Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu  
                     195                    200                    205  
 Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala  
                     210                    215                    220  
 Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His  
                     225                    230                    235                    240

Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly  
 245 250 255  
 Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro  
 260 265 270  
 Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His  
 275 280 285  
 Leu Ala Leu Trp His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly  
 290 295 300  
 Val Leu Val Ala Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp  
 305 310 315 320  
 Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile  
 325 330 335  
 Leu Ser Met Leu Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly  
 340 345 350  
 Arg Met Ala Asp Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile  
 355 360 365  
 Val Leu Leu Trp Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val  
 370 375 380  
 Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile  
 385 390 395 400  
 Pro Leu Ala Ile Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr Arg  
 405 410 415  
 Asn Arg Leu Ser Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val  
 420 425 430  
 Ser Phe Gln Met Leu Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln  
 435 440 445  
 Phe Leu Val Glu Gly Leu Val Val Val Ile Ile Met Met Val Val Arg  
 450 455 460  
 His Gln Pro Ala Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser  
 465 470 475 480  
 Thr Val Leu Val Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val  
 485 490 495  
 Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr  
 500 505 510  
 Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr  
 515 520 525  
 Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val  
 530 535 540  
 Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro  
 545 550 555 560

Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser  
 565 570 575  
 Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro  
 580 585 590  
 Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp  
 595 600 605  
 Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met  
 610 615 620  
 Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn  
 625 630 635 640  
 Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser  
 645 650 655  
 Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe  
 660 665 670  
 Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly  
 675 680 685  
 Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu  
 690 695 700  
 Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala  
 705 710 715 720  
 Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro  
 725 730 735  
 Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn  
 740 745 750  
 Lys Glu Glu Ala Asn Arg  
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 <212> DNA  
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 <222> (101)..(1849)  
 <223> FRXA00606

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 Met Ala Ser Val Pro  
 1 5  
 ccg ttg ctc ggc ttc gtg tcc aaa gaa ggc atg atc aca gcg ttc atg 163  
 Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile Thr Ala Phe Met  
 10 15 20

gac gcc ccc atc ggc aac tcc tat gtt gta tta ctg ctg gtc ggc gca	211
Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu Val Gly Ala	
25 30 35	
gca atc ggc gcg gtc cta acc ttc aca tac tcc gcg aaa ctc gtg ctc	259
Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu	
40 45 50	
ggc gca ttc gtc gac ggc cca cgc gac atg tca cac gtc aag gaa gcc	307
Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His Val Lys Glu Ala	
55 60 65	
ccc gtc tcc ctc tgg ctt ccg gcc gcc ctg cct gga ctt atg tct ctg	355
Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly Leu Met Ser Leu	
70 75 80 85	
cca cta gtc cta gta ctt tcg ctt ttc gac gcc ccc gtc tcc gcc gca	403
Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro Val Ser Ala Ala	
90 95 100	
gcc acc tcc gcc gcg ggg gaa gcg gcg cac atg cac ctg gca ttg tgg	451
Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His Leu Ala Leu Trp	
105 110 115	
cac ggc atc aac acc cca ctg ttg att tcc ttg ggt gtg ctg gtg gcc	499
His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala	
120 125 130	
gga atc ctt ggt gtg ctg ttc cgc aaa gag ctg tgg aaa atc gcc gag	547
Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu	
135 140 145	
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Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu	
150 155 160 165	
gtt tac cga gcc aac ttg ctg ggt aaa ttc ttc ggt cgc atg gct gat	643
Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly Arg Met Ala Asp	
170 175 180	
tcg atg agc cca cgc agg cac ttg gtc agc ctc atc gtg ctg ctc tgg	691
Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Leu Trp	
185 190 195	
gcg ctg gct gct ttt gcc acc att cac ccc tcg gtt cag ctt gca cca	739
Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val Gln Leu Ala Pro	
200 205 210	
aag caa ccg gga att gat cgt tgg atc gac ctc att ccg ctt gcc atc	787
Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile	
215 220 225	
atc gcg cta tct gtc ttc ggc ctg ctc acc acc cga aac cgc ctc agc	835
Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr Arg Asn Arg Leu Ser	
230 235 240 245	
gca gcc gtg ctt gtg ggt acc gtt ggt gtg ggt gtt tcc ttc cag atg	883
Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val Ser Phe Gln Met	
250 255 260	
cta ctt ctg ggc gct ccc gat gtt gca ctt acc cag ttc ctg gta gaa	931

Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr	Gln	Phe	Leu	Val	Glu	
			265					270					275			
ggc	ctc	gtc	gtg	gta	atc	atc	atg	atg	gtt	gtc	cgg	cac	cag	cct	gcc	979
Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val	Arg	His	Gln	Pro	Ala	
		280					285					290				
aac	ttc	aag	cgc	atc	aag	ccc	agc	aga	agg	cgc	agc	acc	gtt	ctt	gtc	1027
Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	Ser	Thr	Val	Leu	Val	
	295					300					305					
gcc	gtc	ctt	gct	gcc	ttc	gcc	gca	ttc	atg	gcg	gtg	tgg	gga	ttg	ctt	1075
Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala	Val	Trp	Gly	Leu	Leu	
310					315					320					325	
ggc	cgt	cac	gaa	cgt	tct	gag	ctg	gcc	atg	tgg	tac	ctc	aac	caa	ggc	1123
Gly	Arg	His	Glu	Arg	Ser	Glu	Leu	Ala	Met	Trp	Tyr	Leu	Asn	Gln	Gly	
				330					335					340		
cca	gag	atc	acc	tct	ggc	gcc	aac	gtg	gtg	aac	acc	atc	ctc	gtg	gaa	1171
Pro	Glu	Ile	Thr	Ser	Gly	Ala	Asn	Val	Val	Asn	Thr	Ile	Leu	Val	Glu	
			345					350					355			
ttc	cgt	gca	ctg	gat	acg	ttg	ggc	gag	ctc	tcc	gtg	ctt	ggc	atg	gca	1219
Phe	Arg	Ala	Leu	Asp	Thr	Leu	Gly	Glu	Leu	Ser	Val	Leu	Gly	Met	Ala	
		360					365					370				
gct	gtc	gtc	atc	ggc	gcg	atg	gtg	gct	tcc	atg	cct	cgt	cat	ccg	ttt	1267
Ala	Val	Val	Ile	Gly	Ala	Met	Val	Ala	Ser	Met	Pro	Arg	His	Pro	Phe	
	375					380					385					
gcc	aag	ggc	acc	cac	cct	cgc	ccc	ttt	ggc	caa	tca	cag	ttg	aac	tcc	1315
Ala	Lys	Gly	Thr	His	Pro	Arg	Pro	Phe	Gly	Gln	Ser	Gln	Leu	Asn	Ser	
390					395				400						405	
att	ccg	ctg	cgc	atg	ctg	ctt	aag	gtg	ctg	gtt	cca	gcg	cta	tgc	ttc	1363
Ile	Pro	Leu	Arg	Met	Leu	Leu	Lys	Val	Leu	Val	Pro	Ala	Leu	Cys	Phe	
				410				415						420		
ttg	agc	ttc	atg	gtg	ttc	atg	cgt	gga	cac	aat	gat	ccg	gga	ggc	ggc	1411
Leu	Ser	Phe	Met	Val	Phe	Met	Arg	Gly	His	Asn	Asp	Pro	Gly	Gly	Gly	
			425					430					435			
ttc	atc	gca	gcc	cta	att	gcc	ggc	ggc	gcg	ctg	atg	ctc	ctg	tac	ctg	1459
Phe	Ile	Ala	Ala	Leu	Ile	Ala	Gly	Gly	Ala	Leu	Met	Leu	Leu	Tyr	Leu	
		440					445					450				
tcc	aag	gcc	aaa	gat	ggc	cgc	att	ttc	cgc	ccg	aat	gtt	cct	ttc	att	1507
Ser	Lys	Ala	Lys	Asp	Gly	Arg	Ile	Phe	Arg	Pro	Asn	Val	Pro	Phe	Ile	
	455					460					465					
ctc	act	ggc	gcg	ggc	atc	ttg	atg	gca	gtg	ttc	tcg	ggc	gta	ctg	gga	1555
Leu	Thr	Gly	Ala	Gly	Ile	Leu	Met	Ala	Val	Phe	Ser	Gly	Val	Leu	Gly	
470					475				480						485	
ctc	acc	cac	ggc	tct	ttc	ctg	tac	gcc	atc	cac	ttc	aac	ttc	gta	ggc	1603
Leu	Thr	His	Gly	Ser	Phe	Leu	Tyr	Ala	Ile	His	Phe	Asn	Phe	Val	Gly	
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cag	cac	tgg	acc	acc	tcg	atg	atc	ttc	gac	ctc	ggc	gtg	tac	ctg	gcc	1651
Gln	His	Trp	Thr	Thr	Ser	Met	Ile	Phe	Asp	Leu	Gly	Val	Tyr	Leu	Ala	

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gtg ttg ggc atg gtg tcc atg gca atc aac ggc ctg ggc gga tac ctg			1699
Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu			
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Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly			
535	540	545	
cca ctg cca gca acg cca acg gtt gaa ccc gaa cca gaa ggc gat gaa			1795
Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro Glu Gly Asp Glu			
550	555	560	565
gac tgg ccc gaa ccc atc aac ccc gca ggc gat aac aaa gag gag gca			1843
Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala			
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aac cga tgattctcgc actgacagtc gcg			1872
Asn Arg			

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 Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser  
 35 40 45  
 Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser  
 50 55 60  
 His Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro  
 65 70 75 80  
 Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala  
 85 90 95  
 Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met  
 100 105 110  
 His Leu Ala Leu Trp His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu  
 115 120 125  
 Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu  
 130 135 140  
 Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp  
 145 150 155 160  
 Ile Leu Ser Met Leu Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe  
 165 170 175

Gly Arg Met Ala Asp Ser Met Ser Pro Arg Arg His Leu Val Ser Leu  
 180 185 190  
 Ile Val Leu Leu Trp Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser  
 195 200 205  
 Val Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu  
 210 215 220  
 Ile Pro Leu Ala Ile Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr  
 225 230 235 240  
 Arg Asn Arg Leu Ser Ala Ala Val Leu Val Gly Thr Val Gly Val Gly  
 245 250 255  
 Val Ser Phe Gln Met Leu Leu Leu Gly Ala Pro Asp Val Ala Leu Thr  
 260 265 270  
 Gln Phe Leu Val Glu Gly Leu Val Val Val Ile Ile Met Met Val Val  
 275 280 285  
 Arg His Gln Pro Ala Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg  
 290 295 300  
 Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala  
 305 310 315 320  
 Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp  
 325 330 335  
 Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn  
 340 345 350  
 Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser  
 355 360 365  
 Val Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met  
 370 375 380  
 Pro Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln  
 385 390 395 400  
 Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val  
 405 410 415  
 Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn  
 420 425 430  
 Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu  
 435 440 445  
 Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro  
 450 455 460  
 Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe  
 465 470 475 480  
 Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His  
 485 490 495

Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu  
 500 505 510  
 Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly  
 515 520 525  
 Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr  
 530 535 540  
 Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu  
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 Asn Lys Glu Glu Ala Asn Arg  
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 Met Ala Met Asp Val  
 1 5  
 ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg 163  
 Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala  
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 gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211  
 Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val  
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 Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala  
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 gaa cac ggc ccg att gct cac aac gtg ggc ctt tat gtc ggt ggc gtg 307  
 Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val  
 55 60 65  
 gca atc ccc ttt gct gcc gat acg ttc agc gcc atc atg ttg atc acc 355  
 Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr  
 70 75 80 85  
 acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt 403  
 Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly  
 90 95 100  
 gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg 451



Glu	Thr	Arg	Ala	Arg	Phe	Tyr	Pro	Ala	Leu	Thr	Leu	Met	Leu	Ile	Thr		
			105					110					115				
ggc	gtc	aac	ggg	gct	ctg	ctg	act	gcc	gat	ctg	ttc	aac	ttc	ttt	gtg	499	
Gly	Val	Asn	Gly	Ala	Leu	Leu	Thr	Ala	Asp	Leu	Phe	Asn	Phe	Phe	Val		
		120					125					130					
ttc	atc	gaa	gtg	atg	ctg	ctg	cct	tcc	tat	ggg	ttg	atc	gcc	atg	acc	547	
Phe	Ile	Glu	Val	Met	Leu	Leu	Pro	Ser	Tyr	Gly	Leu	Ile	Ala	Met	Thr		
	135						140				145						
gga	acg	tgg	gcg	cgc	cta	gcc	tct	gga	cga	atc	ttc	gta	cta	gtc	aat	595	
Gly	Thr	Trp	Ala	Arg	Leu	Ala	Ser	Gly	Arg	Ile	Phe	Val	Leu	Val	Asn		
150					155					160					165		
ctc	tct	gcc	tcc	aca	ttg	ctg	gtt	gca	ggg	gtg	gga	atc	gtc	tac	ggg	643	
Leu	Ser	Ala	Ser	Thr	Leu	Leu	Val	Ala	Gly	Val	Gly	Ile	Val	Tyr	Gly		
				170					175					180			
gtc	ata	ggc	tca	gtc	aac	atc	gca	gct	ctg	caa	gat	gtc	gta	gag	ggc	691	
Val	Ile	Gly	Ser	Val	Asn	Ile	Ala	Ala	Leu	Gln	Asp	Val	Val	Glu	Gly		
		185						190					195				
aac	ccc	ctg	gtt	gcc	agc	gca	atg	ggc	atc	gtg	gtt	att	gcc	atc	gcg	739	
Asn	Pro	Leu	Val	Ala	Ser	Ala	Met	Gly	Ile	Val	Val	Ile	Ala	Ile	Ala		
		200					205					210					
gtt	aaa	gcc	ggg	gta	ttc	cca	gtg	cac	aca	tgg	ctg	cca	cgc	acc	tat	787	
Val	Lys	Ala	Gly	Val	Phe	Pro	Val	His	Thr	Trp	Leu	Pro	Arg	Thr	Tyr		
	215					220					225						
cct	ggg	aca	tca	gca	gct	gtg	atg	ggg	ttg	ttc	tcc	ggg	ttg	cac	acc	835	
Pro	Gly	Thr	Ser	Ala	Ala	Val	Met	Gly	Leu	Phe	Ser	Gly	Leu	His	Thr		
230					235					240					245		
aaa	gtc	gcg	gta	tac	atg	ctc	tat	cgc	att	tgg	gtc	cac	att	ttt	aac	883	
Lys	Val	Ala	Val	Tyr	Met	Leu	Tyr	Arg	Ile	Trp	Val	His	Ile	Phe	Asn		
				250					255					260			
atg	gat	ccc	acg	tgg	aat	tgg	ctg	att	gtc	gca	ttc	atg	gtg	ata	tcc	931	
Met	Asp	Pro	Thr	Trp	Asn	Trp	Leu	Ile	Val	Ala	Phe	Met	Val	Ile	Ser		
			265				270						275				
atg	ctg	gtc	ggg	ggc	ttc	gct	gga	ctt	gct	gaa	aac	tcc	atc	cgt	cgc	979	
Met	Leu	Val	Gly	Gly	Phe	Ala	Gly	Leu	Ala	Glu	Asn	Ser	Ile	Arg	Arg		
		280					285					290					
gtc	ctt	gcc	tac	caa	atg	gtc	aac	ggc	atg	cca	ttt	att	ctc	atc	atg	1027	
Val	Leu	Ala	Tyr	Gln	Met	Val	Asn	Gly	Met	Pro	Phe	Ile	Leu	Ile	Met		
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atg	gcg	ttt	acc	tct	gac	gat	cca	cag	cgc	gca	ctt	gcc	gct	ggg	ctg	1075	
Met	Ala	Phe	Thr	Ser	Asp	Asp	Pro	Gln	Arg	Ala	Leu	Ala	Ala	Gly	Leu		
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ttg	tac	acc	ctg	cac	cac	atg	atc	acc	atc	gcc	gca	ttg	gtg	ctc	act	1123	
Leu	Tyr	Thr	Leu	His	His	Met	Ile	Thr	Ile	Ala	Ala	Leu	Val	Leu	Thr		
				330					335					340			
tcc	ggc	gca	atc	gaa	gaa	acc	tac	ggc	acc	ggg	atg	ttg	tcc	aag	ctg	1171	
Ser	Gly	Ala	Ile	Glu	Glu	Thr	Tyr	Gly	Thr	Gly	Met	Leu	Ser	Lys	Leu		

345										350					355					
tct	ggc	ctt	gca	cgc	cgc	gaa	ccc	gtc	gtc	gca	gca	gtg	ttc	gct	gca	1219				
Ser	Gly	Leu	Ala	Arg	Arg	Glu	Pro	Val	Val	Ala	Ala	Val	Phe	Ala	Ala					
360						365					370									
ggt	gcc	ttc	tct	gtt	gtc	ggt	ttc	cca	ccg	ttt	tcc	ggt	atg	tgg	ggc	1267				
Gly	Ala	Phe	Ser	Val	Val	Gly	Phe	Pro	Pro	Phe	Ser	Gly	Met	Trp	Gly					
375						380					385									
aaa	gcg	ctc	atc	ctg	ctc	gag	atc	gcc	cgc	gtc	ggc	aat	att	gca	gca	1315				
Lys	Ala	Leu	Ile	Leu	Leu	Glu	Ile	Ala	Arg	Val	Gly	Asn	Ile	Ala	Ala					
390						395					400				405					
tgg	atc	gca	atc	gcc	gcc	atc	atc	atc	gcc	agc	ctg	ggc	gca	ctg	ctc	1363				
Trp	Ile	Ala	Ile	Ala	Ala	Ile	Ile	Ile	Ala	Ser	Leu	Gly	Ala	Leu	Leu					
410						415					420									
tcg	atg	atc	cgc	gtg	tgg	cgt	gaa	gtc	ttc	tgg	ggt	ggc	gca	atg	cac	1411				
Ser	Met	Ile	Arg	Val	Trp	Arg	Glu	Val	Phe	Trp	Gly	Gly	Ala	Met	His					
425						430					435									
cag	cgc	ggc	gtc	tcg	ccg	cag	ctg	cgc	atc	agc	cca	gca	aaa	atc	gcc	1459				
Gln	Arg	Gly	Val	Ser	Pro	Gln	Leu	Arg	Ile	Ser	Pro	Ala	Lys	Ile	Ala					
440						445					450									
cca	gcg	ctc	agc	ctg	atc	att	tta	tcg	gta	ggc	atg	ttc	atc	ttc	gcg	1507				
Pro	Ala	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Val	Gly	Met	Phe	Ile	Phe	Ala					
455						460					465									
ggc	ccg	ctt	atc	gac	gcg	acc	ctc	acc	gcc	acc	gac	ggc	ctc	ttg	aac	1555				
Gly	Pro	Leu	Ile	Asp	Ala	Thr	Leu	Thr	Ala	Thr	Asp	Gly	Leu	Leu	Asn					
470						475					480				485					
acc	gat	gca	tac	caa	cag	gct	gtg	ctc	ggt	gaa	aat	gcc	atc	gga	gtg	1603				
Thr	Asp	Ala	Tyr	Gln	Gln	Ala	Val	Leu	Gly	Glu	Asn	Ala	Ile	Gly	Val					
490						495					500									
cca	agc	cct	agc	tac	cag	gga	gga	aac	taatgcttaa	cgccctgaaa						1650				
Pro	Ser	Pro	Ser	Tyr	Gln	Gly	Gly	Asn												
505						510														
ttc																1653				

&lt;210&gt; 688

&lt;211&gt; 510

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 688

Met	Ala	Met	Asp	Val	Leu	Leu	Pro	Ile	Phe	Val	Ala	Val	Pro	Leu	Ala
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Ala	Ser	Ala	Ile	Ala	Val	Leu	Leu	Pro	Trp	Arg	Leu	Ile	Arg	Asp	Ile
			20					25					30		

Leu	His	Ile	Ile	Val	Pro	Phe	Ala	Gly	Ile	Phe	Ala	Gly	Ile	Trp	Leu
		35					40					45			

Phe	Ala	His	Thr	Ala	Glu	His	Gly	Pro	Ile	Ala	His	Asn	Val	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala		
65	70	75
Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe		
	85	90
Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr		
	100	105
Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu		
	115	120
Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly		
	130	135
Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile		
145	150	155
Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val		
	165	170
Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln		
	180	185
Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val		
	195	200
Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp		
	210	215
Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe		
225	230	235
Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp		
	245	250
Val His Ile Phe Asn Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala		
	260	265
Phe Met Val Ile Ser Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu		
	275	280
Asn Ser Ile Arg Arg Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro		
	290	295
Phe Ile Leu Ile Met Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala		
305	310	315
Leu Ala Ala Gly Leu Leu Tyr Thr Leu His His Met Ile Thr Ile Ala		
	325	330
Ala Leu Val Leu Thr Ser Gly Ala Ile Glu Glu Thr Tyr Gly Thr Gly		
	340	345
Met Leu Ser Lys Leu Ser Gly Leu Ala Arg Arg Glu Pro Val Val Ala		
	355	360
Ala Val Phe Ala Ala Gly Ala Phe Ser Val Val Gly Phe Pro Pro Phe		
	370	375
		380

Ser Gly Met Trp Gly Lys Ala Leu Ile Leu Leu Glu Ile Ala Arg Val  
 385 390 395 400  
 Gly Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser  
 405 410 415  
 Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp  
 420 425 430  
 Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser  
 435 440 445  
 Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly  
 450 455 460  
 Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr  
 465 470 475 480  
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 Met Ala Met Asp Val 5  
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 Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala 20  
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 gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211  
 Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val 35  
 25 30  
 cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct 259  
 Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala 50  
 40 45  
 gaa cac ggc ccg att gct cac aac gtg ggc ctt tat gtc ggt ggc gtg 307  
 Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val 65  
 55 60  
 gca atc ccc ttt gct gcc gat acg ttc agc gcc atc atg ttg atc acc 355  
 Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr

70	75	80	85	
acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt				403
Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly				
	90	95	100	
gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg				451
Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr				
	105	110	115	
ggc gtc aac ggt gct ctg ctg act gcc gat ctg ttc aac ttc ttt gtg				499
Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val				
	120	125	130	
ttc atc gaa gtg atg ctg ctg cct tcc tat ggt ttg atc gcc atg acc				547
Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr				
	135	140	145	
gga acg tgg gcg cgc cta gcc tct gga cga atc ttc gta cta gtc aat				595
Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile Phe Val Leu Val Asn				
	150	155	160	165
ctc tct gcc tcc aca ttg ctg gtt gca ggt gtg gga atc gtc tac ggt				643
Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly				
	170	175	180	
gtc ata ggc tca gtc aac atc gca gct ctg caa gat gtc gta gag ggc				691
Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly				
	185	190	195	
aac ccc ctg gtt gcc agc gca atg ggc atc gtg gtt att gcc atc gcg				739
Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala				
	200	205	210	
gtt aaa gcc ggt gta ttc cca gtg cac aca tgg ctg cca cgc acc tat				787
Val Lys Ala Gly Val Phe Pro Val His Thr Trp Leu Pro Arg Thr Tyr				
	215	220	225	
cct ggt aca tca gca gct gtg atg ggg ttg ttc tcc ggt ttg cac acc				835
Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr				
	230	235	240	245
aaa gtc gcg gta tac atg ctc tat cgc att				865
Lys Val Ala Val Tyr Met Leu Tyr Arg Ile				
	250	255		

&lt;210&gt; 690

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 690

Met	Ala	Met	Asp	Val	Leu	Leu	Pro	Ile	Phe	Val	Ala	Val	Pro	Leu	Ala
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Ala	Ser	Ala	Ile	Ala	Val	Leu	Leu	Pro	Trp	Arg	Leu	Ile	Arg	Asp	Ile
			20					25					30		

Leu	His	Ile	Ile	Val	Pro	Phe	Ala	Gly	Ile	Phe	Ala	Gly	Ile	Trp	Leu
		35					40					45			

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu  
 50 55 60  
 Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala  
 65 70 75 80  
 Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe  
 85 90 95  
 Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr  
 100 105 110  
 Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu  
 115 120 125  
 Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly  
 130 135 140  
 Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile  
 145 150 155 160  
 Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val  
 165 170 175  
 Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln  
 180 185 190  
 Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val  
 195 200 205  
 Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp  
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 Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe  
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 Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile  
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 <223> RXA00913

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 ctt gca ctg acc gtt gcg cac tcc ttg ttt aag gca aca ttg ttc atg 96  
 Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met  
 20 25 30  
 aca gtt ggt gcc att gac cac acc acc gga act cgt gat att cgt aaa 144

Thr	Val	Gly	Ala	Ile	Asp	His	Thr	Thr	Gly	Thr	Arg	Asp	Ile	Arg	Lys	
		35					40					45				
ctc	tcc	ggg	ctg	tgg	cgt	aaa	caa	ccg	atc	ctg	ttc	gcc	gtt	gct	gct	192
Leu	Ser	Gly	Leu	Trp	Arg	Lys	Gln	Pro	Ile	Leu	Phe	Ala	Val	Ala	Ala	
	50					55					60					
gtt	tcg	gcg	gcg	tcc	atg	gct	ggg	att	ccg	cca	ctg	ttt	ggg	ttt	atc	240
Val	Ser	Ala	Ala	Ser	Met	Ala	Gly	Ile	Pro	Pro	Leu	Phe	Gly	Phe	Ile	
	65				70					75					80	
gcc	aag	gaa	aca	gcg	ctg	gat	acc	gtg	ttg	aat	gag	cag	atg	ttg	cat	288
Ala	Lys	Glu	Thr	Ala	Leu	Asp	Thr	Val	Leu	Asn	Glu	Gln	Met	Leu	His	
			85						90					95		
ggc	atg	cca	ggg	cga	ttg	atg	ctg	gct	ggc	atc	gtt	ttg	ggg	tcc	atc	336
Gly	Met	Pro	Gly	Arg	Leu	Met	Leu	Ala	Gly	Ile	Val	Leu	Gly	Ser	Ile	
			100					105					110			
ttc	acc	atg	gca	tat	tcc	tgc	tac	ttc	ctg	tac	gaa	gcc	ttt	gcc	acg	384
Phe	Thr	Met	Ala	Tyr	Ser	Cys	Tyr	Phe	Leu	Tyr	Glu	Ala	Phe	Ala	Thr	
		115					120					125				
aag	cac	tcc	aaa	ttc	cca	gag	gcc	aac	ggg	gtc	tca	cct	gca	gtg	gag	432
Lys	His	Ser	Lys	Phe	Pro	Glu	Ala	Asn	Gly	Val	Ser	Pro	Ala	Val	Glu	
	130					135					140					
gca	atg	cat	ccg	gtg	aag	ttt	aag	ctg	tgg	atc	gca	cct	gtc	atc	ctg	480
Ala	Met	His	Pro	Val	Lys	Phe	Lys	Leu	Trp	Ile	Ala	Pro	Val	Ile	Leu	
	145				150					155					160	
gct	att	ttg	acc	gta	gtg	ttt	ggg	gtt	ttc	ccc	aag	cca	gtg	tcg	gaa	528
Ala	Ile	Leu	Thr	Val	Val	Phe	Gly	Val	Phe	Pro	Lys	Pro	Val	Ser	Glu	
				165					170					175		
gca	att	gtc	acg	cat	ctt	gat	aac	gtc	acg	cca	tcg	ctt	gat	gat	gtc	576
Ala	Ile	Val	Thr	His	Leu	Asp	Asn	Val	Thr	Pro	Ser	Leu	Asp	Asp	Val	
			180					185					190			
cac	acc	aaa	ctg	gcc	ttg	tgg	cat	ggg	ctg	aat	cta	ccg	ctg	ctg	ctg	624
His	Thr	Lys	Leu	Ala	Leu	Trp	His	Gly	Leu	Asn	Leu	Pro	Leu	Leu	Leu	
		195					200					205				
tct	gtg	gtg	atc	atc	att	tcc	gga	ttc	atc	atc	ttc	tgg	gag	cga	gac	672
Ser	Val	Val	Ile	Ile	Ile	Ser	Gly	Phe	Ile	Ile	Phe	Trp	Glu	Arg	Asp	
	210					215					220					
acc	gtc	gaa	cgt	ttg	cgc	cct	aac	acc	gca	gcg	ttt	ggc	agt	gcc	gat	720
Thr	Val	Glu	Arg	Leu	Arg	Pro	Asn	Thr	Ala	Ala	Phe	Gly	Ser	Ala	Asp	
	225				230					235				240		
acc	gcc	tac	gac	gcc	att	ctt	gat	gca	ctg	cgt	gtg	ctc	tcc	cac	cgc	768
Thr	Ala	Tyr	Asp	Ala	Ile	Leu	Asp	Ala	Leu	Arg	Val	Leu	Ser	His	Arg	
				245					250					255		
ctg	act	gca	tcc	acc	cag	cgt	ggg	tct	ttg	acc	ctg	aac	gtc	ggg	gtg	816
Leu	Thr	Ala	Ser	Thr	Gln	Arg	Gly	Ser	Leu	Thr	Leu	Asn	Val	Gly	Val	
			260				265						270			
atc	ttc	ttc	gtc	ctc	acg	att	gtt	ccg	ctg	atc	gct	ttg	atc	act	ggc	864
Ile	Phe	Phe	Val	Leu	Thr	Ile	Val	Pro	Leu	Ile	Ala	Leu	Ile	Thr	Gly	

275					280					285										
gaa	caa	agc	gat	gtc	cgc	atg	gag	ctg	tgg	gat	agc	cct	att	cag	ggc	912				
Glu	Gln	Ser	Asp	Val	Arg	Met	Glu	Leu	Trp	Asp	Ser	Pro	Ile	Gln	Gly					
290					295					300										
ttc	atc	gcg	gcc	atc	att	atc	gtc	gtt	gcg	att	gtg	gca	acc	acc	atg	960				
Phe	Ile	Ala	Ala	Ile	Ile	Ile	Val	Val	Ala	Ile	Val	Ala	Thr	Thr	Met					
305					310					315					320					
gat	aac	cgt	ttg	tct	gcg	ctg	att	ttg	gtg	ggg	gtg	aca	ggg	tat	ggc	1008				
Asp	Asn	Arg	Leu	Ser	Ala	Leu	Ile	Leu	Val	Gly	Val	Thr	Gly	Tyr	Gly					
325					330					335										
att	gcc	gtt	atc	ttc	gcg	cta	cat	ggc	gca	ccg	gac	ttg	gcg	cta	acc	1056				
Ile	Ala	Val	Ile	Phe	Ala	Leu	His	Gly	Ala	Pro	Asp	Leu	Ala	Leu	Thr					
340					345					350										
cag	gtg	ctg	gtg	gag	acc	atc	gtc	atg	gtg	gta	ttc	atg	ctg	gtg	ctg	1104				
Gln	Val	Leu	Val	Glu	Thr	Ile	Val	Met	Val	Val	Phe	Met	Leu	Val	Leu					
355					360					365										
cgt	aaa	atg	ccg	aca	gaa	gtt	gcg	tgg	aag	gca	gaa	cct	aaa	cag	tct	1152				
Arg	Lys	Met	Pro	Thr	Glu	Val	Ala	Trp	Lys	Ala	Glu	Pro	Lys	Gln	Ser					
370					375					380										
cgc	gtg	cga	gcg	tgg	ctt	gct	ggc	gcc	acc	gga	ttg	tcc	gtt	gtt	att	1200				
Arg	Val	Arg	Ala	Trp	Leu	Ala	Gly	Ala	Thr	Gly	Leu	Ser	Val	Val	Ile					
385					390					395					400					
gtc	acc	att	ttt	gcc	atg	aat	gct	cgc	acc	act	gaa	ccg	atc	tct	gta	1248				
Val	Thr	Ile	Phe	Ala	Met	Asn	Ala	Arg	Thr	Thr	Glu	Pro	Ile	Ser	Val					
405					410					415										
tac	atg	cag	gat	ctg	gcc	tat	gag	atc	gga	cat	ggc	gca	aac	acc	gtc	1296				
Tyr	Met	Gln	Asp	Leu	Ala	Tyr	Glu	Ile	Gly	His	Gly	Ala	Asn	Thr	Val					
420					425					430										
aac	gta	ctg	ctc	gta	gac	ctg	cgt	ggg	ttt	gat	acc	ttc	ggg	gaa	att	1344				
Asn	Val	Leu	Leu	Val	Asp	Leu	Arg	Gly	Phe	Asp	Thr	Phe	Gly	Glu	Ile					
435					440					445										
tcc	gtc	ctt	gtg	atc	gcg	gca	acc	ggg	atc	gcc	tcc	ctg	gtc	tac	cga	1392				
Ser	Val	Leu	Val	Ile	Ala	Ala	Thr	Gly	Ile	Ala	Ser	Leu	Val	Tyr	Arg					
450					455					460										
aac	cgc	agc	ttc	cgc	aag	gat	tct	cgc	aga	cca	acc	ctg	gct	acc	act	1440				
Asn	Arg	Ser	Phe	Arg	Lys	Asp	Ser	Arg	Arg	Pro	Thr	Leu	Ala	Thr	Thr					
465					470					475					480					
ggg	cgc	cgt	tgg	ttg	gct	gct	gct	gtt	gat	acc	gaa	agg	gcg	cag	aac	1488				
Gly	Arg	Arg	Trp	Leu	Ala	Ala	Ala	Val	Asp	Thr	Glu	Arg	Ala	Gln	Asn					
485					490					495										
cgc	tcg	ctg	atg	gtt	gat	gtg	gca	acg	cgc	atc	ctc	ttc	cct	gcc	atg	1536				
Arg	Ser	Leu	Met	Val	Asp	Val	Ala	Thr	Arg	Ile	Leu	Phe	Pro	Ala	Met					
500					505					510										
atc	atg	ttg	tct	gtg	tac	ttc	ttc	ttc	gcc	gga	cac	aac	gcg	ccg	ggc	1584				
Ile	Met	Leu	Ser	Val	Tyr	Phe	Phe	Phe	Ala	Gly	His	Asn	Ala	Pro	Gly					
515					520					525										



ggc gga ttc gcc ggc ggc ctt gtt gcc tcc ttg gcg ttc gcc ttg cgc 1632  
 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg  
 530 535 540

tac ctt gcc ggt gga cgt gaa gaa ctt gaa gaa gcg ttg cct atc gac 1680  
 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp  
 545 550 555 560

gcc ggc cgt atc ttg gga act gga cta ttt gtt tct gca act gca gtg 1728  
 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val  
 565 570 575

ctg tgg ccc atg gtt ctt ctt ggt gaa cca ccg ctg acc tcc cat att 1776  
 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile  
 580 585 590

tgg gat ctc aca ctg cca ctt atc ggt gag att cac att gca tcc gcg 1824  
 Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala  
 595 600 605

ctg ctc ttt gac ctt ggt gtc tac ctg atc gtc atc ggt ttg acc atg 1872  
 Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met  
 610 615 620

cac att ctc aac agt ttg ggc ggc cag ctc gac cgc gat gag gaa atg 1920  
 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met  
 625 630 635 640

cgt aag cag cgt gcg cgc gac cga gct cga cgc ttg gcg cgc aac cag 1968  
 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln  
 645 650 655

cgt cga gaa gca gca acc gtc ggc gca cgc agg tcg aac gag aaa tcg 2016  
 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser  
 660 665 670

aca cgc caa atg ccg acg att cgg cct cca ggg gca gac aca gaa tcg 2064  
 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser  
 675 680 685

gtg gag cag aac ggt gag aac cag acg tcg ata agc aca aag cgt tta 2112  
 Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu  
 690 695 700

aag cag 2118  
 Lys Gln  
 705

&lt;210&gt; 692

&lt;211&gt; 706

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 692

Ile Ile Ser Val Val Gly Ile Gly Thr Arg Glu Ala Leu Leu Ala Gly  
 1 5 10 15

Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met  
 20 25 30

Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys  
 35 40 45  
 Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala  
 50 55 60  
 Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile  
 65 70 75 80  
 Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His  
 85 90 95  
 Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile  
 100 105 110  
 Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr  
 115 120 125  
 Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu  
 130 135 140  
 Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu  
 145 150 155 160  
 Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu  
 165 170 175  
 Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val  
 180 185 190  
 His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu  
 195 200 205  
 Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp  
 210 215 220  
 Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp  
 225 230 235 240  
 Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg  
 245 250 255  
 Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val  
 260 265 270  
 Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly  
 275 280 285  
 Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly  
 290 295 300  
 Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met  
 305 310 315 320  
 Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly  
 325 330 335  
 Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr  
 340 345 350

Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu  
 355 360 365  
 Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser  
 370 375 380  
 Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile  
 385 390 395 400  
 Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val  
 405 410 415  
 Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val  
 420 425 430  
 Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile  
 435 440 445  
 Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg  
 450 455 460  
 Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr  
 465 470 475 480  
 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn  
 485 490 495  
 Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met  
 500 505 510  
 Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly  
 515 520 525  
 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg  
 530 535 540  
 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp  
 545 550 555 560  
 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val  
 565 570 575  
 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile  
 580 585 590  
 Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala  
 595 600 605  
 Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met  
 610 615 620  
 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met  
 625 630 635 640  
 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln  
 645 650 655  
 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser  
 660 665 670  
 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser

675                      680                      685

Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu  
690                      695                      700

Lys Gln  
705

<210> 693  
<211> 955  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(955)  
<223> RXA00909

<400> 693  
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cagagtaatc cacaacgcgc aaaggggaac tggagaacac gtg ctc att ctt ttt 115  
Val Leu Ile Leu Phe  
1 5

ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act 163  
Leu Ala Leu Thr Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr  
10 15 20

ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt 211  
Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly  
25 30 35

ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga 259  
Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly  
40 45 50

ggt gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat 307  
Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn  
55 60 65

atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc 355  
Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val  
70 75 80 85

tta ggc gtg ggc gcc cta gtg ctg ctg tac tgc tgg gga tat ttt gat 403  
Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys Trp Gly Tyr Phe Asp  
90 95 100

tcc aac gcg ggt cgc ctc agt gcc ttt ggt gct gaa ctg gtg gcc ttc 451  
Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala Glu Leu Val Ala Phe  
105 110 115

gcc atg gcg atg ttt ggt ctt gtc att tca gac aac atc ctg ctg atg 499  
Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp Asn Ile Leu Leu Met  
120 125 130

tac gtc ttc tgg gaa atc acc tcc gtt tta tcc ttc ctc ctg gtt ggt 547  
Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser Phe Leu Leu Val Gly  
135 140 145

tat tac ggc gaa cgc gca tct tca cgt cgc tct gca ggt caa gcc ttg 595  
 Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser Ala Gly Gln Ala Leu  
 150 155 160 165  
  
 atg gtg acc acc ctg ggt gga ttg gcc atg ctg gtg ggc atc att ttg 643  
 Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu Val Gly Ile Ile Leu  
 170 175 180  
  
 atg ggt acc caa act ggc gtg tgg cga ttc tct gag atc cct gcc tac 691  
 Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser Glu Ile Pro Ala Tyr  
 185 190 195  
  
 tca agc tcc tgg gca gat gtg ccg tat att tcc gct gct gct gcc ctt 739  
 Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser Ala Ala Ala Leu  
 200 205 210  
  
 atc ttg gct ggc gca cta tcc aaa tcg gct atc gca cca acc cac ttc 787  
 Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile Ala Pro Thr His Phe  
 215 220 225  
  
 tgg ctt ccc ggc gcg atg gcc gca cca acg ccg gtg tct gct tac ctg 835  
 Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro Val Ser Ala Tyr Leu  
 230 235 240 245  
  
 cac tcc gca gcg atg gtg aag gcg ggt att tac ctt gtg gct cgc ctc 883  
 His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr Leu Val Ala Arg Leu  
 250 255 260  
  
 tct cca gac ctc aac gta gtt ggt tcg tgg tac ctg atc atc atc ccg 931  
 Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr Leu Ile Ile Ile Pro  
 265 270 275  
  
 ttg ggc atg ttg acc atg ctc atg 955  
 Leu Gly Met Leu Thr Met Leu Met  
 280 285

<210> 694  
 <211> 285  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 694  
 Val Leu Ile Leu Phe Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro  
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 Ile Leu Ile Arg Thr Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu  
 20 25 30  
  
 Val Pro Gly Ile Gly Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly  
 35 40 45  
  
 Thr Phe Lys Asp Gly Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro  
 50 55 60  
  
 Ser Ala His Leu Asn Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu  
 65 70 75 80  
  
 Phe Ser Leu Ile Val Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys  
 85 90 95

Trp Gly Tyr Phe Asp Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala  
 100 105 110  
 Glu Leu Val Ala Phe Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp  
 115 120 125  
 Asn Ile Leu Leu Met Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser  
 130 135 140  
 Phe Leu Leu Val Gly Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser  
 145 150 155 160  
 Ala Gly Gln Ala Leu Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu  
 165 170 175  
 Val Gly Ile Ile Leu Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser  
 180 185 190  
 Glu Ile Pro Ala Tyr Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser  
 195 200 205  
 Ala Ala Ala Ala Leu Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile  
 210 215 220  
 Ala Pro Thr His Phe Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro  
 225 230 235 240  
 Val Ser Ala Tyr Leu His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr  
 245 250 255  
 Leu Val Ala Arg Leu Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr  
 260 265 270  
 Leu Ile Ile Ile Pro Leu Gly Met Leu Thr Met Leu Met  
 275 280 285

&lt;210&gt; 695

&lt;211&gt; 927

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(904)

&lt;223&gt; RXA00700

&lt;400&gt; 695

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tctcggccgt gaaagctgcg ctagggcatg gtgaaatctc atg atc aac gcc atc 115  
 Met Ile Asn Ala Ile  
 1 5

aca ctc aag ccc aaa acc ttc ctc acc tta agc ttc ctt gcg gtt ttg 163  
 Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser Phe Leu Ala Val Leu  
 10 15 20

agc atc gtg att ttc ttc tgg ccg ctg atc gtc aac ccg gaa tcc ttc 211  
 Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val Asn Pro Glu Ser Phe

				25				30				35								
ctg	tcc	gac	aaa	gcc	caa	gcg	ccc	ctc	tac	atc	gcg	atc	gtc	att	ccc		259			
Leu	Ser	Asp	Lys	Ala	Gln	Ala	Pro	Leu	Tyr	Ile	Ala	Ile	Val	Ile	Pro					
			40				45				50									
ctc	gtg	ctg	gcc	gct	gtc	atc	gcc	gaa	atc	agt	gaa	aac	gga	ttc	gac		307			
Leu	Val	Leu	Ala	Ala	Val	Ile	Ala	Glu	Ile	Ser	Glu	Asn	Gly	Phe	Asp					
			55				60				65									
gtt	aaa	gcc	gta	gcc	atg	ctc	ggc	gtc	ctc	acc	gcc	atg	gtt	gcc	gta		355			
Val	Lys	Ala	Val	Ala	Met	Leu	Gly	Val	Leu	Thr	Ala	Met	Val	Ala	Val					
			70				75				80			85						
gtc	cga	cca	ttc	ggg	gcc	ggc	gca	gca	ggc	ttt	gaa	gca	gtc	ttc	ttt		403			
Val	Arg	Pro	Phe	Gly	Ala	Gly	Ala	Ala	Gly	Phe	Glu	Ala	Val	Phe	Phe					
				90							95			100						
gtc	ctc	atc	ctc	ggc	gga	cga	gcc	ttc	gga	ccc	ggc	ttc	gga	ttc	atc		451			
Val	Leu	Ile	Leu	Gly	Gly	Arg	Ala	Phe	Gly	Pro	Gly	Phe	Gly	Phe	Ile					
			105							110			115							
ctc	ggc	aac	acc	gga	ctg	ttc	gca	tcc	gcg	ctg	ctc	acc	gca	gga	atc		499			
Leu	Gly	Asn	Thr	Gly	Leu	Phe	Ala	Ser	Ala	Leu	Leu	Thr	Ala	Gly	Ile					
			120				125						130							
gga	ccg	tgg	ctc	ccc	tac	caa	atg	ctc	gca	gcc	gcc	tgg	gtc	agc	ttc		547			
Gly	Pro	Trp	Leu	Pro	Tyr	Gln	Met	Leu	Ala	Ala	Ala	Trp	Val	Ser	Phe					
			135				140						145							
ggc	gcc	ggc	cta	ctc	ccc	caa	gta	cgc	ggc	aaa	aag	gaa	atg	ctc	atc		595			
Gly	Ala	Gly	Leu	Leu	Pro	Gln	Val	Arg	Gly	Lys	Lys	Glu	Met	Leu	Ile					
			150				155			160			165							
atc	gtc	cta	tac	gcc	atc	gtc	tct	tca	ctc	ggc	tac	gga	acc	atg	atg		643			
Ile	Val	Leu	Tyr	Ala	Ile	Val	Ser	Ser	Leu	Gly	Tyr	Gly	Thr	Met	Met					
				170							175			180						
aac	atg	agc	ttc	tgg	ccc	tac	gcc	atc	ggg	gtc	acc	agc	ggg	ctt	tcc		691			
Asn	Met	Ser	Phe	Trp	Pro	Tyr	Ala	Ile	Gly	Val	Thr	Ser	Gly	Leu	Ser					
			185				190						195							
ttc	aca	ccc	ggc	gcg	ccc	gtc	ctg	gaa	aac	ctc	cac	acc	ttc	atg	ctg		739			
Phe	Thr	Pro	Gly	Ala	Pro	Val	Leu	Glu	Asn	Leu	His	Thr	Phe	Met	Leu					
			200				205						210							
ttc	tgc	ctc	acc	aca	tcc	atg	ggg	tgg	gat	ctc	ggc	cgc	gcc	ttc	ttc		787			
Phe	Cys	Leu	Thr	Thr	Ser	Met	Gly	Trp	Asp	Leu	Gly	Arg	Ala	Phe	Phe					
			215				220						225							
acc	tca	gtg	cta	tta	ctg	ctc	aca	gcc	aaa	ccc	gtt	tta	ggg	gct	tta		835			
Thr	Ser	Val	Leu	Leu	Leu	Leu	Thr	Ala	Lys	Pro	Val	Leu	Gly	Ala	Leu					
			230				235			240			245							
cga	cgc	gcc	agc	cgc	cgc	gcc														

&lt;210&gt; 696

&lt;211&gt; 268

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 696

Met Ile Asn Ala Ile Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser  
 1 5 10 15

Phe Leu Ala Val Leu Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val  
 20 25 30

Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile  
 35 40 45

Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser  
 50 55 60

Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr  
 65 70 75 80

Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe  
 85 90 95

Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro  
 100 105 110

Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu  
 115 120 125

Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala  
 130 135 140

Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys  
 145 150 155 160

Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly  
 165 170 175

Tyr Gly Thr Met Met Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val  
 180 185 190

Thr Ser Gly Leu Ser Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu  
 195 200 205

His Thr Phe Met Leu Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu  
 210 215 220

Gly Arg Ala Phe Phe Thr Ser Val Leu Leu Leu Leu Thr Ala Lys Pro  
 225 230 235 240

Val Leu Gly Ala Leu Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val  
 245 250 255

Glu Arg Asp Phe Gly Glu Ala Gly Val Pro Arg Val  
 260 265

&lt;210&gt; 697



&lt;211&gt; 1587

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1564)

&lt;223&gt; RXN00483

&lt;400&gt; 697

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agaccaaga gtaaaatccc aggatttgct tataacttgcg ctcatggata atcaacttcg 60

tcccactttg cattatcaag ctcaaaaccc gcaccggcga gtg ctg gtc acc ggt 115
                               Val Leu Val Thr Gly
                               1 5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163
Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
              10              15              20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211
Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg
              25              30              35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259
Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp
              40              45              50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307
Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr
              55              60              65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355
Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu
              70              75              80              85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403
Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile
              90              95              100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451
Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile
              105              110              115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499
Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile
              120              125              130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att 547
Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile
              135              140              145

att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag 595
Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu
              150              155              160              165

cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag 643
Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu
              170              175              180

cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat 691

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Pro	Leu	Ala	Ile	Arg	Asp	Val	Leu	His	Tyr	Leu	Ile	Ser	Ala	Ala	Asp		
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tta	aag	gat	cca	gtc	aac	cgc	tcc	tgc	gat	att	ggg	tgt	gga	aag	tcg	739	
Leu	Lys	Asp	Pro	Val	Asn	Arg	Ser	Cys	Asp	Ile	Gly	Cys	Gly	Lys	Ser		
		200					205					210					
tat	gaa	ttt	gcg	gat	cta	ttg	cgt	atc	tat	gcc	gat	gtt	cgg	gga	ctg	787	
Tyr	Glu	Phe	Ala	Asp	Leu	Leu	Arg	Ile	Tyr	Ala	Asp	Val	Arg	Gly	Leu		
	215					220					225						
aaa	cgt	cat	gta	aat	tcc	gta	cct	ctc	aat	ttg	ccc	atg	gac	aag	cta	835	
Lys	Arg	His	Val	Asn	Ser	Val	Pro	Leu	Asn	Leu	Pro	Met	Asp	Lys	Leu		
230					235					240					245		
tcc	ggt	ctt	tgg	att	agt	cta	gtg	aca	cct	gtt	cca	ttt	caa	ttg	tct	883	
Ser	Gly	Leu	Trp	Ile	Ser	Leu	Val	Thr	Pro	Val	Pro	Phe	Gln	Leu	Ser		
				250					255					260			
ttc	cct	tta	gct	caa	tca	atg	gct	gag	gat	gcc	gtc	act	gaa	gag	cac	931	
Phe	Pro	Leu	Ala	Gln	Ser	Met	Ala	Glu	Asp	Ala	Val	Thr	Glu	Glu	His		
			265					270					275				
agc	att	aaa	gat	att	att	tca	gat	cca	ccc	gat	ggt	ttt	att	gag	tat	979	
Ser	Ile	Lys	Asp	Ile	Ile	Ser	Asp	Pro	Pro	Asp	Gly	Phe	Ile	Glu	Tyr		
		280					285					290					
cgg	gaa	gca	gtg	gag	ctg	gca	tta	gct	gca	gaa	ttt	gat	cgt	gga	gtt	1027	
Arg	Glu	Ala	Val	Glu	Leu	Ala	Leu	Ala	Ala	Glu	Phe	Asp	Arg	Gly	Val		
	295					300					305						
cca	acg	tca	tgg	gat	cga	agc	tgg	act	gta	caa	caa	ccg	tgg	gct	ggc	1075	
Pro	Thr	Ser	Trp	Asp	Arg	Ser	Trp	Thr	Val	Gln	Gln	Pro	Trp	Ala	Gly		
310					315					320					325		
cag	cct	acc	gat	cca	gag	tgg	gcg	ggc	aaa	gct	gta	tat	gaa	gac	gtc	1123	
Gln	Pro	Thr	Asp	Pro	Glu	Trp	Ala	Gly	Lys	Ala	Val	Tyr	Glu	Asp	Val		
				330					335					340			
cgc	aca	gaa	gat	act	gat	ctc	cga	gca	gcg	cag	gtc	tgg	ccg	atc	att	1171	
Arg	Thr	Glu	Asp	Thr	Asp	Leu	Arg	Ala	Ala	Gln	Val	Trp	Pro	Ile	Ile		
			345					350					355				
gaa	ggt	ttg	ggt	ggc	gtg	aac	ggc	tgg	tat	tct	gca	cca	ctg	cta	tgg	1219	
Glu	Gly	Leu	Gly	Gly	Val	Asn	Gly	Trp	Tyr	Ser	Ala	Pro	Leu	Leu	Trp		
		360					365					370					
cga	ttg	cgg	ggt	atc	gct	gac	aga	ctc	atc	ggc	ggt	cca	ggt	ttg	ggc	1267	
Arg	Leu	Arg	Gly	Ile	Ala	Asp	Arg	Leu	Ile	Gly	Gly	Pro	Gly	Leu	Gly		
	375					380					385						
gga	cgg	cgg	gat	ccc	cgt	cat	ttg	aaa	ctt	ggg	gat	cgc	att	gat	tgg	1315	
Gly	Arg	Arg	Asp	Pro	Arg	His	Leu	Lys	Leu	Gly	Asp	Arg	Ile	Asp	Trp		
390					395					400					405		
tgg	cgg	gtt	act	gag	atc	gat	cca	cca	cat	aga	tta	gtg	ctc	acc	gca	1363	
Trp	Arg	Val	Thr	Glu	Ile	Asp	Pro	Pro	His	Arg	Leu	Val	Leu	Thr	Ala		
				410					415					420			
gag	atg	aaa	gta	gat	ggt	ggc	gct	tgg	ctg	atc	ctg	gaa	gtt	gcg	gac	1411	
Glu	Met	Lys	Val	Asp	Gly	Gly	Ala	Trp	Leu	Ile	Leu	Glu	Val	Ala	Asp		

425										430					435					
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Lys	Glu	Asn	Gly	Gly	Cys	Thr	Tyr	Thr	Gln	Arg	Ala	Ile	Phe	Glu	Pro					
440						445					450									
aag	ggt	ttg	ccc	ggt	tat	ctc	tat	tgg	tgg	gtt	gtt	tca	ccg	ttc	cat	1507				
Lys	Gly	Leu	Pro	Gly	Tyr	Leu	Tyr	Trp	Trp	Val	Val	Ser	Pro	Phe	His					
455						460					465									
gcg	att	att	ttt	cct	tat	atg	cgt	tcg	aat	att	tta	aaa	gct	gcg	cgt	1555				
Ala	Ile	Ile	Phe	Pro	Tyr	Met	Arg	Ser	Asn	Ile	Leu	Lys	Ala	Ala	Arg					
470						475					480				485					
aaa ctc act taatcgcaga gtaggcgtct aaa																1587				
Lys Leu Thr																				

&lt;210&gt; 698

&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 698

Val	Leu	Val	Thr	Gly	Ala	Thr	Gly	Tyr	Ile	Gly	Gly	Arg	Leu	Ile	Thr
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Glu	Leu	Leu	Ala	Ala	Gly	Phe	Gln	Val	Arg	Ala	Thr	Ser	Arg	Lys	Lys
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Thr	Ser	Leu	Gln	Arg	Phe	Asp	Trp	Tyr	Glu	Asp	Val	Glu	Ala	Val	Glu
		35					40					45			

Ala	Asp	Leu	Thr	Asp	Ala	Thr	Glu	Leu	Asp	Thr	Leu	Phe	Lys	Asp	Val
	50					55					60				

Asp	Val	Val	Tyr	Tyr	Leu	Val	His	Ser	Met	Gly	Gly	Lys	Asn	Val	Asp
65					70					75					80

Phe	Glu	Glu	Gln	Glu	Gln	Arg	Thr	Ala	Glu	Asn	Val	Ile	Gln	Ala	Ala
			85						90					95	

Asp	Gln	Ala	Gly	Ile	Lys	Gln	Ile	Val	Tyr	Leu	Ser	Gly	Leu	His	Pro
		100						105					110		

Arg	Asn	Arg	Lys	Ile	Glu	Glu	Leu	Ser	Lys	His	Met	Arg	Ser	Arg	Glu
		115					120					125			

Lys	Val	Ala	Gln	Ile	Leu	Leu	Ala	Gly	Gln	Thr	Pro	Ala	Leu	Ile	Leu
	130					135					140				

Arg	Ala	Ala	Thr	Ile	Ile	Gly	Ser	Gly	Ser	Ala	Ser	Phe	Glu	Ile	Ile
145				150						155				160	

Arg	His	Leu	Thr	Glu	Arg	Leu	Pro	Arg	Met	Ile	Ala	Pro	Gln	Trp	Ile
			165						170					175	

Thr	Asn	Gln	Ile	Glu	Pro	Leu	Ala	Ile	Arg	Asp	Val	Leu	His	Tyr	Leu
		180						185					190		

Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile  
 195 200 205  
 Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala  
 210 215 220  
 Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu  
 225 230 235 240  
 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val  
 245 250 255  
 Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala  
 260 265 270  
 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp  
 275 280 285  
 Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu  
 290 295 300  
 Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln  
 305 310 315 320  
 Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala  
 325 330 335  
 Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln  
 340 345 350  
 Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser  
 355 360 365  
 Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly  
 370 375 380  
 Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly  
 385 390 395 400  
 Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg  
 405 410 415  
 Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile  
 420 425 430  
 Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg  
 435 440 445  
 Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val  
 450 455 460  
 Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile  
 465 470 475 480  
 Leu Lys Ala Ala Arg Lys Leu Thr  
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&lt;210&gt; 699

&lt;211&gt; 1587

&lt;212&gt; DNA

cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat 691  
Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp  
185 190 195

tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg	739
Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser	
200 205 210	
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg	787
Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu	
215 220 225	
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta	835
Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu	
230 235 240 245	
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct	883
Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser	
250 255 260	
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac	931
Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His	
265 270 275	
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat	979
Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr	
280 285 290	
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt	1027
Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val	
295 300 305	
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc	1075
Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly	
310 315 320 325	
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc	1123
Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val	
330 335 340	
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att	1171
Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile	
345 350 355	
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg	1219
Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp	
360 365 370	
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc	1267
Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly	
375 380 385	
gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg	1315
Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp	
390 395 400 405	
tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca	1363
Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala	
410 415 420	
gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac	1411
Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp	
425 430 435	

aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459  
Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro  
440 445 450  
  
aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507  
Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His  
455 460 465  
  
gcg att att ttt cct tat atg cgt tgc aat att tta aaa gct gcg cgt 1555  
Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg  
470 475 480 485  
  
aaa ctc act taatcgcaga gtaggcgtct aaa 1587  
Lys Leu Thr

<210> 700  
<211> 488  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 700  
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Glu Leu Leu Ala Ala Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys  
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Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu  
35 40 45  
  
Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val  
50 55 60  
  
Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp  
65 70 75 80  
  
Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala  
85 90 95  
  
Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro  
100 105 110  
  
Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu  
115 120 125  
  
Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu  
130 135 140  
  
Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile  
145 150 155 160  
  
Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile  
165 170 175  
  
Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu  
180 185 190  
  
Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile  
195 200 205

Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala  
 210 215 220  
 Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu  
 225 230 235 240  
 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val  
 245 250 255  
 Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala  
 260 265 270  
 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp  
 275 280 285  
 Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu  
 290 295 300  
 Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln  
 305 310 315 320  
 Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala  
 325 330 335  
 Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln  
 340 345 350  
 Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser  
 355 360 365  
 Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly  
 370 375 380  
 Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly  
 385 390 395 400  
 Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg  
 405 410 415  
 Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile  
 420 425 430  
 Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg  
 435 440 445  
 Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val  
 450 455 460  
 Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile  
 465 470 475 480  
 Leu Lys Ala Ala Arg Lys Leu Thr  
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&lt;210&gt; 701

&lt;211&gt; 612

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(589)

&lt;223&gt; RXA01534

&lt;400&gt; 701

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                                         Met Thr Ser Ala Ile
                                         1 5

acc acc gca act gat ctt cgc tcc gta ctg cga aac gta cca acc cca 163
Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg Asn Val Pro Thr Pro
                        10                        15                        20

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Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro Leu Gly Met Ile Val
                        25                        30                        35

ggg tca ttc gtc agc att agc gcc gaa cca cca ttg gta ggc atc ttc 259
Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro Leu Val Gly Ile Phe
                        40                        45                        50

ttg cag aag agc tct tct tca tgg cca gct atc gag cag gca tta gtt 307
Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile Glu Gln Ala Leu Val
                        55                        60                        65

acc ggc caa gag cta ggc att tct atc ctc ggc ggg gca cac gca gac 355
Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly Gly Ala His Ala Asp
70                        75                        80                        85

cat gtg cgt aag ctt tct ggc cca tcc gac cag cgc ttt gaa aac ctt 403
His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln Arg Phe Glu Asn Leu
                        90                        95                        100

ggg tgg gca tcc acc gaa aac ggt gcg att cac ctt gaa ggc gct gat 451
Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His Leu Glu Gly Ala Asp
                        105                        110                        115

gca caa cta acc acg aaa ctt cat gat ctc cag gaa atc ggc gat cac 499
Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln Glu Ile Gly Asp His
120                        125                        130

ttc ttt gca gtt cta gaa gtt att gac gct tcc gct gac caa gac ttc 547
Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser Ala Asp Gln Asp Phe
135                        140                        145

agc tca gcg ctg gtg tac cac cgc tca cag gtg tcc tcg ctg 589
Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val Ser Ser Leu
150                        155                        160

taggacacta aattttaaga ggg 612

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&lt;210&gt; 702

&lt;211&gt; 163

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 702

Met Thr Ser Ala Ile Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg  
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 Asn Val Pro Thr Pro Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro  
 20 25 30  
 Leu Gly Met Ile Val Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro  
 35 40 45  
 Leu Val Gly Ile Phe Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile  
 50 55 60  
 Glu Gln Ala Leu Val Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly  
 65 70 75 80  
 Gly Ala His Ala Asp His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln  
 85 90 95  
 Arg Phe Glu Asn Leu Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His  
 100 105 110  
 Leu Glu Gly Ala Asp Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln  
 115 120 125  
 Glu Ile Gly Asp His Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser  
 130 135 140  
 Ala Asp Gln Asp Phe Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val  
 145 150 155 160  
 Ser Ser Leu

<210> 703  
 <211> 1134  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1111)  
 <223> RXA00288

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 Met Ser Ala Gln Met  
 1 5  
 gat acc cct gat ccc act atg tct gct gtt gca atg tta gat tcc atc 163  
 Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala Met Leu Asp Ser Ile  
 10 15 20  
 cct tct gat caa cca gat ttc ctg atc gat gta gaa gta gat cga cca 211  
 Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val Glu Val Asp Arg Pro  
 25 30 35  
 act ccc gga cca cat gat ctg cta gtc cac att gag gcg gtc tca att 259  
 Thr Pro Gly Pro His Asp Leu Leu Val His Ile Glu Ala Val Ser Ile

40	45	50	
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cct aaa att tta ggt ttt gat gct gca ggt gag gtg gtg gct gtt gga Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu Val Val Ala Val Gly 70 75 80 85			355
tcg cag gtc acg ctc ttc aat gtt ggt gac aaa gtg ttc tac gca gga Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys Val Phe Tyr Ala Gly 90 95 100			403
tcc aat cag cgt cca gga agt aac gca gag tac cag gtg gtg gat gaa Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr Gln Val Val Asp Glu 105 110 115			451
cgg ctg gtg ggt cac gca cca caa agc ttg ggg gca cac gac gcc gct Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly Ala His Asp Ala Ala 120 125 130			499
gct ctc cca ctt gtc gcg ctc act gca tgg gag tca ctt ttt gac cga Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu Ser Leu Phe Asp Arg 135 140 145			547
ttg gga gta act cag tca act act gga aca ctg ttg gtc ttg ggc ggt Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu Leu Val Leu Gly Gly 150 155 160 165			595
tca gga ggt gtg cct tca gct ctt att caa ctt gct cga gct ctc act Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu Ala Arg Ala Leu Thr 170 175 180			643
ggg ctg aaa gta gtg gca aca gct tct cgc cct gaa tca caa gaa tgg Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro Glu Ser Gln Glu Trp 185 190 195			691
gtg aca aag ctc ggt gct cat gag gtg att gat cac tcc aag gat ttg Val Thr Lys Leu Gly Ala His Glu Val Ile Asp His Ser Lys Asp Leu 200 205 210			739
agt gag caa atc tcc gac gtg gat ttt gtt ttc agc tcg tgg act act Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe Ser Ser Trp Thr Thr 215 220 225			787
ggg cgt gaa gta gag ctc gcc acg ttg atg aaa ccc cag tcc cac cta Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys Pro Gln Ser His Leu 230 235 240 245			835
gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln 250 255 260			883
aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe 265 270 275			931
aac act cct gat atg ggt gaa caa ggg aaa att ctg aat aag atc gcc Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala 280 285 290			979

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			20					25					30			
Glu	Val	Asp	Arg	Pro	Thr	Pro	Gly	Pro	His	Asp	Leu	Leu	Val	His	Ile	
		35					40					45				
Glu	Ala	Val	Ser	Ile	Asn	Pro	Val	Asp	Thr	Lys	Val	Arg	Met	Arg	Ala	
	50					55					60					
Gly	Lys	Gln	Lys	His	Pro	Lys	Ile	Leu	Gly	Phe	Asp	Ala	Ala	Gly	Glu	
65					70					75					80	
Val	Val	Ala	Val	Gly	Ser	Gln	Val	Thr	Leu	Phe	Asn	Val	Gly	Asp	Lys	
				85					90					95		
Val	Phe	Tyr	Ala	Gly	Ser	Asn	Gln	Arg	Pro	Gly	Ser	Asn	Ala	Glu	Tyr	
			100					105					110			
Gln	Val	Val	Asp	Glu	Arg	Leu	Val	Gly	His	Ala	Pro	Gln	Ser	Leu	Gly	
		115					120					125				
Ala	His	Asp	Ala	Ala	Ala	Leu	Pro	Leu	Val	Ala	Leu	Thr	Ala	Trp	Glu	
	130					135					140					
Ser	Leu	Phe	Asp	Arg	Leu	Gly	Val	Thr	Gln	Ser	Thr	Thr	Gly	Thr	Leu	
145				150						155					160	
Leu	Val	Leu	Gly	Gly	Ser	Gly	Gly	Val	Pro	Ser	Ala	Leu	Ile	Gln	Leu	
				165					170					175		
Ala	Arg	Ala	Leu	Thr	Gly	Leu	Lys	Val	Val	Ala	Thr	Ala	Ser	Arg	Pro	
			180					185					190			
Glu	Ser	Gln	Glu	Trp	Val	Thr	Lys	Leu	Gly	Ala	His	Glu	Val	Ile	Asp	
		195					200					205				

His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe  
 210 215 220  
 Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys  
 225 230 235 240  
 Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu  
 245 250 255  
 Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe  
 260 265 270  
 Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile  
 275 280 285  
 Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val  
 290 295 300  
 Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly  
 305 310 315 320  
 His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg  
 325 330 335  
 Val

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 <212> DNA  
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 <223> RXA02741

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 Met Lys Ala Ile Leu  
 1 5  
 gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac 163  
 Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp  
 10 15 20  
 gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct 211  
 Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala  
 25 30 35  
 ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct 259  
 Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln Gly Glu Tyr His Ala  
 40 45 50  
 cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag 307  
 Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu  
 55 60 65

gat ccg cag ggg ttg att gcg gcg ggt acc aag gtg gcg tgg tgt gat	355
Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys Val Ala Trp Cys Asp	
70 75 80 85	
gcc atg ggt tcg tat gct cag cag gtg tgt gtg ccg cgg gat cgc ttg	403
Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val Pro Arg Asp Arg Leu	
90 95 100	
gtg gcg gtt ccc gag ggc gtg agt tcg gaa gtg gct gcg tcg atg ttg	451
Val Ala Val Pro Glu Gly Val Ser Ser Glu Val Ala Ala Ser Met Leu	
105 110 115	
atg cag gga atc act gcg cat tat cta acc aat ggt gtg tat gag ctt	499
Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn Gly Val Tyr Glu Leu	
120 125 130	
gaa gag ggc gat tct tgc ctc atc act gct ggc gcg ggt ggt gtt gga	547
Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly Ala Gly Gly Val Gly	
135 140 145	
ttg ttg gct acg cag atg gcg gcg gcc aag gga gtg cgc gtg tac agc	595
Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly Val Arg Val Tyr Ser	
150 155 160 165	
gtg gtg tcc acg gat gaa aaa gct gag ctt gct ttg gat gcc ggt gct	643
Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala Leu Asp Ala Gly Ala	
170 175 180	
tat gag gtg ttt cgt tat tcc gat aat ttg gcg gag cag gtt cgt cgg	691
Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala Glu Gln Val Arg Arg	
185 190 195	
cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag	739
His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln	
200 205 210	
tcc acg ttc aat gag tcc tta gag gct gtt cgt ccg cgc ggc act gtg	787
Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val	
215 220 225	
tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag	835
Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln	
230 235 240 245	
ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc	883
Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly	
250 255 260	
gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc	931
Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val	
265 270 275	
acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca	979
Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr	
280 285 290	
tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt	1027
Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg	
295 300 305	
agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca	1076

Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp  
 310 315 320

taaaaagatc ctg

1089

<210> 706

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

Met Lys Ala Ile Leu Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu  
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Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val  
 20 25 30

Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln  
 35 40 45

Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr  
 50 55 60

Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys  
 65 70 75 80

Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val  
 85 90 95

Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val  
 100 105 110

Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn  
 115 120 125

Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly  
 130 135 140

Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly  
 145 150 155 160

Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala  
 165 170 175

Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala  
 180 185 190

Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr  
 195 200 205

Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg  
 210 215 220

Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu  
 225 230 235 240

Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr  
 245 250 255

Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys

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							Met	Gln	Gly	Asn	Ser					
							1				5					
ctt	aat	ctg	gca	gac	aac	agc	gag	aga	aag	aag	ccc	atg	ccg	tca	cca	163
Leu	Asn	Leu	Ala	Asp	Asn	Ser	Glu	Arg	Lys	Lys	Pro	Met	Pro	Ser	Pro	
				10					15					20		
gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca						211										
Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro	
				25					30					35		
ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt	259
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val	
				40					45					50		
cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att	307
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile	
				55					60					65		
att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att	355
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile	
70					75					80					85	
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg	403
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly	
				90					95					100		
atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg	451
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu	
				105					110					115		
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa	499



Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu  
 120 125 130  
 gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547  
 Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly  
 135 140 145  
 ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595  
 Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu  
 150 155 160 165  
 tca ctt gga ttg gga acg ctc tat ttg ggt tgc gtg cgc aac gat gcg 643  
 Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala  
 170 175 180  
 gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691  
 Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val  
 185 190 195  
 gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739  
 Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile  
 200 205 210  
 aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787  
 Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr  
 215 220 225  
 gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835  
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr  
 230 235 240 245  
 tac tat tct cgc tac ggc cag cac cag ctc tgg tgc aag cag acg gcg 883  
 Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala  
 250 255 260  
 cat agg gcg gcg tgc aaa agc ttt tca aaa acc aac agg cag ttc ctt 931  
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu  
 265 270 275  
 agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977  
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg  
 280 285  
 attatggacg cct 990

&lt;210&gt; 708

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 708

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys  
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Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro  
 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His  
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp  
 50 55 60  
 Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser  
 65 70 75 80  
 Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg  
 85 90 95  
 Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln  
 100 105 110  
 Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala  
 115 120 125  
 Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp  
 130 135 140  
 Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala  
 145 150 155 160  
 Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser  
 165 170 175  
 Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro  
 180 185 190  
 Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro  
 195 200 205  
 Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His  
 210 215 220  
 Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp  
 225 230 235 240  
 Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp  
 245 250 255  
 Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr  
 260 265 270  
 Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu  
 275 280 285

Arg

<210> 709  
 <211> 922  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(922)  
 <223> FRXA02560

<400> 709  
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Met Gln Gly Asn Ser	
1 5	
ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca	163
Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro	
10 15 20	
gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca	211
Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro	
25 30 35	
ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt	259
Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val	
40 45 50	
cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att	307
Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile	
55 60 65	
att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att	355
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile	
70 75 80 85	
tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg	403
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly	
90 95 100	
atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg	451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu	
105 110 115	
att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa	499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu	
120 125 130	
gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg	547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly	
135 140 145	
ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag	595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu	
150 155 160 165	
tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg	643
Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala	
170 175 180	
gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc	691
Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val	
185 190 195	
gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att	739
Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile	
200 205 210	
aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc	787
Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr	
215 220 225	

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835  
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr  
 230 235 240 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883  
 Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala  
 250 255 260

cat agg gcg gcg tct aaa cgc tgt tac aag aac caa gaa 922  
 His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn Gln Glu  
 265 270

<210> 710

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 710

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys  
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Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro  
 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His  
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp  
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser  
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg  
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln  
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala  
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp  
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala  
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser  
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro  
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro  
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His  
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp  
225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp  
245 250 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn  
260 265 270

Gln Glu

<210> 711

<211> 870

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(847)

<223> RXA01311

<400> 711

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Met Lys Leu Thr Leu  
1 5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163  
Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr  
10 15 20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211  
Val Gln Val Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu  
25 30 35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259  
Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala  
40 45 50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307  
Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu  
55 60 65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355  
Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala  
70 75 80 85

cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca 403  
Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro  
90 95 100

ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc 451  
Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg  
105 110 115

tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac 499  
Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn  
120 125 130

gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc 547  
 Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr  
 135 140 145  
 gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt 595  
 Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys  
 150 155 160 165  
 gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag 643  
 Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys  
 170 175 180  
 ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg 691  
 Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu  
 185 190 195  
 cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc 739  
 Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys  
 200 205 210  
 tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg 787  
 Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu  
 215 220 225  
 acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga 835  
 Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg  
 230 235 240 245  
 ggc aaa gac gac tagtctttaa tcçaagtaag tac 870  
 Gly Lys Asp Asp

&lt;210&gt; 712

&lt;211&gt; 249

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 712

Met Lys Leu Thr Leu Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu  
 1 5 10 15  
 Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser  
 20 25 30  
 Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly  
 35 40 45  
 Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly  
 50 55 60  
 Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn  
 65 70 75 80  
 Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr  
 85 90 95  
 Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp  
 100 105 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly  
 115 120 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His  
 130 135 140

Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile  
 145 150 155 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu  
 165 170 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys  
 180 185 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr  
 195 200 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro  
 210 215 220

Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala  
 225 230 235 240

Arg Ala Ala Phe Arg Gly Lys Asp Asp  
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<210> 713  
 <211> 929  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(906)  
 <223> RXN03014

<400> 713  
 tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc 48  
 Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr  
 1 5 10 15

ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg 96  
 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met  
 20 25 30

gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt 144  
 Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val  
 35 40 45

tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg 192  
 Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met  
 50 55 60

gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc 240  
 Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu  
 65 70 75 80

gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg 288  
 Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu

85										90					95					
ccg	gac	tcc	tac	ccc	acc	gcg	cca	tcg	ctg	gtc	acc	gcg	gtg	ttc	gca	336				
Pro	Asp	Ser	Tyr	Pro	Thr	Ala	Pro	Ser	Leu	Val	Thr	Ala	Val	Phe	Ala					
			100					105					110							
ggt	ctg	ttg	acc	aag	gtg	ggt	gtg	tat	tcc	atc	att	cga	gca	cgc	tcg	384				
Gly	Leu	Leu	Thr	Lys	Val	Gly	Val	Tyr	Ser	Ile	Ile	Arg	Ala	Arg	Ser					
		115					120					125								
att	att	ttc	acc	gat	gga	tcc	ctt	gac	acc	atg	ctg	atg	tgg	gtg	gca	432				
Ile	Ile	Phe	Thr	Asp	Gly	Ser	Leu	Asp	Thr	Met	Leu	Met	Trp	Val	Ala					
		130				135					140									
ctc	gcc	acc	atg	ctc	att	ggt	att	ttg	ggc	gcg	atg	gcg	caa	aac	gat	480				
Leu	Ala	Thr	Met	Leu	Ile	Gly	Ile	Leu	Gly	Ala	Met	Ala	Gln	Asn	Asp					
145					150				155						160					
atc	aaa	cgt	ttg	ttg	tca	ttt	act	ctg	gtc	agc	cac	atc	ggc	tac	atg	528				
Ile	Lys	Arg	Leu	Leu	Ser	Phe	Thr	Leu	Val	Ser	His	Ile	Gly	Tyr	Met					
			165					170						175						
atc	ttc	ggc	gta	gcc	ctt	gga	tct	gca	cag	ggt	ttg	tct	ggt	gcg	atc	576				
Ile	Phe	Gly	Val	Ala	Leu	Gly	Ser	Ala	Gln	Gly	Leu	Ser	Gly	Ala	Ile					
			180					185					190							
ttc	tac	gca	atc	cac	cac	att	ctg	gtt	cag	act	tcc	ctg	ttc	ctg	gtg	624				
Phe	Tyr	Ala	Ile	His	His	Ile	Leu	Val	Gln	Thr	Ser	Leu	Phe	Leu	Val					
		195					200					205								
gtc	ggt	ctg	gtg	gaa	cgc	caa	gcc	gga	tcc	tcc	tcg	ctg	cga	cgc	ctt	672				
Val	Gly	Leu	Val	Glu	Arg	Gln	Ala	Gly	Ser	Ser	Ser	Leu	Arg	Arg	Leu					
	210					215					220									
gga	tcc	ctg	gca	tat	atc	tcc	cca	ctt	ctt	gcg	att	ttg	tac	ttc	atc	720				
Gly	Ser	Leu	Ala	Tyr	Ile	Ser	Pro	Leu	Leu	Ala	Ile	Leu	Tyr	Phe	Ile					
225					230					235					240					
ccc	gcc	atc	aac	ctg	ggt	ggt	atc	cca	ccg	ttc	tcc	ggc	ttc	ctg	ggc	768				
Pro	Ala	Ile	Asn	Leu	Gly	Gly	Ile	Pro	Pro	Phe	Ser	Gly	Phe	Leu	Gly					
			245					250					255							
aag	atc	atg	ctc	atc	gaa	gcc	ggc	gcc	cga	aga	tgg	cag	ttg	gct	ggc	816				
Lys	Ile	Met	Leu	Ile	Glu	Ala	Gly	Ala	Arg	Arg	Trp	Gln	Leu	Ala	Gly					
		260					265					270								
atg	ggt	cct	tat	cgc	agg	cgc	cgt	tgt	cac	ctc	act	gct	cac	ctt	gta	864				
Met	Gly	Pro	Tyr	Arg	Arg	Arg	Arg	Cys	His	Leu	Thr	Ala	His	Leu	Val					
		275					280					285								
cac	cat	ggt	tct	ggt	ctg	gtc	caa	ggc	ctt	ctg	gcg	cga	ccg			906				
His	His	Gly	Ser	Gly	Leu	Val	Gln	Gly	Leu	Leu	Ala	Arg	Pro							
	290					295					300									
taaagacgcc	cccgatggag	caa														929				

&lt;210&gt; 714

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum



&lt;400&gt; 714

Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr  
 1 5 10 15  
 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met  
 20 25 30  
 Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val  
 35 40 45  
 Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met  
 50 55 60  
 Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu  
 65 70 75 80  
 Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu  
 85 90 95  
 Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala  
 100 105 110  
 Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser  
 115 120 125  
 Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala  
 130 135 140  
 Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp  
 145 150 155 160  
 Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met  
 165 170 175  
 Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile  
 180 185 190  
 Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val  
 195 200 205  
 Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu  
 210 215 220  
 Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile  
 225 230 235 240  
 Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly  
 245 250 255  
 Lys Ile Met Leu Ile Glu Ala Gly Ala Arg Arg Trp Gln Leu Ala Gly  
 260 265 270  
 Met Gly Pro Tyr Arg Arg Arg Arg Cys His Leu Thr Ala His Leu Val  
 275 280 285  
 His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro  
 290 295 300

&lt;210&gt; 715

&lt;211&gt; 1280

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1257)

&lt;223&gt; FRXA00910

&lt;400&gt; 715

tac gtt ggt ttc gaa gtg ctg ctg gtg gcg tca tac gtg ctg ctc acc	48
Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr	
1 5 10 15	
ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg	96
Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met	
20 25 30	
gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt	144
Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val	
35 40 45	
tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg	192
Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met	
50 55 60	
gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc	240
Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu	
65 70 75 80	
gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg	288
Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu	
85 90 95	
ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca	336
Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala	
100 105 110	
ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg	384
Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser	
115 120 125	
att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca	432
Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala	
130 135 140	
ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat	480
Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp	
145 150 155 160	
atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg	528
Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met	
165 170 175	
atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc	576
Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile	
180 185 190	
ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg	624
Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val	
195 200 205	

gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt	672
Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu	
210 215 220	
gga tcc ctg gca tat atc tcc cca ctt ctt gcg att ttg tac ttc atc	720
Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile	
225 230 235 240	
ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc	768
Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly	
245 250 255	
aag atc atg ctc atc gaa gcc ggc gcc gaa gat ggc agt tgg ctg gca	816
Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala	
260 265 270	
tgg gtc ctt atc gca ggc gcc gtt gtc acc tca ctg ctc acc ttg tac	864
Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr	
275 280 285	
acc atg gtt ctg gtc tgg tcc aag gcc ttc tgg cgc gac cgt aaa gac	912
Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp	
290 295 300	
gcc ccc gat gga gca acc gca ctt gcg cga ccc gca cct ttg gta gat	960
Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp	
305 310 315 320	
gtc caa gac gaa gtc gcc gtt aaa gac cgc aac gat gtc gga cgg atg	1008
Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met	
325 330 335	
cct tgg ggc atg gtc ttc tcc act gct ctc ctg gtt tca gca tct ctt	1056
Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu	
340 345 350	
gct gta tcc gtg ctc gca gga cca ctg tca tct att act gga cgc gcc	1104
Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala	
355 360 365	
gcc gaa tcc gca caa gat gtc aac atc tac cgc gcc gca gta ctc ggc	1152
Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly	
370 375 380	
ccc aac tac ctc gac cca tca cgc aca ctc gag atg gag cgt tac gac	1200
Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp	
385 390 395 400	
gcc aac cgc gat gac atc aac cac cgc gtc gac acc aac gga acg gag	1248
Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu	
405 410 415	
gac caa cca tgatcagtggt attcaaacga cga	1280
Asp Gln Pro	

&lt;210&gt; 716

&lt;211&gt; 419

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 716

Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr  
 1 5 10 15

Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met  
 20 25 30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val  
 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met  
 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu  
 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu  
 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala  
 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser  
 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala  
 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp  
 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met  
 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile  
 180 185 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val  
 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu  
 210 215 220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile  
 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly  
 245 250 255

Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala  
 260 265 270

Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr  
 275 280 285

Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp  
 290 295 300

Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp

<400> 717																		
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caca	agcttt	aagat	ccacg	atcag	gagac	tttg	acaaat	atg	tca	ggt	aac	cca	115					
								Met	Ser	Val	Asn	Pro	5					
								1										
acc	cgc	ccc	gaa	ggc	ggc	cgt	cac	cac	gtc	gtc	gtc	atc	ggg	tct	ggg	163		
Thr	Arg	Pro	Glu	Gly	Gly	Arg	His	His	Val	Val	Val	Ile	Gly	Ser	Gly			
				10					15					20				
ttt	ggg	ggc	ctt	ttt	gct	gcc	aag	aac	ctg	gcc	aag	gca	gac	gtc	gat	211		
Phe	Gly	Gly	Leu	Phe	Ala	Ala	Lys	Asn	Leu	Ala	Lys	Ala	Asp	Val	Asp			
			25				30				35							
gtc	act	ctg	att	gac	cgc	acc	aac	cac	cac	ctc	ttc	cag	cca	ctg	ctg	259		
Val	Thr	Leu	Ile	Asp	Arg	Thr	Asn	His	His	Leu	Phe	Gln	Pro	Leu	Leu			
			40				45				50							
tac	caa	gtg	gca	acc	ggg	atc	ctc	tcc	tcc	ggg	gaa	atc	gca	cct	tcc	307		
Tyr	Gln	Val	Ala	Thr	Gly	Ile	Leu	Ser	Ser	Gly	Glu	Ile	Ala	Pro	Ser			
		55			60			65										
act	cga	cag	atc	ctg	ggc	tcc	cag	gaa	aac	gtc	aac	gtc	atc	aag	ggc	355		
Thr	Arg	Gln	Ile	Leu	Gly	Ser	Gln	Glu	Asn	Val	Asn	Val	Ile	Lys	Gly			
70					75					80					85			

gaa gtc acc gac atc aac gtc gag tcc cag act gtg acc gcc tcc ctg	403
Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr Val Thr Ala Ser Leu	
90 95 100	
ggc gag ttc acc cgc gtt ttt gag tac gat tcc ttg gtc gtt ggt gct	451
Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser Leu Val Val Gly Ala	
105 110 115	
ggc gca ggt cag tcc tac ttc ggc aat gat cac ttc gct gag ttc gca	499
Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His Phe Ala Glu Phe Ala	
120 125 130	
cct ggc atg aag tcc atc gac gat gca ctg gag att cgt gca cgc atc	547
Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu Ile Arg Ala Arg Ile	
135 140 145	
atc ggt gct ttc gag cgc gct gag atc tgc gag gat cca gct gag cgc	595
Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu Asp Pro Ala Glu Arg	
150 155 160 165	
gaa cgc ctg ctc acc ttc gtc gtt gtt ggc gct ggc cca acc ggt gtt	643
Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala Gly Pro Thr Gly Val	
170 175 180	
gag ctt gct ggc cag ttg gct gag atg gct cac cgc acc ctt gct ggt	691
Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His Arg Thr Leu Ala Gly	
185 190 195	
gag tac aag aac ttc aac acc aac tcc gca aag atc atc ctg ctt gat	739
Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys Ile Ile Leu Leu Asp	
200 205 210	
ggc gct cca cag gtt ctt cct cca ttc ggt aag cgc cta ggc cgc aac	787
Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys Arg Leu Gly Arg Asn	
215 220 225	
gca cag cgc acc ctg gaa aag atg ggt gtc aac gtt cgc ctg aac gct	835
Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn Val Arg Leu Asn Ala	
230 235 240 245	
atg gtc acc aac gtt gac gct acc tcg gtc acc tac aag acc aag gac	883
Met Val Thr Asn Val Asp Ala Thr Ser Val Thr Tyr Lys Thr Lys Asp	
250 255 260	
ggc gaa gag cac acc atc gaa tct ttc tgc aag att tgg tcc gct ggt	931
Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly	
265 270 275	
gtt gcg gca tcc cca ctg ggc aag ctc gtc gca gag cag acc ggt gtt	979
Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala Glu Gln Thr Gly Val	
280 285 290	
gag acc gac cgc gca ggc cgc gtc atg gtt aac gat gac ctg tct gtt	1027
Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val	
295 300 305	
ggc gat cag aag aac gtc ttc gtt	1051
Gly Asp Gln Lys Asn Val Phe Val	
310 315	

&lt;210&gt; 718

&lt;211&gt; 317

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 718

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Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val
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Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala
      20           25           30

Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu
      35           40           45

Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
      50           55           60

Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val
      65           70           75           80

Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr
      85           90           95

Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser
      100          105          110

Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His
      115          120          125

Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu
      130          135          140

Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu
      145          150          155          160

Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala
      165          170          175

Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
      180          185          190

Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys
      195          200          205

Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
      210          215          220

Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn
      225          230          235          240

Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr
      245          250          255

Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys
      260          265          270

Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala
      275          280          285

Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn

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290          295          300
Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
305          310          315

<210> 719
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(816)
<223> FRXA01895

<400> 719
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His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu
1          5          10          15

tcc tcc ggt gaa atc gca cct tcc act cga cag atc ctg ggc tcc cag 96
Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln
20          25          30

gaa aac gtc aac gtc atc aag ggc gaa gtc acc gac atc aac gtc gag 144
Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
35          40          45

tcc cag act gtg acc gcc tcc ctg ggc gag ttc acc cgc gtt ttt gag 192
Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
50          55          60

tac gat tcc ttg gtc gtt ggt gct ggc gca ggt cag tcc tac ttc ggc 240
Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
65          70          75          80

aat gat cac ttc gct gag ttc gca cct ggc atg aag tcc atc gac gat 288
Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
85          90          95

gca ctg gag att cgt gca cgc atc atc ggt gct ttc gag cgc gct gag 336
Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
100          105          110

atc tgc gag gat cca gct gag cgc gaa cgc ctg ctc acc ttc gtc gtt 384
Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
115          120          125

gtt ggc gct ggc cca acc ggt gtt gag ctt gct ggc cag ttg gct gag 432
Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
130          135          140

atg gct cac cgc acc ctt gct ggt gag tac aag aac ttc aac acc aac 480
Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
145          150          155          160

tcc gca aag atc atc ctg ctt gat ggt gct cca cag gtt ctt cct cca 528
Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
165          170          175

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ttc ggt aag cgc cta ggc cgc aac gca cag cgc acc ctg gaa aag atg 576  
 Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met  
                   180                                  185                                  190

ggt gtc aac gtt cgc ctg aac gct atg gtc acc aac gtt gac gct acc 624  
 Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr  
                   195                                  200                                  205

tcg gtc acc tac aag acc aag gac ggc gaa gag cac acc atc gaa tct 672  
 Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser  
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ttc tgc aag att tgg tcc gct ggt gtt gcg gca tcc cca ctg ggc aag 720  
 Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys  
                   225                                  230                                  235                                  240

ctc gtc gca gag cag acc ggt gtt gag acc gac cgc gca ggc cgc gtc 768  
 Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val  
                                   245                                  250                                  255

atg gtt aac gat gac ctg tct gtt ggc gat cag aag aac gtc ttc gtt 816  
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                   20                                  25                                  30

Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu  
                   35                                  40                                  45

Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu  
                   50                                  55                                  60

Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly  
                   65                                  70                                  75                                  80

Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp  
                                   85                                  90                                  95

Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu  
                   100                                  105                                  110

Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val  
                   115                                  120                                  125

Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu  
                   130                                  135                                  140

Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn  
                   145                                  150                                  155                                  160

Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro  
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Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met  
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Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr  
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Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser  
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Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys  
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 Met Thr Thr Pro Pro  
 1 5

act gag att tcg aac gtg aat ccc acc gcg aat gaa ttt gat gat ccg 163  
 Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn Glu Phe Asp Asp Pro  
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gat gtg gga cgg cgc att act tct gct gct ggt gtg cca ggc gtt ttg 211  
 Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly Val Pro Gly Val Leu  
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cat gcg ctc cag cat gct gtt ccg aat cgt gcc ctg ctg ccg ttg ctc 259  
 His Ala Leu Gln His Ala Val Pro Asn Arg Ala Leu Leu Pro Leu Leu  
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acc atg aat aaa cca ggc ggc atc gac tgt cct ggt tgt gct tgg cct 307  
 Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro Gly Cys Ala Trp Pro  
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gag cct tcc act gcc aac ctt ggt gtg gtt gag ttc tgc gag aac ggt 355  
 Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu Phe Cys Glu Asn Gly  
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gcc aag gcg gtc gcc gag gaa aca aca cct gat cgt gcc ggc aaa gag	403
Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp Arg Ala Gly Lys Glu	
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Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg Glu Lys Thr Asp His	
105 110 115	
tgg ctg gga aag cgt ggc cga atc acc gag ccc atg ttt tat gat cgt	499
Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro Met Phe Tyr Asp Arg	
120 125 130	
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Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser Trp Asp Arg Ala Phe	
135 140 145	
gcg atc att gcg tcg aag ctc cgc gag atc gag cca gat gaa gcg gtg	595
Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu Pro Asp Glu Ala Val	
150 155 160 165	
ttt tac acc tct ggt cga gca ccc aat gag ccg gct tat atg ctg cag	643
Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro Ala Tyr Met Leu Gln	
170 175 180	
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Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu Pro Asp Cys Gly Asn	
185 190 195	
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Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly Glu Thr Leu Gly Leu	
200 205 210	
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Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr Asn Thr Asp Leu Leu	
215 220 225	
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Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His Pro Arg Ala Leu Thr	
230 235 240 245	
gct ttc aaa gaa ttg aag gaa aac ggt ggc aag att ctg gcg ctg aac	883
Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys Ile Leu Ala Leu Asn	
250 255 260	
ccc atg cca gag acc ggt ctg atg aaa ttc cgt gag ccc caa tca gtc	931
Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg Glu Pro Gln Ser Val	
265 270 275	
aag ggc gcg ttg agc att tca gac aaa ctt gct gat gaa tac ttg cag	979
Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala Asp Glu Tyr Leu Gln	
280 285 290	
atc cgt ctt gat gga gac cgc gca ttc ttc cag gcg ctc aac aag gaa	1027
Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln Ala Leu Asn Lys Glu	
295 300 305	
ctc atc cgt aga gat gcc cta gat cat gca ttc ttg gat aaa ttc tgt	1075
Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe Leu Asp Lys Phe Cys	
310 315 320 325	

tca ggt gtg gat gaa acc atc gag cac ctc aaa tca ctc gat gat gag	1123
Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys Ser Leu Asp Asp Glu	
330 335 340	
gtt ctg ctc aag gga tgc ggt ctg acg gca gcg gag atc aac aag gcc	1171
Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala Glu Ile Asn Lys Ala	
345 350 355	
gct gac atg gtg gaa aag tct gac acc gtg gtg gtg tca tgg act ctc	1219
Ala Asp Met Val Glu Lys Ser Asp Thr Val Val Val Ser Trp Thr Leu	
360 365 370	
ggg gtc acc cag cat aag aac gct gtg tac acc atc cgt gaa atg gtg	1267
Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr Ile Arg Glu Met Val	
375 380 385	
aac ttc ctg ctg ctt act gga aat att ggt aag cct ggc gca ggc act	1315
Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys Pro Gly Ala Gly Thr	
390 395 400 405	
gcc ccg ctt cgt ggg cac tca aac gtc cag ggt gat cga acc atg ggt	1363
Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly Asp Arg Thr Met Gly	
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Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala Ala Leu Glu Asn Glu	
425 430 435	
ttt ggt ttc gat gtg ccc cgc aag cac ggc ttc gac acg gta aat tcc	1459
Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe Asp Thr Val Asn Ser	
440 445 450	
ctg cga gcc atg cgc gaa ggc aag acc aag ttc ttt ctc tcc ctc ggt	1507
Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe Phe Leu Ser Leu Gly	
455 460 465	
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Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser Val Val Glu Lys Gly	
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Met Glu Ser Asn Glu Leu Thr Val His Leu Ser Thr Lys Pro Asn Gly	
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Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile Leu Pro Val Ile Ala	
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Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val Gln Arg Val Thr Val	
520 525 530	
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Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr Gly Lys Arg Thr Ala	
535 540 545	
aac aag gat ctg aat ttg aag tcc gaa tgc gac atc att gga acc atc	1795
Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp Ile Ile Gly Thr Ile	
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Gly	Lys	Gln	Thr	Phe	Gly	Asp	Ala	Phe	Trp	Gln	Pro	Met	Ile	Asp	Asn		
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tac	gat	gtg	gtc	cgc	gat	cac	atc	gag	gcc	acc	att	cct	ggg	ttc	cac	1891	
Tyr	Asp	Val	Val	Arg	Asp	His	Ile	Glu	Ala	Thr	Ile	Pro	Gly	Phe	His		
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gat	ttc	aac	cgt	cgc	atc	gac	aac	ccc	ggg	gga	ttc	ctc	ctc	ccc	aac	1939	
Asp	Phe	Asn	Arg	Arg	Ile	Asp	Asn	Pro	Gly	Gly	Phe	Leu	Leu	Pro	Asn		
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gga	cct	cgt	gag	cgc	atc	ttc	aac	aca	tcc	aat	ggc	aag	gcc	caa	ttg	1987	
Gly	Pro	Arg	Glu	Arg	Ile	Phe	Asn	Thr	Ser	Asn	Gly	Lys	Ala	Gln	Leu		
	615					620					625						
acg	gtt	aat	gaa	acc	aat	gtg	att	gag	cta	ccc	aag	gac	tat	ttg	ctt	2035	
Thr	Val	Asn	Glu	Thr	Asn	Val	Ile	Glu	Leu	Pro	Lys	Asp	Tyr	Leu	Leu		
	630				635					640					645		
atg	aac	acg	gta	cgt	tca	cat	gat	caa	tac	aac	tcc	acg	att	tac	ggg	2083	
Met	Asn	Thr	Val	Arg	Ser	His	Asp	Gln	Tyr	Asn	Ser	Thr	Ile	Tyr	Gly		
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ctg	gat	gac	cgc	tac	cgc	ggg	gtt	cgc	aat	ggg	cgc	cgc	gta	gtg	ttc	2131	
Leu	Asp	Asp	Arg	Tyr	Arg	Gly	Val	Arg	Asn	Gly	Arg	Arg	Val	Val	Phe		
			665				670						675				
gtc	aat	cct	caa	gat	tgt	aag	caa	cgt	ggg	ctc	aag	gat	gga	gac	atc	2179	
Val	Asn	Pro	Gln	Asp	Cys	Lys	Gln	Arg	Gly	Leu	Lys	Asp	Gly	Asp	Ile		
		680					685					690					
gtc	gat	atc	gtc	tct	gtc	ttt	gat	gat	ggc	gaa	cgc	cga	gca	ccg	aat	2227	
Val	Asp	Ile	Val	Ser	Val	Phe	Asp	Asp	Gly	Glu	Arg	Arg	Ala	Pro	Asn		
	695					700					705						
ttc	cga	gtg	gtg	gaa	tat	gac	acc	gcg	agg	gac	tgc	gtc	acc	acg	tat	2275	
Phe	Arg	Val	Val	Glu	Tyr	Asp	Thr	Ala	Arg	Asp	Cys	Val	Thr	Thr	Tyr		
	710				715					720					725		
ttc	cct	gag	gcc	aac	gta	ttg	gtt	cca	ttg	gat	tca	gta	gct	gaa	aaa	2323	
Phe	Pro	Glu	Ala	Asn	Val	Leu	Val	Pro	Leu	Asp	Ser	Val	Ala	Glu	Lys		
			730					735					740				
tcc	aac	act	cca	gtg	tcc	aag	tca	gtt	gtg	gtt	cgc	ctt	gaa	gca	aca	2371	
Ser	Asn	Thr	Pro	Val	Ser	Lys	Ser	Val	Val	Val	Arg	Leu	Glu	Ala	Thr		
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Gly	Arg	Thr	Ala	Ser													
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&lt;210&gt; 722

&lt;211&gt; 762

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 722

Met Thr Thr Pro Pro Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn

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5

10

15

Glu Phe Asp Asp Pro Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly  
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 Val Pro Gly Val Leu His Ala Leu Gln His Ala Val Pro Asn Arg Ala  
                   35                  40                  45  
 Leu Leu Pro Leu Leu Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro  
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 Gly Cys Ala Trp Pro Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu  
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 Phe Cys Glu Asn Gly Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp  
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 Arg Ala Gly Lys Glu Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg  
                  100                 105                 110  
 Glu Lys Thr Asp His Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro  
   115                 120                 125  
 Met Phe Tyr Asp Arg Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser  
   130                 135                 140  
 Trp Asp Arg Ala Phe Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu  
  145                 150                 155                 160  
 Pro Asp Glu Ala Val Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro  
                  165                 170                 175  
 Ala Tyr Met Leu Gln Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu  
                  180                 185                 190  
 Pro Asp Cys Gly Asn Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly  
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 Glu Thr Leu Gly Leu Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr  
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 Asn Thr Asp Leu Leu Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His  
  225                 230                 235                 240  
 Pro Arg Ala Leu Thr Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys  
                  245                 250                 255  
 Ile Leu Ala Leu Asn Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg  
                  260                 265                 270  
 Glu Pro Gln Ser Val Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala  
   275                 280                 285  
 Asp Glu Tyr Leu Gln Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln  
   290                 295                 300  
 Ala Leu Asn Lys Glu Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe  
  305                 310                 315                 320  
 Leu Asp Lys Phe Cys Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys  
                  325                 330                 335  
 Ser Leu Asp Asp Glu Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala

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Glu	Ile	Asn	Lys	Ala	Ala	Asp	Met	Val	Glu	Lys	Ser	Asp	Thr	Val	Val				
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Val	Ser	Trp	Thr	Leu	Gly	Val	Thr	Gln	His	Lys	Asn	Ala	Val	Tyr	Thr				
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Ile	Arg	Glu	Met	Val	Asn	Phe	Leu	Leu	Leu	Thr	Gly	Asn	Ile	Gly	Lys				
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Pro	Gly	Ala	Gly	Thr	Ala	Pro	Leu	Arg	Gly	His	Ser	Asn	Val	Gln	Gly				
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Asp	Arg	Thr	Met	Gly	Ile	Trp	Glu	Lys	Met	Pro	Glu	Ala	Phe	Leu	Ala				
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Ala	Leu	Glu	Asn	Glu	Phe	Gly	Phe	Asp	Val	Pro	Arg	Lys	His	Gly	Phe				
	435						440					445							
Asp	Thr	Val	Asn	Ser	Leu	Arg	Ala	Met	Arg	Glu	Gly	Lys	Thr	Lys	Phe				
	450					455					460								
Phe	Leu	Ser	Leu	Gly	Gly	Asn	Leu	Val	Arg	Val	Ser	Ser	Asp	Thr	Ser				
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Thr	Lys	Pro	Asn	Gly	Ser	Gln	Ala	Trp	Pro	Gly	Glu	Gln	Ser	Leu	Ile				
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Leu	Pro	Val	Ile	Ala	Arg	Thr	Asp	Lys	Asp	Val	Gln	Lys	Ser	Gly	Val				
	515						520					525							
Gln	Arg	Val	Thr	Val	Glu	Asp	Ser	Ala	Gly	Ala	Val	His	Ala	Ser	Thr				
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Gly	Lys	Arg	Thr	Ala	Asn	Lys	Asp	Leu	Asn	Leu	Lys	Ser	Glu	Cys	Asp				
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Pro	Met	Ile	Asp	Asn	Tyr	Asp	Val	Val	Arg	Asp	His	Ile	Glu	Ala	Thr				
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Ile	Pro	Gly	Phe	His	Asp	Phe	Asn	Arg	Arg	Ile	Asp	Asn	Pro	Gly	Gly				
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Phe	Leu	Leu	Pro	Asn	Gly	Pro	Arg	Glu	Arg	Ile	Phe	Asn	Thr	Ser	Asn				
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Gly	Lys	Ala	Gln	Leu	Thr	Val	Asn	Glu	Thr	Asn	Val	Ile	Glu	Leu	Pro				
625					630					635					640				
Lys	Asp	Tyr	Leu	Leu	Met	Asn	Thr	Val	Arg	Ser	His	Asp	Gln	Tyr	Asn				
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Ser	Thr	Ile	Tyr	Gly	Leu	Asp	Asp	Arg	Tyr	Arg	Gly	Val	Arg	Asn	Gly				
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Arg Arg Val Val Phe Val Asn Pro Gln Asp Cys Lys Gln Arg Gly Leu  
 675 680 685

Lys Asp Gly Asp Ile Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu  
 690 695 700

Arg Arg Ala Pro Asn Phe Arg Val Val Glu Tyr Asp Thr Ala Arg Asp  
 705 710 715 720

Cys Val Thr Thr Tyr Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp  
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Ser Val Ala Glu Lys Ser Asn Thr Pro Val Ser Lys Ser Val Val Val  
 740 745 750

Arg Leu Glu Ala Thr Gly Arg Thr Ala Ser  
 755 760

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 <223> RXN00705

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 Met Gly Arg Ile Thr  
 1 5

caa aac ttg cag gtc cca cgc gtt gtg tcc act gac gag caa gtt ttt 163  
 Gln Asn Leu Gln Val Pro Arg Val Val Ser Thr Asp Glu Gln Val Phe  
 10 15 20

gtt aac act cgt ccg gat act gtt gcg gtg gag gag cct cta gaa att 211  
 Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile  
 25 30 35

cgg gtt aat ggc act gcg ctt acc acc act atg cgc acg ccc ggc cat 259  
 Arg Val Asn Gly Thr Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His  
 40 45 50

gat att gag ttg gtg cat ggc ctc ctc ttg tca gaa ggt ctg atc acg 307  
 Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr  
 55 60 65

gat gct tct gag gtt ttt acc gcc cgc tat tgt gca gga gct gtt ggc 355  
 Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly  
 70 75 80 85

cca gat aat caa aat acg tac aac gtc tta gaa ctt gat gtc atc ccc 403  
 Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro  
 90 95 100



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aaa gac aat ccg gcc cgg gat ccc gtc cag aat ccc tcc cat aat ccc 451
Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro
105 110 115

gaa ggc agc caa cac gaa gca ctc cac atc cca act ttc caa ccg gta 499
Glu Gly Ser Gln His Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val
120 125 130

cgc gaa cta aac ctc gtg gca gcc caa cgc aat gtg ctg act acg tct 547
Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser
135 140 145

gct tgt ggt gtt tgt ggc acg acg tct att gag cag ttg atg aac aag 595
Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys
150 155 160 165

aag ggc tgg ccc att acg ccg att aca ccg gat cct cgg atg att gtg 643
Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val
170 175 180

tcg ttg cca gat aag ttg aag tcg aag cag aag att ttc gac aaa act 691
Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr
185 190 195

ggt ggg gtt cat gct gct ggt ttg gcc acg ctt gat ggt gag atg ttg 739
Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu
200 205 210

att att cga gag gat gtc ggt cgg cat aac gca gct gac aaa gtt ata 787
Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala Ala Asp Lys Val Ile
215 220 225

gga aac atg ctg atg gcg gga aag ctc ccc ttg gaa aac act att ttg 835
Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu
230 235 240 245

gtg atg agt tct agg gcg tct ttt gag ctt gtc caa aag gct gcc atg 883
Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met
250 255 260

gct gga att tcg ggt gta atc gct gtt ggt gct gca aca tcg ctg gca 931
Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala
265 270 275

atc gag gcg gcg cag gat tca ggt att ttc ctt gct ggt ttt gtt cgg 979
Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg
280 285 290

ggc aac aag ttt aac cac tat gcg ggc gag ctc gga taatgccaga 1025
Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu Gly
295 300 305

acaggtagaa cag 1038

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&lt;210&gt; 724

&lt;211&gt; 305

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 724

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 Asp Glu Gln Val Phe Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu  
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 Glu Pro Leu Glu Ile Arg Val Asn Gly Thr Ala Leu Thr Thr Thr Met  
 35 40 45  
 Arg Thr Pro Gly His Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser  
 50 55 60  
 Glu Gly Leu Ile Thr Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys  
 65 70 75 80  
 Ala Gly Ala Val Gly Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu  
 85 90 95  
 Leu Asp Val Ile Pro Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn  
 100 105 110  
 Pro Ser His Asn Pro Glu Gly Ser Gln His Glu Ala Leu His Ile Pro  
 115 120 125  
 Thr Phe Gln Pro Val Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn  
 130 135 140  
 Val Leu Thr Thr Ser Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu  
 145 150 155 160  
 Gln Leu Met Asn Lys Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp  
 165 170 175  
 Pro Arg Met Ile Val Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys  
 180 185 190  
 Ile Phe Asp Lys Thr Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu  
 195 200 205  
 Asp Gly Glu Met Leu Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala  
 210 215 220  
 Ala Asp Lys Val Ile Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu  
 225 230 235 240  
 Glu Asn Thr Ile Leu Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val  
 245 250 255  
 Gln Lys Ala Ala Met Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala  
 260 265 270  
 Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu  
 275 280 285  
 Ala Gly Phe Val Arg Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu  
 290 295 300  
 Gly  
 305

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<220>  
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 <223> FRXA00705

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 gat act gtt gcg gtg gag gag cct cta gaa att cgg gtt aat ggc act 96  
 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr  
 20 25 30  
 gcg ctt acc acc act atg cgc acg ccc ggc cat gat att gag ttg gtg 144  
 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val  
 35 40 45  
 cat ggc ctc ctc ttg tca gaa ggt ctg atc acg gat gct tct gag gtt 192  
 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val  
 50 55 60  
 ttt acc gcc cgc tat tgt gca gga gct gtt ggc cca gat aat caa aat 240  
 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn  
 65 70 75 80  
 acg tac aac gtc tta gaa ctt gat gtc atc ccc aaa gac aat ccg gcc 288  
 Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala  
 85 90 95  
 cgg gat ccc gtc cag aat ccc tcc cat aat ccc gaa ggc agc caa cac 336  
 Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His  
 100 105 110  
 gaa gca ctc cac atc cca act ttc caa ccg gta cgc gaa cta aac ctc 384  
 Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu  
 115 120 125  
 gtg gca gcc caa cgc aat gtg ctg act acg tct gct tgt ggt gtt tgt 432  
 Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser Ala Cys Gly Val Cys  
 130 135 140  
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 Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys Lys Gly Trp Pro Ile  
 145 150 155 160  
 acg ccg att aca ccg gat cct cgg atg att gtg tcg ttg cca gat aag 528  
 Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys  
 165 170 175  
 ttg aag tcg aag cag aag att ttc gac aaa act ggt ggg gtt cat gct 576  
 Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr Gly Gly Val His Ala  
 180 185 190  
 gct ggt ttg gcc acg ctt gat ggt gag atg ttg att att cga gag gat 624  
 Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu Ile Ile Arg Glu Asp

195	200	205	
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Val Gly Arg His Asn Ala Ala Asp Lys Val Ile Gly Asn Met Leu Met			
210	215	220	
gcg gga aag ctc ccc ttg gaa aac act att ttg gtg atg agt tct agg			720
Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu Val Met Ser Ser Arg			
225	230	235	240
gcg tct ttt gag ctt gtc caa aag gct gcc atg gct gga att tcg ggt			768
Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met Ala Gly Ile Ser Gly			
245	250	255	
gta atc gct gtt ggt gct gca aca tcg ctg gca atc gag gcg gcg cag			816
Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln			
260	265	270	
gat tca ggt att ttc ctt gct ggt ttt gtt cgg ggc aac aag ttt aac			864
Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg Gly Asn Lys Phe Asn			
275	280	285	
cac tat gcg ggc gag ctc gga taatgccaga acaggtagaa cag			~ 908
His Tyr Ala Gly Glu Leu Gly			
290	295		

&lt;210&gt; 726

&lt;211&gt; 295

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 726

Pro	Arg	Val	Val	Ser	Thr	Asp	Glu	Gln	Val	Phe	Val	Asn	Thr	Arg	Pro
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Asp	Thr	Val	Ala	Val	Glu	Glu	Pro	Leu	Glu	Ile	Arg	Val	Asn	Gly	Thr
		20						25						30	

Ala	Leu	Thr	Thr	Thr	Met	Arg	Thr	Pro	Gly	His	Asp	Ile	Glu	Leu	Val
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His	Gly	Leu	Leu	Leu	Ser	Glu	Gly	Leu	Ile	Thr	Asp	Ala	Ser	Glu	Val
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Phe	Thr	Ala	Arg	Tyr	Cys	Ala	Gly	Ala	Val	Gly	Pro	Asp	Asn	Gln	Asn
65					70					75					80

Thr	Tyr	Asn	Val	Leu	Glu	Leu	Asp	Val	Ile	Pro	Lys	Asp	Asn	Pro	Ala
			85						90					95	

Arg	Asp	Pro	Val	Gln	Asn	Pro	Ser	His	Asn	Pro	Glu	Gly	Ser	Gln	His
		100						105					110		

Glu	Ala	Leu	His	Ile	Pro	Thr	Phe	Gln	Pro	Val	Arg	Glu	Leu	Asn	Leu
	115						120					125			

Val	Ala	Ala	Gln	Arg	Asn	Val	Leu	Thr	Thr	Ser	Ala	Cys	Gly	Val	Cys
	130					135					140				

Gly	Thr	Thr	Ser	Ile	Glu	Gln	Leu	Met	Asn	Lys	Lys	Gly	Trp	Pro	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145		150		155		160									
Thr	Pro	Ile	Thr	Pro	Asp	Pro	Arg	Met	Ile	Val	Ser	Leu	Pro	Asp	Lys
				165					170					175	
Leu	Lys	Ser	Lys	Gln	Lys	Ile	Phe	Asp	Lys	Thr	Gly	Gly	Val	His	Ala
			180					185					190		
Ala	Gly	Leu	Ala	Thr	Leu	Asp	Gly	Glu	Met	Leu	Ile	Ile	Arg	Glu	Asp
		195					200					205			
Val	Gly	Arg	His	Asn	Ala	Ala	Asp	Lys	Val	Ile	Gly	Asn	Met	Leu	Met
	210					215					220				
Ala	Gly	Lys	Leu	Pro	Leu	Glu	Asn	Thr	Ile	Leu	Val	Met	Ser	Ser	Arg
225					230					235					240
Ala	Ser	Phe	Glu	Leu	Val	Gln	Lys	Ala	Ala	Met	Ala	Gly	Ile	Ser	Gly
				245					250					255	
Val	Ile	Ala	Val	Gly	Ala	Ala	Thr	Ser	Leu	Ala	Ile	Glu	Ala	Ala	Gln
			260					265					270		
Asp	Ser	Gly	Ile	Phe	Leu	Ala	Gly	Phe	Val	Arg	Gly	Asn	Lys	Phe	Asn
		275					280					285			
His	Tyr	Ala	Gly	Glu	Leu	Gly									
	290					295									

&lt;210&gt; 727

&lt;211&gt; 1134

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1111)

&lt;223&gt; RXN00388

&lt;400&gt; 727

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acatcgaagc	agttttcaca	aagaataagg	ttggaaaatt	atg	ttg	ccc	gtc	aac	115
				Met	Leu	Pro	Val	Asn	
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caa	acg	tat	gcg	cag	ttc	tca	gac	act	gcc	ttc	gta	tcg	gca	tac	atc	163
Gln	Thr	Tyr	Ala	Gln	Phe	Ser	Asp	Thr	Ala	Phe	Val	Ser	Ala	Tyr	Ile	
			10						15					20		

atc	tac	gtt	ctg	gca	ctc	atc	ctc	tcc	ctc	gtc	tac	tac	gta	aaa	caa	211
Ile	Tyr	Val	Leu	Ala	Leu	Ile	Leu	Ser	Leu	Val	Tyr	Tyr	Val	Lys	Gln	
			25					30					35			

caa	ggc	att	atc	gac	gcc	cgc	cgc	gag	caa	acc	cgc	gtc	agc	gaa	ctc	259
Gln	Gly	Ile	Ile	Asp	Ala	Arg	Arg	Glu	Gln	Thr	Arg	Val	Ser	Glu	Leu	
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gtt	ggt	gca	ggc	ggc	agc	gct	gat	gtt	gat	act	gac	ctg	cct	gat	gac	307
Val	Gly	Ala	Gly	Gly	Ser	Ala	Asp	Val	Asp	Thr	Asp	Leu	Pro	Asp	Asp	

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cag tcc ttc tgg ttc ccg atc cac gtt tcc tcc gtc tcc atc ggc gca Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser Val Ser Ile Gly Ala 185 190 195			691
tcc atc ggt atc gtc tcc ggt att gca tcc ctg ctg tac ata ctg cgc Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu Leu Tyr Ile Leu Arg 200 205 210			739
atg tgg caa cca aag ggt aaa gaa aag ggc ttc ttc ggc gca gta gca Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe Phe Gly Ala Val Ala 215 220 225			787
aaa cca ctc cca tcc gga aaa acc ctg gat aac ctg gca tac aag acc Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn Leu Ala Tyr Lys Thr 230 235 240 245			835
gcg atc tgg act gtc cca atc ttc ggc ctg ggc atc atc ttg ggt gcc Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly Ile Ile Leu Gly Ala 250 255 260			883
atc tgg gca gaa gca gcc tgg ggt cgt ttc tgg gga tgg gat cct aag Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp Gly Trp Asp Pro Lys 265 270 275			931
gaa aca gtc tcc ttc atc acc tgg gtt ctc tac gct ggt tac ctc cac Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His 280 285 290			979
gca cgt gca act gct ggt tgg cgc aac acc aac gct gca tgg atc aac Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn Ala Ala Trp Ile Asn 295 300 305			1027

atc ctg gcg ctg gtc acg atg att ttt aat ctg ttc ttc atc aac atg 1075  
 Ile. Leu Ala Leu Val Thr Met Ile Phe Asn Leu Phe Phe Ile Asn Met  
 310 315 320 325

gtc gta tct ggt ctg cac tct tac gcc gga ctg aac taagcacttt 1121  
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 330 335

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Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr  
 35 40 45

Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr  
 50 55 60

Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu  
 65 70 75 80

Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser  
 85 90 95

Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg  
 100 105 110

Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile  
 115 120 125

Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln  
 130 135 140

Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu  
 145 150 155 160

Ala Leu Leu Phe Tyr Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro  
 165 170 175

Val Val Pro Ala Leu Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser  
 180 185 190

Val Ser Ile Gly Ala Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu  
 195 200 205

Leu Tyr Ile Leu Arg Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe  
 210 215 220

Phe Gly Ala Val Ala Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn

225                      230                      235                      240  
 Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly  
                                  245                      250                      255  
 Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp  
                                  260                      265                      270  
 Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr  
                                  275                      280                      285  
 Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn  
                                  290                      295                      300  
 Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu  
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 Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu  
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 Asn

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   1                                    5                                    10                                    15  
 ttc ggc ctg ggc atc atc ttg ggt gcc atc tgg gca gaa gca gcc tgg      96  
 Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp  
                                  20                                    25                                    30  
 ggt cgt ttc tgg gga tgg gat cct aag gaa aca gtc tcc ttc atc acc      144  
 Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr  
                                  35                                    40                                    45  
 tgg gtt ctc tac gct ggt tac ctc cac gca cgt gca act gct ggt tgg      192  
 Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp  
                                  50                                    55                                    60  
 cgc aac acc aac gct gca tgg atc aac atc ctg gcg ctg gtc acg atg      240  
 Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met  
   65                                    70                                    75                                    80  
 att ttt aat ctg ttc ttc atc aac atg gtc gta tct ggt ctg cac tct      288  
 Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser  
                                  85                                    90                                    95  
 tac gcc gga ctg aac taagcacttt tggttggcgg ggt      326  
 Tyr Ala Gly Leu Asn



100

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 <211> 101  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 730  
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                   20                  25                  30  
 Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr  
           35                  40                  45  
 Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp  
       50                  55                  60  
 Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met  
   65                  70                  75                  80  
 Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser  
                   85                  90                  95  
 Tyr Ala Gly Leu Asn  
           100

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 <213> Corynebacterium glutamicum

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 <223> FRXA00386

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   Met Leu Pro Val Asn  
   1                  5  
 caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc 163  
 Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile  
                   10                  15                  20  
 atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa 211  
 Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln  
                   25                  30                  35  
 caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc 259  
 Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu  
                   40                  45                  50  
 gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac 307

Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp  
55 60 65  
atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa 355  
Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu  
70 75 80 85  
acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc 403  
Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly  
90 95 100  
gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc 451  
Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser  
105 110 115  
cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc 499  
Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu  
120 125 130  
ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc 547  
Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg  
135 140 145  
gtg gta tgg cca tgg atc ctc acc cca atg gct ggc act tgg ttt tct 595  
Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala Gly Thr Trp Phe Ser  
150 155 160 165  
acg gtg gca ccc agc 610  
Thr Val Ala Pro Ser  
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20 25 30  
Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr  
35 40 45  
Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr  
50 55 60  
Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu  
65 70 75 80  
Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser  
85 90 95  
Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg  
100 105 110  
Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile  
115 120 125

Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln  
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Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala  
 145 150 155 160

Gly Thr Trp Phe Ser Thr Val Ala Pro Ser  
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<210> 733

<211> 1095

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1072)

<223> RXA00945

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 Met Leu Glu Arg Leu  
 1 5

aaa cgc cta gat ccg ctc att gtc ctc att gtg ctg gct gtc att gtg 163  
 Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val Leu Ala Val Ile Val  
 10 15 20

gcg atc atc att cca gtt cgc ggg gtt gct gcg gat tgg ttt gat gtc 211  
 Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val  
 25 30 35

gcc gtc aag att gcc att gcg ctg ctg ttt ttt ctt tat ggt gcc cgc 259  
 Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg  
 40 45 50

cta tcc acc caa gag gcg ctg aat ggt ctg aag cac tgg agg ctt cac 307  
 Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys His Trp Arg Leu His  
 55 60 65

ctg act att ttg gcg atc act ttc gga ata ttc cca ctt atc ggc att 355  
 Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe Pro Leu Ile Gly Ile  
 70 75 80 85

ggg ctc gag ccg atg act gca ttt gtg tcg gaa gat att tat cgg gga 403  
 Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly  
 90 95 100

att ttg ttc ctc acg ctc gtt ccg tcc acc gtg cag tca tcg gtg gcg 451  
 Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala  
 105 110 115

ttt acc tcg atc gct aaa ggc aac gta gct ggt gcg att gtg tcg gca 499  
 Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala  
 120 125 130

tcg ctc tcc aac ctt gcg ggt gtt ttc ctc act ccg ctg ctg gtc atg 547

Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met  
 135 140 145  
 ctc atc atg tct gcg ggc ggg gga gtt cac gtg gat tcc cag gtc ttc 595  
 Leu Ile Met Ser Ala Gly Gly Gly Val His Val Asp Ser Gln Val Phe  
 150 155 160 165  
 ctc gac att gcg att cag ctt ctg ctg ccg ttc atc ctc ggc cag gta 643  
 Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val  
 170 175 180  
 tgt agg cgt tgg gtg aag aat ttt gcg gcc aac aaa gca aca aaa atc 691  
 Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile  
 185 190 195  
 gtg gac cgc ggc tgc atc gcg atg gtc gtg tac tcc gcg ttt tct gcc 739  
 Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Ala Phe Ser Ala  
 200 205 210  
 ggc atg gtg gct ggc att tgg tcc act gtg agc gtt cta gag att atc 787  
 Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile  
 215 220 225  
 tac ctc att gtt ttc gct att ctg ctg gtg atg gcc atg ctg tgg ttc 835  
 Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe  
 230 235 240 245  
 acg ctg ttc atg gct aca cgc ctt gga ttt aac cgg gca gat tcc atc 883  
 Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile  
 250 255 260  
 gct att cag ttc tgc gga acc aag aaa tcc ctg gcc aca ggc ctc cca 931  
 Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu Ala Thr Gly Leu Pro  
 265 270 275  
 atg gcg gca gtc atc ttc ggt ggc gcc aat atc ggc ctg ctc atc ttg 979  
 Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile Gly Leu Leu Ile Leu  
 280 285 290  
 ccg ttg atg atc ttc cac caa gtc cag ctg atg att tgt gca tgg ctt 1027  
 Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu  
 295 300 305  
 gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc 1072  
 Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala  
 310 315 320  
 taaaagtcct cagtagctag cca 1095

&lt;210&gt; 734

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 734

Met Leu Glu Arg Leu Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val  
 1 5 10 15

Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala  
 20 25 30

Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe  
           35                          40                          45  
 Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys  
           50                          55                          60  
 His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe  
           65                          70                          75                          80  
 Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu  
                           85                          90                          95  
 Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val  
                           100                          105                          110  
 Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly  
           115                          120                          125  
 Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr  
           130                          135                          140  
 Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val  
   145                          150                          155                          160  
 Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe  
                           165                          170                          175  
 Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn  
                           180                          185                          190  
 Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr  
           195                          200                          205  
 Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser  
           210                          215                          220  
 Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met  
   225                          230                          235                          240  
 Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn  
           245                          250                          255  
 Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu  
           260                          265                          270  
 Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile  
           275                          280                          285  
 Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met  
           290                          295                          300  
 Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln  
   305                          310                          315                          320  
 Lys Ala Asn Ala

&lt;210&gt; 735

&lt;211&gt; 1281

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1258)

&lt;223&gt; RXN02556

&lt;400&gt; 735

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tgccatcata ttaaggccaa attgcttgga tcctgggatt tatttaatta gattaaatcc 60

gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115
                                   Leu Ile Val Ser Thr
                                   1 5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163
Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
                                   10 15 20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211
Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
                                   25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259
Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
                                   40 45 50

aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg 307
Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
                                   55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355
Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp
                                   70 75 80 85

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val
                                   90 95 100

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
                                   105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
                                   120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu
                                   135 140 145

atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc 595
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly
                                   150 155 160 165

gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca 643
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala
                                   170 175 180

acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca 691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro

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	185	190	195	
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag				739
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln				
200 . 205 210				
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att				787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile				
215 220 225				
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta				835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val				
230 235 240 245				
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt				883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val				
250 255 260				
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc				931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly				
265 270 275				
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac				979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp				
280 285 290				
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg				1027
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val				
295 300 305				
gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa				1075
Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu				
310 315 320 325				
atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att				1123
Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile				
330 335 340				
cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag				1171
Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys				
345 350 355				
aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta				1219
Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val				
360 365 370				
aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca				1268
Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser				
375 380 385				
ccccagaact tcc				1281

&lt;210&gt; 736

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 736

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 Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His  
                   35                                  40                                  45  
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly  
                   50                                  55                                  60  
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met  
                   65                                  70                                  75                                  80  
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile  
                                   85                                  90                                  95  
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile  
                                   100                                  105                                  110  
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu  
                   115                                  120                                  125  
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile  
                   130                                  135                                  140  
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn  
                   145                                  150                                  155                                  160  
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys  
                                   165                                  170                                  175  
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu  
                                   180                                  185                                  190  
 Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp  
                   195                                  200                                  205  
 Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp  
                   210                                  215                                  220  
 Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe  
                   225                                  230                                  235                                  240  
 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala  
                                   245                                  250                                  255  
 Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile  
                                   260                                  265                                  270  
 Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met  
                   275                                  280                                  285  
 Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser  
                   290                                  295                                  300  
 Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro  
                   305                                  310                                  315                                  320  
 Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu  
                                   325                                  330                                  335



Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly  
340 345 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu  
355 360 365

Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu  
370 375 380

Ile Ser  
385

<210> 737

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> FRXA02556

<400> 737

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gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115  
Leu Ile Val Ser Thr  
1 5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163  
Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val  
10 15 20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211  
Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr  
25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259  
Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala  
40 45 50

aac acc ttc aac ggt ggc aat cag aag caa ggc gat cag cag aag gcg 307  
Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala  
55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355  
Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp  
70 75 80 85

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403  
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val  
90 95 100

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451  
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu  
105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499  
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro  
120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu 135 140 145	547
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly 150 155 160 165	595
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala 170 175 180	643
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro 185 190 195	691
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln 200 205 210	739
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile 215 220 225	787
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val 230 235 240 245	835
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val 250 255 260	883
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly 265 270 275	931
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp 280 285 290	979
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val 295 300 305	1027
gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu 310 315 320 325	1075
atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile 330 335 340	1123
cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys 345 350 355	1171
aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val 360 365 370	1219

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268  
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser  
       375                      380                      385

ccccagaact tcc 1281

<210> 738

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 738

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Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys  
                       20                      25                      30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His  
                       35                      40                      45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly  
       50                      55                      60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met  
       65                      70                      75                      80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile  
                       85                      90                      95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile  
                       100                      105                      110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu  
                       115                      120                      125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile  
       130                      135                      140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn  
       145                      150                      155                      160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys  
                       165                      170                      175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu  
                       180                      185                      190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp  
                       195                      200                      205

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp  
       210                      215                      220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe  
       225                      230                      235                      240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala  
                       245                      250                      255

Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile  
 260 265 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met  
 275 280 285

Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser  
 290 295 300

Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro  
 305 310 315 320

Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu  
 325 330 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly  
 340 345 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu  
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Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu  
 370 375 380

Ile Ser  
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<210> 739  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> (101)..(1177)  
 <223> RXA01392

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 Val Ala Asn Thr Ser  
 1 5

tcc gat tgg gca ggc gcc cca caa aat gca tca gca gac ggc gag ttc 163  
 Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser Ala Asp Gly Glu Phe  
 10 15 20

gtt cgc gat acc aac tac atc gat gac cgc atc gtc gca gac gtt cca 211  
 Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile Val Ala Asp Val Pro  
 25 30 35

gcg gga tcc gaa cca att gct cag gaa gat ggc act ttc cat tgg cct 259  
 Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly Thr Phe His Trp Pro  
 40 45 50

gtc gag gct ggt cgc tac cgt tta gtc gct gcc cgc gca tgt cca tgg 307  
 Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala Arg Ala Cys Pro Trp  
 55 60 65

gca cac cgc act gtt atc acc cgt cgt ctt ctc ggc ctg gag aac gtg	355
Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu Gly Leu Glu Asn Val	
70 75 80 85	
atc tcg ctt ggt ctg acc ggc ccg act cac gac gtt cgt tcc tgg act	403
Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp Val Arg Ser Trp Thr	
90 95 100	
ttc gat tta gat cca aac cat ctt gat ccc gtg ctg cag att cct cgt	451
Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val Leu Gln Ile Pro Arg	
105 110 115	
cta cag gac gcg tat ttc aac cgc ttc ccc gat tac ccg cgc ggc att	499
Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp Tyr Pro Arg Gly Ile	
120 125 130	
act gtc cca gcg ctc gtg gag gaa tcg tct aag aag gtc gtc acc aac	547
Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys Lys Val Val Thr Asn	
135 140 145	
gat tac cct tcc atc acc atc gat ttc aat ctt gag tgg aag cag ttc	595
Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu Glu Trp Lys Gln Phe	
150 155 160 165	
cac cgt gag ggt gcg cct aac ctc tac ccc gcg gag ctg cgc gag gag	643
His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala Glu Leu Arg Glu Glu	
170 175 180	
atg gcg ccg gtg atg aag cgc atc ttc act gag gtc aac aac ggc gta	691
Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu Val Asn Asn Gly Val	
185 190 195	
tac agg acc ggc ttt gcc ggt agc cag gaa gcg cac aac gag gcg tac	739
Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala His Asn Glu Ala Tyr	
200 205 210	
aag cgg ctt tgg gtt gcg ttg gac tgg cta gaa gat cgc tta tcg acg	787
Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu Asp Arg Leu Ser Thr	
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cga cgt tac ctc atg ggg gat cac atc acc gag gcg gat atc cgc ctc	835
Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu Ala Asp Ile Arg Leu	
230 235 240 245	
tac cca acc ctc gtg cgt ttc gat gcc gtc tac cac gga cac ttc aag	883
Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr His Gly His Phe Lys	
250 255 260	
tgt ggc cgc aac aag atc acc gaa atg ccg aat cta tgg ggc tac ctg	931
Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn Leu Trp Gly Tyr Leu	
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cgg gat ctt ttc cag acc cca ggc ttt ggc gac acc acc gat ttc acc	979
Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp Thr Thr Asp Phe Thr	
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gaa atc aag cag cac tac tac atc acc cac gcg gag att aac ccc acc	1027
Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala Glu Ile Asn Pro Thr	
295 300 305	
cgg atc gtt cca gtc gga cca gat ctg tct ggt ttc gcg aca cca cac	1075

Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly Phe Ala Thr Pro His  
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 Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala Glu Gly Val Thr Leu  
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Thr Phe His Trp Pro Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala  
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Arg Ala Cys Pro Trp Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu  
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Gly Leu Glu Asn Val Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp  
 85 90 95

Val Arg Ser Trp Thr Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val  
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Leu Gln Ile Pro Arg Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp  
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Tyr Pro Arg Gly Ile Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys  
 130 135 140

Lys Val Val Thr Asn Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu  
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Glu Trp Lys Gln Phe His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala  
 165 170 175

Glu Leu Arg Glu Glu Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu  
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Val Asn Asn Gly Val Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala  
 195 200 205

His Asn Glu Ala Tyr Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu  
 210 215 220  
 Asp Arg Leu Ser Thr Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu  
 225 230 235 240  
 Ala Asp Ile Arg Leu Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr  
 245 250 255  
 His Gly His Phe Lys Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn  
 260 265 270  
 Leu Trp Gly Tyr Leu Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp  
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 Thr Thr Asp Phe Thr Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala  
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 Glu Ile Asn Pro Thr Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly  
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 Met Ser Thr Val Val  
 1 5  
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 Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro Val Glu Lys Val Asn  
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 Val Val Val Pro Asp Pro Gly Ala Asn Asp Val Ile Val Lys Ile Gln  
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 Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr Arg Asp Gly Asp Ile  
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Ser	Asp	Glu	Phe	Pro	Tyr	Leu	Leu	Gly	His	Glu	Ala	Ala	Gly	Ile	Val		
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Glu	Glu	Val	Gly	Glu	Ser	Val	Thr	His	Val	Glu	Val	Gly	Asp	Phe	Val	85	
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Ile	Leu	Asn	Trp	Arg	Ala	Val	Cys	Gly	Glu	Cys	Arg	Ala	Cys	Lys	Lys	100	
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Gly	Glu	Pro	Lys	Tyr	Cys	Phe	Asn	Thr	His	Asn	Ala	Ser	Lys	Lys	Met	115	
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Thr	Leu	Glu	Asp	Gly	Thr	Glu	Leu	Ser	Pro	Ala	Leu	Gly	Ile	Gly	Ala		
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Phe	Leu	Glu	Lys	Thr	Leu	Val	His	Glu	Gly	Gln	Cys	Thr	Lys	Val	Asn		
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Pro	Glu	Glu	Asp	Pro	Ala	Ala	Ala	Gly	Leu	Leu	Gly	Cys	Gly	Ile	Met	165	
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Ser	Val	Ala	Val	Phe	Gly	Leu	Gly	Gly	Val	Gly	Met	Ala	Ala	Ile	Ala		
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Gly	Ala	Lys	Ile	Ala	Gly	Ala	Ser	Lys	Ile	Ile	Ala	Val	Asp	Ile	Asp		
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Glu	Lys	Lys	Leu	Glu	Trp	Ala	Lys	Glu	Phe	Gly	Ala	Thr	His	Thr	Ile		
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Asn	Ser	Ser	Gly	Leu	Gly	Gly	Glu	Gly	Asp	Ala	Ser	Glu	Val	Val	Ala		
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His	Ala	Gly	Arg	Met	Val	Met	Val	Gly	Val	Pro	Asn	Leu	Thr	Ser	Arg		
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Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg Asp Phe Pro Thr Tyr			
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gtg gat ctg cac ctg cag ggt cgt ttc cca ctg gat aag ttt gtt tct			1123
Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu Asp Lys Phe Val Ser			
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Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala Phe Asn Thr Met Lys			
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gct ggc gac gtg ctg cgt tct gtg gtg gag atc taaatggctc acgacggatt			1224
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gcg			1227

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 Arg Asp Gly Asp Ile Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu  
 50 55 60  
 Ala Ala Gly Ile Val Glu Glu Val Gly Glu Ser Val Thr His Val Glu  
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 Val Gly Asp Phe Val Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys  
 85 90 95  
 Arg Ala Cys Lys Lys Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn  
 100 105 110  
 Ala Ser Lys Lys Met Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala  
 115 120 125  
 Leu Gly Ile Gly Ala Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln  
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 Cys Thr Lys Val Asn Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu  
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Pro	Gln	Thr	Pro	Glu	Gly	Asn	Ser	Met	Ala	Lys	Pro	Ser	Ala	Lys	Lys	
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Leu	Thr	Ile	Gly	Leu	Ser	Gly	Ala	Gly	Ile	Leu	Ala	Thr	Ala	Ile	Thr		
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Pro	Asp	Ala	Gln	Val	Ala	Thr	Ala	Gln	Arg	Asp	Asp	Gln	Ala	Leu	Ile		
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Gly	Gly	Asp	Leu	Phe	Arg	Leu	Asn	Cys	Ala	Ser	Cys	His	Asn	Phe	Thr		
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Gly	Arg	Gly	Gly	Ala	Leu	Ser	Ser	Gly	Lys	Tyr	Ala	Pro	Asn	Leu	Asp		
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Asn	Met	Pro	Lys	Phe	Ser	Asp	Arg	Gln	Leu	Ser	Ala	Asp	Glu	Lys	Lys		
	230				235					240					245		
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Asp	Ile	Ile	Ala	Phe	Ile	Lys	Ser	Thr	Lys	Glu	Thr	Pro	Ser	Pro	Gly		
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Gly	Tyr	Ser	Leu	Gly	Ser	Leu	Gly	Pro	Val	Ala	Glu	Gly	Leu	Phe	Met		

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 35 40 45  
 Ala Thr Ala Ile Thr Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp  
 50 55 60  
 Asp Gln Ala Leu Ile Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys  
 65 70 75 80  
 Ile Thr Cys His Gly Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro  
 85 90 95  
 Ser Leu Val Gly Val Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser  
 100 105 110  
 Gly Arg Met Pro Ile Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala  
 115 120 125  
 Pro Arg Tyr Thr Glu Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala  
 130 135 140  
 Ala Asn Gly Gly Gly Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu  
 145 150 155 160  
 Ala Met Glu Glu Leu Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser  
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 Ala Asp Val Ala Arg Gly Gly Asp Leu Phe Arg Leu Asn Cys Ala Ser  
 180 185 190  
 Cys His Asn Phe Thr Gly Arg Gly Gly Ala Leu Ser Ser Gly Lys Tyr  
 195 200 205  
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Met Val Leu Val Trp																
1 5																
tcc aag gcc ttc tgg cgc gac cgt aaa gac gcc ccc gat gga gca acc																163
Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala Pro Asp Gly Ala Thr																
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gca cta gca aga ccc gca cct ttg gta gat atc caa gac gaa gtc gcc																211
Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile Gln Asp Glu Val Ala																
25 30 35																
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Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro Trp Gly Met Val Phe																
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Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala Val Ser Val Leu Ala																
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Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala Glu Ser Ala Gln Asp																
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Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro Thr Thr Ser Thr His																
90 95 100																
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His Ala His Ser Arg Trp Ser Val Thr Thr Pro Thr Ala Met Thr Ser																
105 110 115																
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Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro  
35 40 45  
Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala  
50 55 60  
Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala  
65 70 75 80  
Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro  
85 90 95  
Thr Thr Ser Thr His His Ala His Ser Arg Trp Ser Val Thr Thr Pro  
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Val His Ile Pro Phe  
1 5  
ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163  
Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys  
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gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211  
 Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser  
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acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259  
 Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala  
                   40                                  45                                  50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307  
 Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val  
                   55                                  60                                  65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355  
 Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe  
                   70                                  75                                  80                                  85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403  
 Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe  
                                   90                                  95                                  100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451  
 Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys  
                                   105                                  110                                  115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg 501  
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<211> 127

<212> PRT

<213> Corynebacterium glutamicum

<400> 748

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Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro  
                   20                                  25                                  30

Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala  
                   35                                  40                                  45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala  
                   50                                  55                                  60

Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala  
                   65                                  70                                  75                                  80

Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile  
                                   85                                  90                                  95

Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg  
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Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn  
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ttcaacccat ggccgtatcc tcgcggattt taggagataa atg tct aat caa tta 115																
Met Ser Asn Gln Leu 5																
ccc gat cac gtc cgc gac gcc ttc caa gta ggt gcg gga cct gcc gaa 163																
Pro Asp His Val Arg Asp Ala Phe Gln Val Gly Ala Gly Pro Ala Glu 20																
caa ctc ggt caa gct tgg gac ttc gga ttc cgc gtc ggc aac act gtg 211																
Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg Val Gly Asn Thr Val 35																
ttc gcc aaa gtg acg gcg ccg gaa gtg tcg ggc tgg tcg tcg aaa acc 259																
Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly Trp Ser Ser Lys Thr 50																
cgc gaa acc ctg aaa cca gaa ggc gtg cgc gtc gta cga ccg atc cgc 307																
Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val Val Arg Pro Ile Arg 65																
tcc acc gac ggc cga ttt gtg gtt gcg ggg tgg cgc gca tcg gtg ttc 355																
Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp Arg Ala Ser Val Phe 85																
tct acg gga acg atc agc aag cga gtc gat gag acg gtc gtt gcg ggt 403																
Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu Thr Val Val Ala Gly 100																
ctt cgt ttg gca gat gca tta gtg gat acg cat gca ccg gaa cct gtg 451																
Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His Ala Pro Glu Pro Val 115																
gac aat gtg ttt aac cgt gct gat gtg cag gcc tgg gaa gag cag ccc 499																
Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala Trp Glu Glu Gln Pro 130																
ggc cga atc ggt gaa ttg ttg gag ccg att aat cgc gtg aac cag gtt 547																
Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn Arg Val Asn Gln Val 145																
ggc cat gcg gat atg ttg gcg aca acg ctg tat gcg gga act cag cca 595																
Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro 165																
cct gca gtg acg gat ttg gtg cca gtg ctg cgt ccg cat ggt ttc act 643																
Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr																



170	175	180	
gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag			691
Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu			
185	190	195	
gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt			739
Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val			
200	205	210	
ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac			787
Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Glu Phe Ser Glu Asn			
215	220	225	
aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc			835
Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu			
230	235	240	245
gtg tcg tat gtt tct gac aag att tgaggtatgt cggaatacaa acc			882
Val Ser Tyr Val Ser Asp Lys Ile			
250			

&lt;210&gt; 750

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 750

Met Ser Asn Gln Leu Pro Asp His Val Arg Asp Ala Phe Gln Val Gly	
1	5
Ala Gly Pro Ala Glu Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg	
20	25
Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly	
35	40
Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val	
50	55
Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp	
65	70
Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu	
85	90
Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His	
100	105
Ala Pro Glu Pro Val Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala	
115	120
Trp Glu Glu Gln Pro Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn	
130	135
Arg Val Asn Gln Val Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr	
145	150
Ala Gly Thr Gln Pro Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg	
165	170
	175

Pro His Gly Phe Thr Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu  
 180 185 190

Gly Ala Val Asp Glu Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu  
 195 200 205

Ile Glu Gln Leu Val Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln  
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Glu Phe Ser Glu Asn Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg  
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Val Glu Ser Thr Leu Val Ser Tyr Val Ser Asp Lys Ile  
 245 250

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 <223> RXN02206

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 Met Val Gly Ser Ser  
 1 5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163  
 Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser  
 10 15 20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211  
 Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn  
 25 30 35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259  
 Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val  
 40 45 50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307  
 Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser  
 55 60 65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355  
 Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu  
 70 75 80 85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403  
 Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp  
 90 95 100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451  
 Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val  
 105 110 115

ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499  
 Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu  
 120 125 130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547  
 Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly  
 135 140 145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca 595  
 Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala  
 150 155 160 165

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg 643  
 Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu  
 170 175 180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691  
 Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu  
 185 190 195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739  
 Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr  
 200 205 210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787  
 Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr  
 215 220 225

gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc 835  
 Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile  
 230 235 240 245

att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc 883  
 Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro  
 250 255 260

gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct 931  
 Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala  
 265 270 275

gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag 979  
 Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys  
 280 285 290

gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat 1027  
 Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp  
 295 300 305

gtc tcc ctg tgacttggtc caattacatt cac 1059  
 Val Ser Leu  
 310

&lt;210&gt; 752

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 752

Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr

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Ser Thr Trp Gly	Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe		
20	25	30	
Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn			
35	40	45	
Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala			
50	55	60	
Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn			
65	70	75	80
Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu			
85	90	95	
Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu			
100	105	110	
Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu			
115	120	125	
Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr			
130	135	140	
Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala			
145	150	155	160
Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln			
165	170	175	
Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro			
180	185	190	
Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly			
195	200	205	
Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser			
210	215	220	
Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp			
225	230	235	240
Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly			
245	250	255	
Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg			
260	265	270	
Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu			
275	280	285	
Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr			
290	295	300	
Gln Ala Leu Asp Asp Val Ser Leu			
305	310		

&lt;211&gt; 747

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

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&lt;221&gt; CDS

&lt;222&gt; (101)..(724)

&lt;223&gt; RXN02554

&lt;400&gt; 753

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ggataggctc cataaaaaata accaaaggcg gaaaatttca atg tca cac act aag 115
                                         Met Ser His Thr Lys
                                         1                               5

cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc 163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala
                        10                               15                               20

agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt 211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
                        25                               30                               35

gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg 259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
                        40                               45                               50

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc 307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
                        55                               60                               65

ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta 355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
                        70                               75                               80                               85

gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat 403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
                        90                               95                               100

ggg gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att 451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
                        105                               110                               115

att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac 499
Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
                        120                               125                               130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att 547
Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
                        135                               140                               145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595
Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
                        150                               155                               160                               165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643
Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
                        170                               175                               180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691

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Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn  
 185 190 195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744  
 Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg  
 200 205

aac

747

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 <213> Corynebacterium glutamicum

<400> 754  
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Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys  
 20 25 30

Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile  
 35 40 45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp  
 50 55 60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val  
 65 70 75 80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His  
 85 90 95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg  
 100 105 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val  
 115 120 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly  
 130 135 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala  
 145 150 155 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile  
 165 170 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe  
 180 185 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg  
 195 200 205

<210> 755  
 <211> 933

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(910)

&lt;223&gt; RXN01204

&lt;400&gt; 755

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ccgaacacgg	gagagaacgc	tgagcggtac	aacactgtcc	atg	aag	ggc	gaa	ttc	115
				Met	Lys	Gly	Glu	Phe	
				1				5	

cac	gcc	ccc	gat	ttg	gac	aaa	gaa	ttt	ttc	ccg	ggg	cac	gta	acc	gat	163
His	Ala	Pro	Asp	Leu	Asp	Lys	Glu	Phe	Phe	Pro	Gly	His	Val	Thr	Asp	
				10					15					20		

agt	ggg	gaa	gtc	gtg	aac	atg	ctg	ttc	acc	gat	ttc	gct	aat	ggg	ttg	211
Ser	Gly	Glu	Val	Val	Asn	Met	Leu	Phe	Thr	Asp	Phe	Ala	Asn	Gly	Trp	
			25				30						35			

ttc	gca	atg	gac	cgc	atc	gta	ttg	atc	cgt	ctt	ctt	atg	acg	gca	gtc	259
Phe	Ala	Met	Asp	Arg	Ile	Val	Leu	Ile	Arg	Leu	Leu	Met	Thr	Ala	Val	
		40					45					50				

gtt	gtg	gtc	ttc	ttc	ctt	tgg	gct	atg	cgc	aag	cca	aag	ctt	gtt	ccg	307
Val	Val	Val	Phe	Phe	Leu	Trp	Ala	Met	Arg	Lys	Pro	Lys	Leu	Val	Pro	
	55					60					65					

cat	ggc	gtc	cag	aat	ttt	gca	gag	tac	gca	ctc	gat	ttc	gtt	ggg	att	355
His	Gly	Val	Gln	Asn	Phe	Ala	Glu	Tyr	Ala	Leu	Asp	Phe	Val	Gly	Ile	
70					75					80				85		

cac	atc	gct	gaa	gac	atc	ctc	gga	aag	aag	aaa	ggg	cgt	cgg	ttc	ctg	403
His	Ile	Ala	Glu	Asp	Ile	Leu	Gly	Lys	Lys	Lys	Gly	Arg	Arg	Phe	Leu	
			90					95						100		

ccg	atc	ctg	gcc	acc	atc	ttc	ttc	gcg	gct	ctg	ttg	atg	aac	ctt	gca	451
Pro	Ile	Leu	Ala	Thr	Ile	Phe	Phe	Ala	Ala	Leu	Leu	Met	Asn	Leu	Ala	
			105					110					115			

acg	atc	atc	ccg	gga	cta	aac	atc	tcc	tcc	aac	tca	cgt	att	gca	ttc	499
Thr	Ile	Ile	Pro	Gly	Leu	Asn	Ile	Ser	Ser	Asn	Ser	Arg	Ile	Ala	Phe	
			120				125					130				

cca	atc	gtg	atg	gcg	gta	gct	ggg	tac	atc	gcg	ttt	atc	tac	gca	ggc	547
Pro	Ile	Val	Met	Ala	Val	Ala	Gly	Tyr	Ile	Ala	Phe	Ile	Tyr	Ala	Gly	
	135					140					145					

tct	aag	cgt	tac	gga	ttc	ttc	aaa	tat	gtg	aag	tct	tct	gtt	gtg	att	595
Ser	Lys	Arg	Tyr	Gly	Phe	Phe	Lys	Tyr	Val	Lys	Ser	Ser	Val	Val	Ile	
150					155				160					165		

ccg	aac	att	cca	cca	gca	ctt	cac	gtc	ttg	gtg	gtt	cca	att	gag	ttc	643
Pro	Asn	Ile	Pro	Pro	Ala	Leu	His	Val	Leu	Val	Val	Pro	Ile	Glu	Phe	
				170					175					180		

ttc	tct	aca	ttc	atc	ttg	agg	cca	gtc	acc	ctg	gca	ctg	cgt	ttg	atg	691
Phe	Ser	Thr	Phe	Ile	Leu	Arg	Pro	Val	Thr	Leu	Ala	Leu	Arg	Leu	Met	

185	190	195	
gcc aac ttc ctt gct ggc cac atc atc ctg gtt ctg ctt ttc tcc gca			739
Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val Leu Leu Phe Ser Ala			
200	205	210	
acg aac ttc ttc ttc ttc cag ttc aac gga tgg aca gca atg tcc ggc			787
Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp Thr Ala Met Ser Gly			
215	220	225	
gta acc atc ttg atg gca gta ctc ttc acg gtt tac gag atc att gtt			835
Val Thr Ile Leu Met Ala Val Leu Phe Thr Val Tyr Glu Ile Ile Val			
230	235	240	245
atc ttc ctg cag gca tac atc ttc gct ctg ctg gtc gct gta tac att			883
Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu Val Ala Val Tyr Ile			
250	255	260	
gag ctt tca ctt cac gcg gat tct cac tagatgaaaa aggtcgctat			930
Glu Leu Ser Leu His Ala Asp Ser His			
265	270		
taa			933
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Gly His Val Thr Asp Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp			
20	25	30	
Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu			
35	40	45	
Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys			
50	55	60	
Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu			
65	70	75	80
Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys			
85	90	95	
Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu			
100	105	110	
Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn			
115	120	125	
Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala			
130	135	140	
Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys			
145	150	155	160



Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val  
 165 170 175

Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu  
 180 185 190

Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val  
 195 200 205

Leu Leu Phe Ser Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp  
 210 215 220

Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val  
 225 230 235 240

Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu  
 245 250 255

Val Ala Val Tyr Ile Glu Leu Ser Leu His Ala Asp Ser His  
 260 265 270

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 Met Lys Gly Glu Phe  
 1 5

cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163  
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp  
 10 15 20

agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211  
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp  
 25 30 35

ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259  
 Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu Leu Met Thr Ala Val  
 40 45 50

gtt gtg gtc ttc ttc ctt tgg gct atg cgc aag cca aag ctt gtt ccg 307  
 Val Val Val Phe Phe Leu Trp Ala Met Arg Lys Pro Lys Leu Val Pro  
 55 60 65

cat ggc gtc cag aat ttt gca gag tac gca ctc gat ttc gtt ggt att 355  
 His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu Asp Phe Val Gly Ile  
 70 75 80 85

cac atc gct gaa gac atc ctc gga aag aag aaa ggt cgt cgg ttc ctg 403  
 His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys Gly Arg Arg Phe Leu

90										95					100					
ccg	atc	ctg	gcc	acc	atc	ttc	ttc	gcg	gct	ctg	ttg	atg	aac	ctt	gca	451				
Pro	Ile	Leu	Ala	Thr	Ile	Phe	Phe	Ala	Ala	Leu	Leu	Met	Asn	Leu	Ala					
			105						110					115						
acg	atc	atc	ccg	gga	cta	aac	atc	tcc	tcc	aac	tca	cgt	att	gca	ttc	499				
Thr	Ile	Ile	Pro	Gly	Leu	Asn	Ile	Ser	Ser	Asn	Ser	Arg	Ile	Ala	Phe					
			120					125					130							
cca	atc	gtg	atg	gcg	gta	gct	ggt	tac	atc	gcg	ttt	atc	tac	gca	ggc	547				
Pro	Ile	Val	Met	Ala	Val	Ala	Gly	Tyr	Ile	Ala	Phe	Ile	Tyr	Ala	Gly					
			135				140							145						
tct	aag	cgt	tac	gga	ttc	ttc	aaa	tat	gtg	aag	tct	tct	ggt	gtg	att	595				
Ser	Lys	Arg	Tyr	Gly	Phe	Phe	Lys	Tyr	Val	Lys	Ser	Ser	Val	Val	Ile					
					155					160					165					
ccg	aac	att	cca	cca	gca	ctt	cac	gtc	ttg	gtg	ggt	cca	att	gag	ttc	643				
Pro	Asn	Ile	Pro	Pro	Ala	Leu	His	Val	Leu	Val	Val	Pro	Ile	Glu	Phe					
				170					175					180						
ttc	tct	aca	ttc	atc	ttg	agg	cca	gtc	acc	ctg	gca	ctg	cgt	ttg	atg	691				
Phe	Ser	Thr	Phe	Ile	Leu	Arg	Pro	Val	Thr	Leu	Ala	Leu	Arg	Leu	Met					
			185					190						195						
gcc	aac	ttc	ctt	gct	ggc	cac	atc	atc	ctg	ggt	ctg	ctt	ttc	ttc	gca	739				
Ala	Asn	Phe	Leu	Ala	Gly	His	Ile	Ile	Leu	Val	Leu	Leu	Phe	Phe	Ala					
			200				205						210							
acg	aac	ttc	ttc	ttc	ttc	cag	ttc	aac	gga	tgg	aca	gca	atg	tcc	ggc	787				
Thr	Asn	Phe	Phe	Phe	Phe	Gln	Phe	Asn	Gly	Trp	Thr	Ala	Met	Ser	Gly					
			215				220				225									
gta	acc	atc	ttg	atg	gca	gta	ctc	ttc	acg	ggt	tac	gag	atc	att	ggt	835				
Val	Thr	Ile	Leu	Met	Ala	Val	Leu	Phe	Thr	Val	Tyr	Glu	Ile	Ile	Val					
			230			235				240					245					
atc	ttc	ctg	cag	gca	tac	atc	ttc	gct								862				
Ile	Phe	Leu	Gln	Ala	Tyr	Ile	Phe	Ala												
				250																

&lt;210&gt; 758

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 758

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Gly	His	Val	Thr	Asp	Ser	Gly	Glu	Val	Val	Asn	Met	Leu	Phe	Thr	Asp
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Phe	Ala	Asn	Gly	Trp	Phe	Ala	Met	Asp	Arg	Ile	Val	Leu	Ile	Arg	Leu
		35					40					45			

Leu	Met	Thr	Ala	Val	Val	Val	Val	Phe	Phe	Leu	Trp	Ala	Met	Arg	Lys
	50					55					60				

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu  
 65 70 75 80  
 Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys  
 85 90 95  
 Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu  
 100 105 110  
 Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn  
 115 120 125  
 Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala  
 130 135 140  
 Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys  
 145 150 155 160  
 Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val  
 165 170 175  
 Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu  
 180 185 190  
 Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val  
 195 200 205  
 Leu Leu Phe Phe Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp  
 210 215 220  
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 Met Ala Glu Leu Thr  
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 atc tcc tcc gat gag atc cgt agc gcg att gcg aac tac acc tcg agc 163  
 Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala Asn Tyr Thr Ser Ser  
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 Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly Val Val Ile Ser Ala  
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gct gac ggt atc gcc cag gtt tcg ggc ctc ccg tca gta atg gcg aat	259
Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro Ser Val Met Ala Asn	
40 45 50	
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Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly Val Ala Gln Asn Leu	
55 60 65	
gaa gct gac cga gtc ggc gtc gtg gtc ctg ggt aac tac gag cta ctt	355
Glu Ala Asp Arg Val Gly Val Val Val Leu Gly Asn Tyr Glu Leu Leu	
70 75 80 85	
aaa gaa ggc gac caa gtt cgt cgt act gga gac gtt ctg tct atc cca	403
Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp Val Leu Ser Ile Pro	
90 95 100	
gtc ggc gag gca ttc ctt ggc cgc gtt atc aac ccc ctt ggc cag cca	451
Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn Pro Leu Gly Gln Pro	
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Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu Asp Arg Val Leu Glu	
120 125 130	
ctt cag gca cca acc gtg ctt gag cgc cag cct gtc gag gag cct ttg	547
Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro Val Glu Glu Pro Leu	
135 140 145	
gca acc ggc atc aag gct atc gat gca atg acc cca atc ggc cgc ggt	595
Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr Pro Ile Gly Arg Gly	
150 155 160 165	
cag cgt cag ctg atc att ggt gac cgt aag act ggc aag acc gca gtc	643
Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr Gly Lys Thr Ala Val	
170 175 180	
tgt gtc gat acc atc ctt aac cag aag gcc aac tgg gag acc ggc gac	691
Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn Trp Glu Thr Gly Asp	
185 190 195	
aag acc aag cag gtt cgc tgc atc tac gtc gca atc ggt cag aag ggc	739
Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala Ile Gly Gln Lys Gly	
200 205 210	
tcc acc att gca gcc ctg cgt aag acc ctc gag gag cag ggc gct ctc	787
Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu Glu Gln Gly Ala Leu	
215 220 225	
gag tac acc acc atc gtg gct gca ccc gct tcc gat gct gca ggc ttc	835
Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser Asp Ala Ala Gly Phe	
230 235 240 245	
aag tgg ctt gca cca ttc gct ggc gct gct ctc gcc cag cac tgg atg	883
Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu Ala Gln His Trp Met	
250 255 260	
tac cag ggc aac cac gtc ctg gtc atc tac gat gat ctg acc aag cag	931
Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp Asp Leu Thr Lys Gln	
265 270 275	

gct gag gca tac cgt gct atc tcc ctg ctg ctg cgt cgc cca ccg ggc	979
Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly	
280 285 290	
cgc gaa gca tac cca ggt gac gtc ttc tac ctg cac tcc cgt ctg ctg	1027
Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu	
295 300 305	
gag cgc gct gcg aag ctg tcc gat gaa cta ggc gca ggt tct att aca	1075
Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly Ala Gly Ser Ile Thr	
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Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp Val Ser Ala Phe Ile	
330 335 340	
cct acc aac gtg att tcc atc acc gac ggt cag gta ttc ctt gag tcc	1171
Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln Val Phe Leu Glu Ser	
345 350 355	
gac ctg ttc aac cgt ggc gtt cgc ccg gcg atc aac gtc ggt gta tcc	1219
Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile Asn Val Gly Val Ser	
360 365 370	
gtc tcc cgt gtc ggt ggc gca gct cag acc aag ggt atg aag aag gtt	1267
Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys Gly Met Lys Lys Val	
375 380 385	
gcc ggt tct ctc cgt ctg gat ctg gct gca ttc cgc gac ctg gaa gca	1315
Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe Arg Asp Leu Glu Ala	
390 395 400 405	
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Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala Ser Lys Ser Gln Leu	
410 415 420	
gag cgt ggc cag cgc ctc gtt cag ctg ttg att cag tct gag aac gca	1411
Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile Gln Ser Glu Asn Ala	
425 430 435	
cct cag gct gtt gag tac cag atc att tct ctc tgg ctt gca ggc gaa	1459
Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu Trp Leu Ala Gly Glu	
440 445 450	
ggc gca ttc gac aac gtt cct gtt gaa gat gtt cgt cgc ttc gag tcc	1507
Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val Arg Arg Phe Glu Ser	
455 460 465	
gaa ctg cac gag tac tta ggc tcc aac gct gca cag gtc tac gag cag	1555
Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala Gln Val Tyr Glu Gln	
470 475 480 485	
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Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser Lys Glu Thr Leu Leu	
490 495 500	
aag gca acc gaa gat ttc aag agc gct ttc cag acc acc gat ggc acc	1651
Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln Thr Thr Asp Gly Thr	
505 510 515	
cct gtc atc aac gag cct gag gtt gaa gca ctc gat gca ggc cag gtc	1699

Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu Asp Ala Gly Gln Val  
 520 525 530

aag aaa gac cag ctc acc gtt tcc cgc aag gtc agc aag aag 1741  
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taaggcagcg agcctacact aaa 1764

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<212> PRT

<213> Corynebacterium glutamicum

<400> 760

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Val Val Ile Ser Ala Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro  
 35 40 45

Ser Val Met Ala Asn Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly  
 50 55 60

Val Ala Gln Asn Leu Glu Ala Asp Arg Val Gly Val Val Val Leu Gly  
 65 70 75 80

Asn Tyr Glu Leu Leu Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp  
 85 90 95

Val Leu Ser Ile Pro Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn  
 100 105 110

Pro Leu Gly Gln Pro Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu  
 115 120 125

Asp Arg Val Leu Glu Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro  
 130 135 140

Val Glu Glu Pro Leu Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr  
 145 150 155 160

Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr  
 165 170 175

Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn  
 180 185 190

Trp Glu Thr Gly Asp Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala  
 195 200 205

Ile Gly Gln Lys Gly Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu  
 210 215 220

Glu Gln Gly Ala Leu Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser  
 225 230 235 240

Asp Ala Ala Gly Phe Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu  
 245 250 255  
 Ala Gln His Trp Met Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp  
 260 265 270  
 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu  
 275 280 285  
 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu  
 290 295 300  
 His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly  
 305 310 315 320  
 Ala Gly Ser Ile Thr Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp  
 325 330 335  
 Val Ser Ala Phe Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln  
 340 345 350  
 Val Phe Leu Glu Ser Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile  
 355 360 365  
 Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys  
 370 375 380  
 Gly Met Lys Lys Val Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe  
 385 390 395 400  
 Arg Asp Leu Glu Ala Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala  
 405 410 415  
 Ser Lys Ser Gln Leu Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile  
 420 425 430  
 Gln Ser Glu Asn Ala Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu  
 435 440 445  
 Trp Leu Ala Gly Glu Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val  
 450 455 460  
 Arg Arg Phe Glu Ser Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala  
 465 470 475 480  
 Gln Val Tyr Glu Gln Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser  
 485 490 495  
 Lys Glu Thr Leu Leu Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln  
 500 505 510  
 Thr Thr Asp Gly Thr Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu  
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 <223> RXN01193

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 Met Thr Thr Ala Leu  
 1 5  
 gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163  
 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg  
 10 15 20  
 gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211  
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro  
 25 30 35  
 gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259  
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys  
 40 45 50  
 aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307  
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile  
 55 60 65  
 cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355  
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala  
 70 75 80 85  
 gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403  
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val  
 90 95 100  
 aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451  
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser  
 105 110 115  
 ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499  
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro  
 120 125 130  
 cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc 547  
 Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly  
 135 140 145  
 atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc 595  
 Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile  
 150 155 160 165  
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 Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu  
 170 175 180



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Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala	
185 190 195	
ggt gtt ggt gag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg	739
Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met	
200 205 210	
gaa gaa atg ggc gtt ctc cag gac acc gcc ctg gtg ttc ggt cag atg	787
Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu Val Phe Gly Gln Met	
215 220 225	
gat gag cca cca gga gtc ggt atg cgc gtg gct ctg tcc ggc ctg acc	835
Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala Leu Ser Gly Leu Thr	
230 235 240 245	
atg gcg gag tac ttc cgc gat gtt cag aac cag gac gtg ctg ctg ttc	883
Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe	
250 255 260	
atc gac aac atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc	931
Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr	
265 270 275	
ctt ctg ggt cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct	979
Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala	
280 285 290	
gac gag atg ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt	1027
Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg	
295 300 305	
tcg att acc tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc	1075
Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr	
310 315 320 325	
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Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu	
330 335 340	
ctt gac cgc tcc att gct tcc aag ggt att tac cca gca gtg aac cca	1171
Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro	
345 350 355	
ctg acc tcc acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt	1219
Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg	
360 365 370	
cac tac gag gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag	1267
His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys	
375 380 385	
gaa ctt cag gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa	1315
Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu	
390 395 400 405	
gag gac aag atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg	1363
Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu	
410 415 420	
ggt cag aac ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc	1411

Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser  
 425 430 435

tac gtg cca ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac 1459  
 Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn  
 440 445 450

ggc gac ttc gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt 1507  
 Gly Asp Phe Asp His Tyr Pro Glu Lys Ala Phe Asn Gly Leu Gly Gly  
 455 460 465

ttg gac gat gtc gaa gct gca tac aag aag ctg acc gga aag 1549  
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Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr  
 35 40 45

Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu  
 50 55 60

Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu  
 65 70 75 80

Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro  
 85 90 95

Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys  
 100 105 110

Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly  
 115 120 125

Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu  
 130 135 140

Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val  
 145 150 155 160

Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr  
 165 170 175

Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly  
 180 185 190

Thr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp

195					200					205					
Leu	Phe	Leu	Glu	Met	Glu	Glu	Met	Gly	Val	Leu	Gln	Asp	Thr	Ala	Leu
210					215					220					
Val	Phe	Gly	Gln	Met	Asp	Glu	Pro	Pro	Gly	Val	Gly	Met	Arg	Val	Ala
225					230					235					240
Leu	Ser	Gly	Leu	Thr	Met	Ala	Glu	Tyr	Phe	Arg	Asp	Val	Gln	Asn	Gln
				245					250					255	
Asp	Val	Leu	Leu	Phe	Ile	Asp	Asn	Ile	Phe	Arg	Phe	Thr	Gln	Ala	Gly
			260					265					270		
Ser	Glu	Val	Ser	Thr	Leu	Leu	Gly	Arg	Met	Pro	Ser	Ala	Val	Gly	Tyr
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Gln	Pro	Thr	Leu	Ala	Asp	Glu	Met	Gly	Val	Leu	Gln	Glu	Arg	Ile	Thr
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Ser	Thr	Lys	Gly	Arg	Ser	Ile	Thr	Ser	Leu	Gln	Ala	Val	Tyr	Val	Pro
305					310					315					320
Ala	Asp	Asp	Tyr	Thr	Asp	Pro	Ala	Pro	Ala	Thr	Thr	Phe	Ala	His	Leu
				325					330					335	
Asp	Ala	Thr	Thr	Glu	Leu	Asp	Arg	Ser	Ile	Ala	Ser	Lys	Gly	Ile	Tyr
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Pro	Ala	Val	Asn	Pro	Leu	Thr	Ser	Thr	Ser	Arg	Ile	Leu	Glu	Pro	Ala
			355				360					365			
Ile	Val	Gly	Glu	Arg	His	Tyr	Glu	Val	Ser	Gln	Arg	Val	Ile	Gly	Ile
			370				375					380			
Leu	Gln	Lys	Asn	Lys	Glu	Leu	Gln	Asp	Ile	Ile	Ala	Ile	Leu	Gly	Met
385					390					395					400
Asp	Glu	Leu	Ser	Glu	Glu	Asp	Lys	Ile	Thr	Val	Ala	Arg	Ala	Arg	Arg
				405					410				415		
Ile	Glu	Arg	Phe	Leu	Gly	Gln	Asn	Phe	Phe	Val	Ala	Glu	Lys	Phe	Thr
			420					425					430		
Gly	Leu	Pro	Gly	Ser	Tyr	Val	Pro	Leu	Thr	Asp	Thr	Val	Asp	Ala	Phe
			435				440					445			
Glu	Arg	Ile	Cys	Asn	Gly	Asp	Phe	Asp	His	Tyr	Pro	Glu	Gln	Ala	Phe
			450				455					460			
Asn	Gly	Leu	Gly	Gly	Leu	Asp	Asp	Val	Glu	Ala	Ala	Tyr	Lys	Lys	Leu
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Thr	Gly	Lys													

&lt;210&gt; 763

&lt;211&gt; 778

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (15)..(755)

&lt;223&gt; FRXA01193

&lt;400&gt; 763

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Tyr	Phe	Arg	Asp	Val	Gln	Asn	Gln	Asp	Val	Leu	Leu	Phe	Ile	Asp	Asn	
	15						20					25				
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Ile	Phe	Arg	Phe	Thr	Gln	Ala	Gly	Ser	Glu	Val	Ser	Thr	Leu	Leu	Gly	
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cgt	atg	cct	tcc	gcc	gtg	ggg	tac	cag	cca	acc	ctg	gct	gac	gag	atg	194
Arg	Met	Pro	Ser	Ala	Val	Gly	Tyr	Gln	Pro	Thr	Leu	Ala	Asp	Glu	Met	
	45				50					55					60	
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Gly	Val	Leu	Gln	Glu	Arg	Ile	Thr	Ser	Thr	Lys	Gly	Arg	Ser	Ile	Thr	
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tct	ctg	cag	gcc	gtt	tac	gtt	cct	gcc	gat	gac	tac	acc	gac	ccg	gct	290
Ser	Leu	Gln	Ala	Val	Tyr	Val	Pro	Ala	Asp	Asp	Tyr	Thr	Asp	Pro	Ala	
			80					85					90			
cca	gcg	acc	acc	ttc	gct	cac	ttg	gat	gca	acc	acc	gag	ctt	gac	cgc	338
Pro	Ala	Thr	Thr	Phe	Ala	His	Leu	Asp	Ala	Thr	Thr	Glu	Leu	Asp	Arg	
		95					100					105				
tcc	att	gct	tcc	aag	ggg	att	tac	cca	gca	gtg	aac	cca	ctg	acc	tcc	386
Ser	Ile	Ala	Ser	Lys	Gly	Ile	Tyr	Pro	Ala	Val	Asn	Pro	Leu	Thr	Ser	
	110					115					120					
acc	tct	cgt	att	ctc	gag	cca	gca	atc	gtt	ggg	gag	cgt	cac	tac	gag	434
Thr	Ser	Arg	Ile	Leu	Glu	Pro	Ala	Ile	Val	Gly	Glu	Arg	His	Tyr	Glu	
	125				130				135						140	
gtt	tct	cag	cgt	gtc	atc	ggc	att	ctg	cag	aag	aac	aag	gaa	ctt	cag	482
Val	Ser	Gln	Arg	Val	Ile	Gly	Ile	Leu	Gln	Lys	Asn	Lys	Glu	Leu	Gln	
				145				150						155		
gac	atc	atc	gcc	atc	ctt	ggg	atg	gac	gag	ctt	tct	gaa	gag	gac	aag	530
Asp	Ile	Ile	Ala	Ile	Leu	Gly	Met	Asp	Glu	Leu	Ser	Glu	Glu	Asp	Lys	
			160					165					170			
atc	acc	gtt	gca	cgt	gcg	cgt	cgc	atc	gag	cgc	ttc	ctg	ggg	cag	aac	578
Ile	Thr	Val	Ala	Arg	Ala	Arg	Arg	Ile	Glu	Arg	Phe	Leu	Gly	Gln	Asn	
		175					180					185				
ttc	ttc	gtt	gca	gag	aag	ttc	acc	ggg	ctt	cct	ggc	tcc	tac	gtg	cca	626
Phe	Phe	Val	Ala	Glu	Lys	Phe	Thr	Gly	Leu	Pro	Gly	Ser	Tyr	Val	Pro	
	190					195					200					
ctg	acc	gac	acc	gtc	gac	gct	ttc	gag	cgt	att	tgc	aac	ggc	gac	ttc	674
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			20					25					30			
Thr	Gln	Ala	Gly	Ser	Glu	Val	Ser	Thr	Leu	Leu	Gly	Arg	Met	Pro	Ser	
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Ala	Val	Gly	Tyr	Gln	Pro	Thr	Leu	Ala	Asp	Glu	Met	Gly	Val	Leu	Gln	
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Glu	Arg	Ile	Thr	Ser	Thr	Lys	Gly	Arg	Ser	Ile	Thr	Ser	Leu	Gln	Ala	
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Val	Tyr	Val	Pro	Ala	Asp	Asp	Tyr	Thr	Asp	Pro	Ala	Pro	Ala	Thr	Thr	
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Phe	Ala	His	Leu	Asp	Ala	Thr	Thr	Glu	Leu	Asp	Arg	Ser	Ile	Ala	Ser	
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Lys	Gly	Ile	Tyr	Pro	Ala	Val	Asn	Pro	Leu	Thr	Ser	Thr	Ser	Arg	Ile	
		115					120					125				
Leu	Glu	Pro	Ala	Ile	Val	Gly	Glu	Arg	His	Tyr	Glu	Val	Ser	Gln	Arg	
	130					135					140					
Val	Ile	Gly	Ile	Leu	Gln	Lys	Asn	Lys	Glu	Leu	Gln	Asp	Ile	Ile	Ala	
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Ile	Leu	Gly	Met	Asp	Glu	Leu	Ser	Glu	Glu	Asp	Lys	Ile	Thr	Val	Ala	
				165					170					175		
Arg	Ala	Arg	Arg	Ile	Glu	Arg	Phe	Leu	Gly	Gln	Asn	Phe	Phe	Val	Ala	
			180					185					190			
Glu	Lys	Phe	Thr	Gly	Leu	Pro	Gly	Ser	Tyr	Val	Pro	Leu	Thr	Asp	Thr	
		195					200					205				
Val	Asp	Ala	Phe	Glu	Arg	Ile	Cys	Asn	Gly	Asp	Phe	Asp	His	Tyr	Pro	
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Tyr Lys Lys Leu Thr Gly Lys  
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(739)

<223> FRXA01203

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 Met Thr Thr Ala Leu  
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gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163  
 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg  
 10 15 20

gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211  
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro  
 25 30 35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259  
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys  
 40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307  
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile  
 55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355  
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala  
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403  
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val  
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451  
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser  
 105 110 115

ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499  
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro  
 120 125 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc 547  
 Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly  
 135 140 145

atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc 595

Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile  
 150 155 160 165

ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa 643  
 Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu  
 170 175 180

atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca 691  
 Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala  
 185 190 195

ggt gtt ggt aag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg 739  
 Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met  
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Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr  
 35 40 45

Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu  
 50 55 60

Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu  
 65 70 75 80

Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro  
 85 90 95

Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys  
 100 105 110

Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly  
 115 120 125

Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu  
 130 135 140

Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val  
 145 150 155 160

Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr  
 165 170 175

Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly  
 180 185 190

Thr Ser Val Phe Ala Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp  
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Leu Phe Leu Glu Met  
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<212> DNA  
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<223> RXN02821

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Met Asn Glu Ile Ile  
1 5  
ctg gca cag gac gca acc gag tcc acc atc acc gga ctt ggc gct gtc 163  
Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr Gly Leu Gly Ala Val  
10 15 20  
ggc tac ggc atc gca acc atc gga cct ggc ctc ggc atc ggc atc ctg 211  
Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu  
25 30 35  
gtt ggt aag gct ctc gag ggt atg gca cgt cag cct gag atg gct gga 259  
Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly  
40 45 50  
cag ctc cgt acc acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg 307  
Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu  
55 60 65  
gca ctg atc ggc ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga 360  
Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe  
70 75 80  
aag 363

<210> 768  
<211> 80  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 768  
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Gly Leu Gly Ala Val Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu  
20 25 30  
Gly Ile Gly Ile Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln  
35 40 45  
Pro Glu Met Ala Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala  
50 55 60



Phe Val Glu Ala Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe  
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 Val Gly Tyr Gly Ile  
 1 5  
 gca acc atc gga cct ggc ctc ggc atc ggc atc ttg gtt ggt aag gct 163  
 Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu Val Gly Lys Ala  
 10 15 20  
 ctc gag ggt atg gca cgt cag cct gag atg gct gga cag ctc cgt acc 211  
 Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly Gln Leu Arg Thr  
 25 30 35  
 acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg gca ctg atc ggc 259  
 Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu Ala Leu Ile Gly  
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 ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga aag 303  
 Leu Val Ala Gly Phe Leu Phe  
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 20 25 30  
 Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala  
 35 40 45  
 Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe  
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 <222> (1)..(609)  
 <223> RXA01200

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 1 5 10 15  
 gac gcc gca gag cag acc tgg tcc act cca cgc gag ttc cgc gct gga 96  
 Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly  
 20 25 30  
 cta gtc caa ctt ggc cgt cgc gcc ctt ctt cgc tct gcg gag aaa cag 144  
 Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln  
 35 40 45  
 ggt cag ctt ggt cag gtg gaa gat gaa ctg ttc cga ctc agc cga atc 192  
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile  
 50 55 60  
 ctg gat cgc gaa agc aag ctg act cag ctt ctt tca gat cgc act cag 240  
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln  
 65 70 75 80  
 gaa att ggc ggt cga cgt gac ctc ctg gct aag gtg ctc tac ggc aag 288  
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys  
 85 90 95  
 gta act gct gtt acc gaa gcc ctc gca ctg cag gct att ggt cgc cct 336  
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro  
 100 105 110  
 gag cac aac cca att gac gat atc gca gct ttg gct ggc gct gta gca 384  
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala  
 115 120 125  
 gag cta cag ggt cgt tcc gtt gca cat gtc gtt acc gca gtt gaa ctc 432  
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu  
 130 135 140  
 aac gag gga cag caa caa gcg cta gct gaa aag ctg gga cgt att tat 480  
 Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr  
 145 150 155 160  
 ggt cgt gcg atg agc atc cac tcc gag gtt gat acc agc ctc ctc ggt 528  
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly  
 165 170 175  
 gga atg atc atc cgc gtc gga gac gaa gta att gac ggc agc acc tcg 576  
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser  
 180 185 190  
 ggc aaa ctc gag cgt ctg cgg gca agc ttc gca taaagacacg acgaattaga 629  
 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala

195

200

caa

632

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           20                  25                  30  
 Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln  
           35                  40                  45  
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile  
       50                  55                  60  
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln  
   65                  70                  75                  80  
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys  
           85                  90                  95  
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro  
           100                  105                  110  
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala  
       115                  120                  125  
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu  
   130                  135                  140  
 Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr  
  145                  150                  155                  160  
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly  
           165                  170                  175  
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser  
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 <223> RXA01194

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<213> Corynebacterium glutamicum

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			20					25					30		
Gly	Val	Leu	Pro	Asp	His	Glu	Pro	Leu	Leu	Gly	Gln	Leu	Val	Glu	Asn
		35				40						45			
Gly	Val	Val	Thr	Ile	Gln	Pro	Ile	Asp	Gly	Glu	Lys	Leu	Ile	Ala	Gly
	50					55					60				
Val	Ser	Asp	Gly	Phe	Leu	Ser	Val	Ser	Lys	Glu	Lys	Val	Thr	Ile	Leu
65				70						75				80	

Ala Asp Phe Ala Val Trp Ala Asn Glu Val Asp Thr Ala Ser Ala Glu  
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Ala Asp Leu Asn Ser Asp Asp Glu Leu Ala Lys Ala His Ala Glu Ala  
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Gly Leu Arg Ala Val Arg Arg Ser Ser Glu Gly Leu  
115 120

<210> 775

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1075)

<223> RXA01202

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Met Ala Thr Ile Arg  
1 5

gaa ttg cgt gac cga att cgt tcg gtt aac tca acc aag aag atc acc 163  
Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser Thr Lys Lys Ile Thr  
10 15 20

aag gct caa gag ctc atc gcc acc tct cgc atc acc aag gca cag ggt 211  
Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile Thr Lys Ala Gln Gly  
25 30 35

cgc gtc gcg gca gct gcg ccg tac gcc gag gaa atc cag cgc gtg ctg 259  
Arg Val Ala Ala Ala Pro Tyr Ala Glu Glu Ile Gln Arg Val Leu  
40 45 50

gag cgc ctc gcg tcg gca agc tcc cta gac cac cca atg ctg cgt gag 307  
Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His Pro Met Leu Arg Glu  
55 60 65

cgt gaa ggc ggc aag cga gcc gcc gtg ctc gtg gtt act tct gac cgc 355  
Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val Val Thr Ser Asp Arg  
70 75 80 85

ggc atg gct ggt ggc tac aac cac aac gtt ctg aaa aag gca gcg gag 403  
Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu Lys Lys Ala Ala Glu  
90 95 100

ctg gaa aag ctt ctt gct gaa agt gga tac gaa gtg gtt cgt tat gtc 451  
Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu Val Val Arg Tyr Val  
105 110 115

acc ggc aaa aag ggc gtc gac tac tac aag ttc cgc gct gaa gat gtg 499  
Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe Arg Ala Glu Asp Val  
120 125 130

gct ggc acc tgg act gga ttc tca cag gat cca gac tgg gca gct acc 547  
Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro Asp Trp Ala Ala Thr

135	140	145	
cac aac gtg cgc cgt	cac ctc att gat ggt	ttc acc gcc agc tct gaa	595
His Asn Val Arg Arg	His Leu Ile Asp Gly	Phe Thr Ala Ser Ser Glu	
150	155	160 165	
ggt gaa gct gca tgg	cgc gag gga ctg aac	cta cca gaa ggc cag gat	643
Gly Glu Ala Ala Trp	Arg Glu Gly Leu Asn	Leu Pro Glu Gly Gln Asp	
	170	175 180	
atc cag ggc ttc gac	cag gtt cac gtg gtc	tac acc gag ttc atc tcc	691
Ile Gln Gly Phe Asp	Gln Val His Val Val	Tyr Thr Glu Phe Ile Ser	
	185	190 195	
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Met Leu Thr Gln Asn	Pro Val Val His Gln	Leu Leu Pro Val Glu Pro	
	200	205 210	
gtc atc gaa gat gaa	att ttc gaa aaa ggc	gag gat ctg ctg tcc tct	787
Val Ile Glu Asp Glu	Ile Phe Glu Lys Gly	Glu Asp Leu Leu Ser Ser	
	215	220 225	
tcc ggc gaa gtc gaa	ccc gac tac gag ttc	gag ccg gat gca gac act	835
Ser Gly Glu Val Glu	Pro Asp Tyr Glu Phe	Glu Pro Asp Ala Asp Thr	
	230	235 240 245	
ctg ctt gag gca ctg	ctt ccg cag tac gtc	tct cgt agg ctg ttc tcc	883
Leu Leu Glu Ala Leu	Pro Gln Tyr Val Ser	Arg Arg Leu Phe Ser	
	250	255 260	
atc ttc ttg gag gct	gca gct gca gag tcc	gct tca cgt cga aac gcg	931
Ile Phe Leu Glu Ala	Ala Ala Ala Glu Ser	Ala Ser Arg Arg Asn Ala	
	265	270 275	
atg aag tct gcg act	gac aac gct acg gaa	ctg gtc aag gac ctg tcc	979
Met Lys Ser Ala Thr	Asp Asn Ala Thr Glu	Leu Val Lys Asp Leu Ser	
	280	285 290	
cgt gtg gcc aac cag	gca cgt cag gca cag	atc acc cag gaa atc aca	1027
Arg Val Ala Asn Gln	Ala Arg Gln Ala Gln	Ile Thr Gln Glu Ile Thr	
	295	300 305	
gag att gtt ggt ggc	gca ggc gcg ctc gcc	gac agc gga gaa agt gac	1075
Glu Ile Val Gly Gly	Ala Gly Ala Leu Ala	Asp Ser Gly Glu Ser Asp	
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taattatgac tacagctctt	gaa		1098

&lt;210&gt; 776

&lt;211&gt; 325

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 776

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Thr	Lys	Lys	Ile	Thr	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Thr	Ser	Arg	Ile
			20					25					30		

Thr Lys Ala Gln Gly Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu  
 35 40 45  
 Ile Gln Arg Val Leu Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His  
 50 55 60  
 Pro Met Leu Arg Glu Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val  
 65 70 75 80  
 Val Thr Ser Asp Arg Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu  
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 Lys Lys Ala Ala Glu Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu  
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 Val Val Arg Tyr Val Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe  
 115 120 125  
 Arg Ala Glu Asp Val Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro  
 130 135 140  
 Asp Trp Ala Ala Thr His Asn Val Arg Arg His Leu Ile Asp Gly Phe  
 145 150 155 160  
 Thr Ala Ser Ser Glu Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu  
 165 170 175  
 Pro Glu Gly Gln Asp Ile Gln Gly Phe Asp Gln Val His Val Val Tyr  
 180 185 190  
 Thr Glu Phe Ile Ser Met Leu Thr Gln Asn Pro Val Val His Gln Leu  
 195 200 205  
 Leu Pro Val Glu Pro Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu  
 210 215 220  
 Asp Leu Leu Ser Ser Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu  
 225 230 235 240  
 Pro Asp Ala Asp Thr Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser  
 245 250 255  
 Arg Arg Leu Phe Ser Ile Phe Leu Glu Ala Ala Ala Ala Glu Ser Ala  
 260 265 270  
 Ser Arg Arg Asn Ala Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu  
 275 280 285  
 Val Lys Asp Leu Ser Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile  
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 Ser Gly Glu Ser Asp  
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<210> 777  
 <211> 1773  
 <212> DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1750)

&lt;223&gt; RXN02434

&lt;400&gt; 777

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                                         Met Arg Thr Phe Ala
                                         1           5

gct tat att gcc att gat ggc ctc agc ttt tcc tac ccc aac acc cac 163
Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser Tyr Pro Asn Thr His
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gtt tta agc gat att tcg ctc acc gtt gcc aat ggc gat atc gcc gga 211
Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn Gly Asp Ile Ala Gly
                25                30                35

ctg att ggt gaa aac ggc gca gga aaa tcc acc ctg ctc agc ctc atc 259
Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Leu Ile
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gct ggc gtc atg gaa ccc gac cag ggc agg att tac ctc ccc gaa cgc 307
Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile Tyr Leu Pro Glu Arg
                55                60                65

acc gga ttc atc gcc caa gaa aca gac tta ccg ttt gaa caa ccc gtg 355
Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro Phe Glu Gln Pro Val
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cag tcg ctt atc gac gcc gcc gtc gcc cca gtg cgc gcg gtc gat gcc 403
Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val Arg Ala Val Asp Ala
                90                95                100

gcg att aca gat ttg tcc acc aag ctt ggc gac gcc tcc ctc agc gcc 451
Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp Ala Ser Leu Ser Ala
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gaa gag cag gcg caa gtc gcc aca gat ttc gat gca gcg cta ggc gct 499
Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp Ala Ala Leu Gly Ala
                120                125                130

gca gaa gaa ctc gga ctg tgg gaa tta gat gca cgt att gaa acc atc 547
Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala Arg Ile Glu Thr Ile
                135                140                145

gtc gcg ggt ctc ggc ctt gcc gag gtg gat cgc agc act ccc att ggt 595
Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg Ser Thr Pro Ile Gly
                150                155                160                165

gag ctt tcc ggc ggt cag cgc cgc aga ttc gca ttg gca gcg ctg ctg 643
Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala Leu Ala Ala Leu Leu
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ttg gaa cca cac gat gct ctg att ttc gat gag ccc acc aac cac ctc 691
Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu Pro Thr Asn His Leu
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ggt	cca	gtg	ctg	atc	gcc	agc	cac	gat	cgc	ttc	ttc	ctc	gac	tcc	gtc	787
Gly	Pro	Val	Leu	Ile	Ala	Ser	His	Asp	Arg	Phe	Phe	Leu	Asp	Ser	Val	
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tgt	acc	gag	tta	atc	gac	ctc	gat	cct	gca	ctt	gga	cct	gag	ggc	gga	835
Cys	Thr	Glu	Leu	Ile	Asp	Leu	Asp	Pro	Ala	Leu	Gly	Pro	Glu	Gly	Gly	
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tcc	ggc	gaa	gaa	gta	aaa	caa	gcc	gtg	tct	ttt	ggt	ggt	gga	ttt	tct	883
Ser	Gly	Glu	Glu	Val	Lys	Gln	Ala	Val	Ser	Phe	Gly	Gly	Gly	Phe	Ser	
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Glu	Tyr	Ile	Lys	Glu	Arg	Glu	Thr	Arg	Arg	Thr	Arg	Trp	Ala	Gln	Leu	
			265					270					275			
tac	acc	gca	caa	gaa	acc	gag	cgg	gaa	aaa	ctc	gaa	gaa	acc	acc	ggc	979
Tyr	Thr	Ala	Gln	Glu	Thr	Glu	Arg	Glu	Lys	Leu	Glu	Glu	Thr	Thr	Gly	
		280					285					290				
acc	acc	gaa	tcg	gat	att	ttc	cac	agc	tcg	gtt	tcc	aaa	tcg	gaa	gct	1027
Thr	Thr	Glu	Ser	Asp	Ile	Phe	His	Ser	Ser	Val	Ser	Lys	Ser	Glu	Ala	
	295					300					305					
aaa	atc	acc	gcg	aaa	ttt	tac	gca	gac	cgg	gca	gct	aaa	act	caa	ggc	1075
Lys	Ile	Thr	Ala	Lys	Phe	Tyr	Ala	Asp	Arg	Ala	Ala	Lys	Thr	Gln	Gly	
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aac	cgc	gtc	cgc	tcc	gcc	aaa	aac	cgc	ctg	aag	gaa	ttg	gaa	cgc	tat	1123
Asn	Arg	Val	Arg	Ser	Ala	Lys	Asn	Arg	Leu	Lys	Glu	Leu	Glu	Arg	Tyr	
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Glu	Ile	Pro	Ala	Pro	Pro	Lys	Pro	Leu	Glu	Phe	Gln	Gly	Ile	Pro	Glu	
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Ala	Ser	Gly	Asn	Gly	His	Gly	Glu	Thr	Leu	Glu	Val	Arg	Ala	Ile	Ala	
		360					365					370				
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Val	Glu	Asn	Arg	Leu	Gln	Pro	Leu	Thr	Phe	His	Ile	Asp	Pro	Gly	Asp	
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cac	atc	ctg	gtc	gaa	ggc	ccc	aac	ggt	gtc	ggt	aaa	tcc	acc	ctg	ctg	1315
His	Ile	Leu	Val	Glu	Gly	Pro	Asn	Gly	Val	Gly	Lys	Ser	Thr	Leu	Leu	
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Ser	Val	Leu	Glu	Gly	Val	Leu	Glu	Pro	Thr	Glu	Gly	Glu	Leu	Ile	Val	
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ccc	gaa	ggg	ctg	aaa	gtt	gcg	cgc	ctg	aaa	cag	gac	gat	cag	tgg	acg	1411
Pro	Glu	Gly	Leu	Lys	Val	Ala	Arg	Leu	Lys	Gln	Asp	Asp	Gln	Trp	Thr	
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 Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met Gly Leu Leu Arg Glu  
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cgc gtc tcg ctc ggg ctc atc ctg gcg agc cca cca gat ctt ttg ctt 1603  
 Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro Pro Asp Leu Leu Leu  
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ctt gac gag ccc acc aac cac ctc tcc ctc gcg ctg agc gaa gaa ctc 1651  
 Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala Leu Ser Glu Glu Leu  
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 520 525 530

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&lt;210&gt; 778

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 778

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Gly Asp Ile Ala Gly Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr  
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Leu Leu Ser Leu Ile Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile  
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Tyr Leu Pro Glu Arg Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro  
 65 70 75 80

Phe Glu Gln Pro Val Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val  
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Arg Ala Val Asp Ala Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp  
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Ala Ser Leu Ser Ala Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp

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Ala	Ala	Leu	Gly	Ala	Ala	Glu	Glu	Leu	Gly	Leu	Trp	Glu	Leu	Asp	Ala
130					135					140					
Arg	Ile	Glu	Thr	Ile	Val	Ala	Gly	Leu	Gly	Leu	Ala	Glu	Val	Asp	Arg
145					150					155					160
Ser	Thr	Pro	Ile	Gly	Glu	Leu	Ser	Gly	Gly	Gln	Arg	Arg	Arg	Phe	Ala
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Leu	Ala	Ala	Leu	Leu	Leu	Glu	Pro	His	Asp	Ala	Leu	Ile	Phe	Asp	Glu
			180					185					190		
Pro	Thr	Asn	His	Leu	Asp	Asp	Thr	Ala	Val	Asp	Phe	Leu	Ile	Ser	Glu
			195				200					205			
Ile	Ser	Arg	Phe	Lys	Gly	Pro	Val	Leu	Ile	Ala	Ser	His	Asp	Arg	Phe
			210			215					220				
Phe	Leu	Asp	Ser	Val	Cys	Thr	Glu	Leu	Ile	Asp	Leu	Asp	Pro	Ala	Leu
225					230					235					240
Gly	Pro	Glu	Gly	Gly	Ser	Gly	Glu	Glu	Val	Lys	Gln	Ala	Val	Ser	Phe
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Gly	Gly	Gly	Phe	Ser	Glu	Tyr	Ile	Lys	Glu	Arg	Glu	Thr	Arg	Arg	Thr
			260					265					270		
Arg	Trp	Ala	Gln	Leu	Tyr	Thr	Ala	Gln	Glu	Thr	Glu	Arg	Glu	Lys	Leu
		275					280					285			
Glu	Glu	Thr	Thr	Gly	Thr	Thr	Glu	Ser	Asp	Ile	Phe	His	Ser	Ser	Val
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Ser	Lys	Ser	Glu	Ala	Lys	Ile	Thr	Ala	Lys	Phe	Tyr	Ala	Asp	Arg	Ala
305					310					315					320
Ala	Lys	Thr	Gln	Gly	Asn	Arg	Val	Arg	Ser	Ala	Lys	Asn	Arg	Leu	Lys
				325					330					335	
Glu	Leu	Glu	Arg	Tyr	Glu	Ile	Pro	Ala	Pro	Pro	Lys	Pro	Leu	Glu	Phe
			340					345					350		
Gln	Gly	Ile	Pro	Glu	Ala	Ser	Gly	Asn	Gly	His	Gly	Glu	Thr	Leu	Glu
		355					360					365			
Val	Arg	Ala	Ile	Ala	Val	Glu	Asn	Arg	Leu	Gln	Pro	Leu	Thr	Phe	His
		370				375					380				
Ile	Asp	Pro	Gly	Asp	His	Ile	Leu	Val	Glu	Gly	Pro	Asn	Gly	Val	Gly
385					390					395					400
Lys	Ser	Thr	Leu	Leu	Ser	Val	Leu	Glu	Gly	Val	Leu	Glu	Pro	Thr	Glu
				405					410					415	
Gly	Glu	Leu	Ile	Val	Pro	Glu	Gly	Leu	Lys	Val	Ala	Arg	Leu	Lys	Gln
			420					425					430		
Asp	Asp	Gln	Trp	Thr	Glu	Lys	Gln	Leu	Asn	Thr	Pro	Val	Asp	Glu	Leu
		435					440					445			

Phe Ala Ala Leu Ser Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met  
 450 455 460  
 Gly Leu Leu Arg Glu Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser  
 465 470 475 480  
 Leu Gly Gln Arg Arg Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro  
 485 490 495  
 Pro Asp Leu Leu Leu Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala  
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<210> 779  
 <211> 1407  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1384)  
 <223> RXN00684

<400> 779

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gag tcc acc agc cat cac ggc tac cag cct ttc gat atg cac aac ccg 211  
 Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe Asp Met His Asn Pro  
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 Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu Pro Val Met Phe Asp  
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gag cgc atc ggc tac tgg gtg gta acc aaa tat gac gac atc aaa acc 307  
 Glu Arg Ile Gly Tyr Trp Val Thr Lys Tyr Asp Asp Ile Lys Thr  
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acc ttt gat gac tgg gaa aca ttc tcc tct gaa aat gca caa gcc cca 355  
 Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu Asn Ala Gln Ala Pro  
 70 75 80 85

gtc cgc aag cgt gga cct cag gca acc caa atc atg acc gat ggc ggc 403

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Phe	Thr	Ala	Tyr	Ser	Gly	Leu	Ser	Ala	Arg	Ile	Pro	Pro	Glu	His	Thr		
			105					110					115				
cgc	atc	cgc	gca	atc	gca	caa	aag	gcc	ttc	acg	cca	cgc	cgc	tat	aaa	499	
Arg	Ile	Arg	Ala	Ile	Ala	Gln	Lys	Ala	Phe	Thr	Pro	Arg	Arg	Tyr	Lys		
			120				125					130					
gca	ctc	gaa	cca	gat	atc	cga	gca	atg	gtg	att	gat	cgt	gtg	gag	aaa	547	
Ala	Leu	Glu	Pro	Asp	Ile	Arg	Ala	Met	Val	Ile	Asp	Arg	Val	Glu	Lys		
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Tyr	Asp	Ile	Pro	Thr	Ile	Thr	Ile	Leu	Thr	Leu	Ile	Gly	Ala	Asp	Ile		
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ttc	atg	gtg	gtc	acc	tac	aag	cgg	tgg	tca	gat	tcc	cgt	gcg	gcc	atg	691	
Phe	Met	Val	Val	Thr	Tyr	Lys	Arg	Trp	Ser	Asp	Ser	Arg	Ala	Ala	Met		
			185					190					195				
acc	tgg	ggc	gat	ctt	agt	gat	gaa	gag	cag	atc	cca	cac	gca	cac	aat	739	
Thr	Trp	Gly	Asp	Leu	Ser	Asp	Glu	Glu	Gln	Ile	Pro	His	Ala	His	Asn		
			200				205					210					
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Leu	Val	Glu	Tyr	Trp	Gln	Glu	Cys	Gln	Arg	Met	Val	Ala	Asp	Ala	His		
			215			220					225						
gca	cac	ggt	ggc	gac	aac	ctc	acc	gct	gat	cta	gtg	cga	gca	cag	caa	835	
Ala	His	Gly	Gly	Asp	Asn	Leu	Thr	Ala	Asp	Leu	Val	Arg	Ala	Gln	Gln		
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Leu	Leu	Phe	Ala	Gly	His	Glu	Thr	Thr	Thr	Thr	Leu	Ile	Ser	Asn	Cys		
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Phe	Arg	Val	Leu	Leu	Asp	His	Pro	Glu	Gln	Trp	Gln	Ala	Ile	Leu	Glu		
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Asn	Pro	Lys	Leu	Ile	Pro	Ala	Ala	Val	Asp	Glu	Val	Leu	Arg	Tyr	Ser		
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Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn Gly Glu Glu Phe Asp			
345	350	355	
atc agc cgc gct aat gcg cgc gag cac ctg tct ttt ggt ttc ggc atc			1219
Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser Phe Gly Phe Gly Ile			
360	365	370	
cac tat tgc cta gga aac atg ctg gcc aaa ctt caa gcc aag atc tgt			1267
His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu Gln Ala Lys Ile Cys			
375	380	385	
ctc gag gaa gtc acc agg ctt gtt cct tcc ctg cac ttg gtt gcg gac			1315
Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu His Leu Val Ala Asp			
390	395	400	405
aaa gct atc ggg ttc cgg gag aac ctc tcc ttc cgc gtc ccc act tct			1363
Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe Arg Val Pro Thr Ser			
410	415	420	
gtt ccc gtg act tgg aac gct taacgcttta ttaaataagg aga			1407
Val Pro Val Thr Trp Asn Ala			
425			

&lt;210&gt; 780

&lt;211&gt; 428

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 780

Met Thr Ser Gln Thr Ser Gln Gln Ser Thr Ser Thr Gly Gly Cys Pro	
1 5 10 15	
Phe Gly His Thr Ser Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe	
20 25 30	
Asp Met His Asn Pro Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu	
35 40 45	
Pro Val Met Phe Asp Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr	
50 55 60	
Asp Asp Ile Lys Thr Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu	
65 70 75 80	
Asn Ala Gln Ala Pro Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile	
85 90 95	
Met Thr Asp Gly Gly Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile	
100 105 110	
Pro Pro Glu His Thr Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr	
115 120 125	
Pro Arg Arg Tyr Lys Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile	
130 135 140	
Asp Arg Val Glu Lys Met Leu Ala Asn Asp Gln His Val Gly Asp Met	